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(54) Title: METHODS OF DIAGNOSIS OF LUNG CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF LUNG CANCER

(57) Abstract: Described herein are methods and compositions that can be used for diagnosis and treatment of lung cancer and similar pathologies. Also described herein are methods that can be used to identify modulators of lung cancer and similar pathologies.



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METHODS OF DIAGNOSIS OF LUNG CANCER, COMPOSITIONS AND METHODS
OF SCREENING FOR MODULATORS OF LUNG CANCER

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CROSS-REFERENCES TO RELATED APPLICATIONS

This application is related to USSN 60/284,770, filed April 18, 2001; USSN 60/290,492, filed May 10, 2001; USSN 60/334,370, filed November 29, 2001; USSN 60/339,245, filed November 9, 2001; USSN 60/350,666, filed November 13, 2001; and
10 USSN 60/xxx,xxx, filed April 12, 2002 (Docket OMNI-002P); each of which is incorporated herein by reference in its entirety.

FIELD OF THE INVENTION

The invention relates to the identification of nucleic acid and protein expression
15 profiles and nucleic acids, products, and antibodies thereto that are involved in lung cancer; and to the use of such expression profiles and compositions in diagnosis and therapy of lung cancer. The invention further relates to methods for identifying and using agents and/or targets that inhibit lung cancer or related conditions.

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BACKGROUND OF THE INVENTION

Lung cancer is the second most commonly occurring cancer in the United States and is the leading cause of cancer-related death. It is estimated that there are over 160,000 new cases of lung cancer in the United States every year. Of those who are diagnosed with lung cancer, 86 percent will die within five years. Lung cancer is the most common visceral
25 cancer in men and accounts for nearly one third of all cancer deaths in both men and women. In fact, lung cancer accounts for 7% of all deaths, due to any cause, in both men and women.

Smoking is the primary cause of lung cancer, with more than 80% of lung cancers resulting from smoking. About 400 to 500 separate gaseous substances are present in the smoke of a non-filter cigarette. The most noteworthy substances include nitrogen oxides,
30 hydrogen cyanide, formaldehyde, benzene, and toluene. The particles present in cigarette smoke contain at least 3,500 individual compounds such as nicotine, tobacco alkaloids (nornicotine, anatabine, anabasine), polycyclic aromatic hydrocarbons (e.g., benzo(a)pyrene, B(a)P), naphthalenes, aromatic amines, phenols, and tobacco-specific nitrosamines.

Tobacco-specific nitrosamines are formed during tobacco curing and processing, and are suspected of causing lung cancer in humans. In rodent studies, regardless of the where or how it is applied, the tobacco-specific nitrosamine known as NNK produces lung adenomas and lung adenocarcinomas. The tobacco-specific nitrosamine known as NNAL also produces lung adenocarcinomas in rodents.

Many of the chemicals found in cigarette smoke also affect the nonsmoker inhaling "secondhand" or sidestream smoke. Indeed, the smoke inhaled by non-smokers has a chemical composition similar to the smoke inhaled by smokers, but, importantly, the concentrations of the carcinogenic tobacco-specific nitrosamines are present in higher concentrations in second hand smoke. For this and other reasons, "passive smoking" is an important cause of lung cancer, causing as many as 3,000 lung cancer deaths in nonsmokers each year.

In addition to smoking, other factors thought to be causes of lung cancer include on-the-job exposure to carcinogens such as asbestos and uranium, exposure to chemical hazards such as radon, polycyclic aromatic hydrocarbons, chromium, nickel, and inorganic arsenic, genetic factors, and diet.

Histological classification of various lung cancers define the types of cancer that begin in the lung. See, e.g., Travis, et al. (1999) Histological Typing of Lung and Pleural Tumours (International Histological Classification of Tumours, No 1. Four major cell types make up more than 88% of all primary lung neoplasms. These are: squamous or epidermoid carcinoma, small cell (also called oat cell) carcinoma, adenocarcinoma, and large cell (also called large cell anaplastic) carcinoma. The remainder include undifferentiated carcinomas, carcinoids, bronchial gland tumors, and other rarer types. The various cell types have different natural histories and responses to therapy, and, thus, a correct histologic diagnosis is the first step of effective treatment.

Small cell lung cancer (SCLC) accounts for 18-25% of all lung cancers, and occurs less frequently than non-small cell lung cancers, and generally spread to distant organs more rapidly than non-small cell lung cancer. In general, at the time of presentation small cell lung cancers have already spread beyond the bounds where surgery and curative intent can be undertaken. However, if identified early enough, these cancers are often responsive to chemotherapy and thoracic radiation treatment.

Non-small cell lung cancers (NSCLC) are the more frequently occurring form of lung cancer. They comprise squamous cell carcinoma, adenocarcinoma, and large cell carcinoma

The screening of asymptomatic persons at high risk for lung cancer has often proven ineffective. In general, only 5 to 15 percent of lung cancer patients have their disease detected while they are asymptomatic. Of course, early detection and treatment are critical factors in the fight against lung cancer. The average survival rate is 49% for those whose cancer is detected early, before the cancer has spread from the lung. Lung cancer often spreads outside of the lung, and it may have spread to the bones or brain by the time it is diagnosed. While the prognosis may be better for lung cancers that are detected early, because of the lack of effective curative treatments, early detection does not necessarily alter the total death rate from lung cancer.

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bronchiectasis. Other aspects of the invention will become apparent to the skilled artisan by the following description of the invention.

In one aspect, the present invention provides a method of detecting a lung cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16. Alternatively, the sample may be contacted with a specific binding reagent, e.g., antibody.

In one embodiment, the polynucleotide selectively hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1A-16. In another embodiment, the polynucleotide comprises a sequence as shown in Tables 1A-16.

In one embodiment, the biological sample is a tissue sample, or a body fluid. In another embodiment, the biological sample comprises isolated nucleic acids, e.g., mRNA.

In one embodiment, the polynucleotide is labeled, e.g., with a fluorescent label. In one embodiment, the polynucleotide is immobilized on a solid surface. In one embodiment, the patient is undergoing a therapeutic regimen to treat lung cancer. In another embodiment, the patient is suspected of having lung cancer. In one embodiment, the patient is a primate, e.g., a human.

In one embodiment, the method further comprises the step of amplifying nucleic acids before the step of contacting the biological sample with the polynucleotide.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a lung cancer-associated transcript in the biological sample by contacting the biological sample with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16, thereby monitoring the efficacy of the therapy. Or the sample may be evaluated for protein, e.g., contacting the sample with an antibody.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the lung cancer-associated transcript to a level of the lung cancer-associated transcript in a biological sample from the patient prior to, or earlier in, the therapeutic treatment. Or the sample may be evaluated for comparison of protein.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of: (i) providing a

biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a lung cancer-associated antibody in the biological sample by contacting the biological sample with a polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16, wherein the polypeptide specifically binds to the lung cancer-associated antibody, thereby monitoring the efficacy of the therapy.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the lung cancer-associated antibody to a level of the lung cancer-associated antibody in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a lung cancer-associated polypeptide in the biological sample by contacting the biological sample with an antibody, wherein the antibody specifically binds to a polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16, thereby monitoring the efficacy of the therapy.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the lung cancer-associated polypeptide to a level of the lung cancer-associated polypeptide in a biological sample from the patient prior to, or earlier in, the therapeutic treatment. In one aspect, the present invention provides an isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1A-16. In one embodiment, an expression vector or cell comprises the isolated nucleic acid. In one aspect, the present invention provides an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1A-16.

In another aspect, the present invention provides an antibody that specifically binds to an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1A-16. In one embodiment, the antibody is conjugated to an effector component, e.g., a fluorescent label, a radioisotope or a cytotoxic chemical. In one embodiment, the antibody is an antibody fragment. In another embodiment, the antibody is humanized.

In one aspect, the present invention provides a method of detecting lung cancer in a patient, the method comprising contacting a biological sample from the patient with an antibody or protein as described herein.

In another aspect, the present invention provides a method of detecting antibodies specific to a lung cancer gene in a patient, the method comprising contacting a biological sample from the patient with a polypeptide encoded by a nucleic acid comprises a sequence from Tables 1A-16.

5 In another aspect, the present invention provides a method for identifying a compound that modulates a lung cancer-associated polypeptide, the method comprising the steps of: (i) contacting the compound with a lung cancer-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16; and (ii) determining the functional effect of the
10 compound upon the polypeptide.

In one embodiment, the functional effect is a physical effect, an enzymatic effect, or a chemical effect. In one embodiment, the polypeptide is expressed in a eukaryotic host cell or cell membrane. In another embodiment, the polypeptide is recombinant. In one
15 embodiment, the functional effect is determined by measuring ligand binding to the polypeptide.

In another aspect, the present invention provides a method of inhibiting proliferation or another critical process of a lung cancer-associated cell to treat lung cancer in a patient, the method comprising the step of administering to the subject a therapeutically effective amount of a compound identified as described herein. In one embodiment, the compound is an
20 antibody.

In another aspect, the present invention provides a drug screening assay comprising the steps of: (i) administering a test compound to a mammal having lung cancer or a cell isolated therefrom; (ii) comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables
25 1A-16 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of lung cancer.

In one embodiment, the control is a mammal with lung cancer or a cell therefrom that has not been treated with the test compound. In another embodiment, the control is a normal
30 cell or mammal, or a non-malignant lung disease.

In another aspect, the present invention provides a method for treating a mammal having lung cancer comprising administering a compound identified by the assay described herein.

In another aspect, the present invention provides a pharmaceutical composition for treating a mammal having lung cancer, the composition comprising a compound identified by the assay described herein and a physiologically acceptable excipient.

DETAILED DESCRIPTION OF THE INVENTION

In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and treatment of lung disease or cancer, as well as methods for screening for compositions which modulate lung cancer. "Treatment, monitoring, detection or modulation of lung disease or cancer" includes treatment, monitoring, detection, or modulation of lung disease in those patients who have lung disease (whether malignant or non-malignant, e.g., emphysema, bronchitis, or fibrosis) as well as patients with lung cancers in which gene expression from a gene in Tables 1A-16 is increased or decreased, indicating that the subject is more likely to have disease. In particular, while these targets are identified primarily from lung cancer samples, these same targets are likely to be similarly found in analyses of other medical conditions. These other conditions may result from similar pathological processes which affect similar tissues, e.g., lung cancer, small cell lung carcinoma (oat cell carcinoma), non-small cell carcinomas (e.g., squamous cell carcinoma, adenocarcinoma, large cell lung carcinoma, carcinoid, granulomatous), fibrosis (idiopathic pulmonary fibrosis (IPF), hypersensitivity pneumonitis (HP), interstitial pneumonitis, nonspecific idiopathic pneumonitis (NSIP)), chronic obstructive pulmonary disease (COPD, e.g., emphysema, chronic bronchitis), asthma, bronchiectasis, and esophageal cancer. See, e.g., the NCI webpage and USSN 60/347,349 and USSN 60/xxx,xxx (docket LFBF-001-1P, filed March 29, 2002), each of which is incorporated herein by reference. The treatment may be of lung cancer or related condition itself, or treatment of metastasis.

In particular, identification of markers selectively expressed on these cancers allows for use of that expression in diagnostic, prognostic, or therapeutic methods. As such, the invention defines various compositions, e.g., nucleic acids, polypeptides, antibodies, and small molecule agonists/antagonists, which will be useful to selectively identify those markers. For example, therapeutic methods may take the form of protein therapeutics which use the marker expression for selective localization or modulation of function (for those markers which have a causative disease effect), for vaccines, identification of binding partners, or antagonism, e.g., using antisense or RNAi. The markers may be useful for molecular characterization of subsets of lung diseases, which subsets may actually require

very different treatments. Moreover, the markers may also be important in related diseases to the specific cancers, e.g., which affect similar tissues in non-malignant diseases, or have similar mechanisms of induction/maintenance. Metastatic processes or characteristics may also be targeted. Diagnostic and prognostic uses are made available, e.g., to subset related but distinct diseases, or to determine treatment strategy. The detection methods may be based upon nucleic acid, e.g., PCR or hybridization techniques, or protein, e.g., ELISA, imaging, IHC, etc. The diagnosis may be qualitative or quantitative, and may detect increases or decreases in expression levels.

Tables 1A-16 provide unigene cluster identification numbers for the nucleotide sequence of genes that exhibit increased or decreased expression in lung cancer samples. The tables also provide an exemplar accession number that provides a nucleotide sequence that is part of the unigene cluster. In Table 1A, genes marked as “target 1” or “target 2” are particularly useful as therapeutic targets. Genes marked as “target 3” are particularly useful as diagnostic markers. Genes marked as “chron” are upregulated in chronically diseased lung (e.g., emphysema, bronchitis, fibrosis) relative to lung tumors and normal tissue. In certain analyses, the ratio for the “chron” category was determined using the 70th percentile of chronically diseased lung samples divided by the 90th percentile of normal lung samples. The ratio for the targets was determined using the 70th percentile of lung tumor samples divided by the 90th percentile of normal lung samples.

Definitions

The term “lung cancer protein” or “lung cancer polynucleotide” or “lung cancer-associated transcript” refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologs that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or greater nucleotide sequence identity, preferably over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a unigene cluster of Tables 1A-16; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of or associated with a unigene cluster of Tables 1A-16, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 1A-16 and conservatively modified variants thereof; or (4)

have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or greater amino sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acid, to an amino acid sequence encoded by a nucleotide sequence of or associated with a unigene cluster of Tables 1A-16. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. A "lung cancer polypeptide" and a "lung cancer polynucleotide," include both naturally occurring or recombinant forms.

A "full length" lung cancer protein or nucleic acid refers to a lung cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains the elements normally contained in one or more naturally occurring, wild type lung cancer polynucleotide or polypeptide sequences. The "full length" may be prior to, or after, various stages of post-translational processing or splicing, including alternative splicing.

"Biological sample" as used herein is a sample of biological tissue or fluid that contains nucleic acids or polypeptides, e.g., of a lung cancer protein, polynucleotide, or transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g., humans, or rodents, e.g., mice, and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, frozen sections taken for histologic purposes, archival materials, blood, plasma, serum, sputum, stool, tears, mucus, hair, skin, etc. Biological samples also include explants and primary and/or transformed cell cultures derived from patient tissues. A biological sample is typically obtained from a eukaryotic organism, most preferably a mammal such as a primate, e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, mouse; rabbit; or other mammal; or a bird; reptile; fish. Livestock and domestic animals are of interest.

"Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an animal, but can also be accomplished by using previously isolated cells (e.g., isolated by another person, at another time, and/or for another purpose), or by performing the methods of the invention in vivo. Archival tissues or materials, having treatment or outcome history, will be particularly useful.

The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the

same or have a specified percentage of amino acid residues or nucleotides that are the same (e.g., about 60% identity, preferably 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using, e.g., a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (see, e.g., NCBI web site <http://www.ncbi.nlm.nih.gov/BLAST/> or the like). Such sequences are then said to be “substantially identical.” This definition also refers to, or may be applied to, the complement of a test sequence. The definition also includes sequences that have deletions and/or insertions, substitutions, and naturally occurring, e.g., polymorphic or allelic variants, and man-made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A “comparison window”, as used herein, includes reference to a segment of contiguous positions selected from the group consisting typically of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482, by the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443, by the search for similarity method of Pearson and Lipman (1988) Proc. Nat’l. Acad. Sci. USA 85:2444, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer

Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (see, e.g., Ausubel, et al. (eds. 1995 and supplements) Current Protocols in Molecular Biology.

Preferred examples of algorithms that are suitable for determining percent sequence identity and sequence similarity include the BLAST and BLAST 2.0 algorithms, which are described in Altschul, et al. (1977) Nuc. Acids Res. 25:3389-3402 and Altschul, et al. (1990) J. Mol. Biol. 215:403-410. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul, et al., *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) Proc. Natl. Acad. Sci. USA 89:10915) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin and Altschul (1993) Proc. Nat'l. Acad. Sci. USA 90:5873-5787). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between

two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001. Log values may be negative large numbers, e.g., 5, 10, 20, 30, 40, 40, 70, 90, 110, 150, 170, etc.

An indication that two nucleic acid sequences are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid. Thus, a polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

A "host cell" is a naturally occurring cell or a transformed cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells *in vivo*, and the like. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, and the like (see, e.g., the American Type Culture Collection catalog or web site, www.atcc.org).

The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein or nucleic acid that is the predominant species present in a preparation is substantially purified. In particular, an isolated nucleic acid is separated from some open reading frames that naturally flank the gene and encode proteins other than protein encoded by the gene. The term "purified" in some embodiments denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least about 85% pure, more preferably at least 95% pure, and most preferably at least 99% pure. "Purify" or "purification" in other embodiments means removing at least one contaminant or component from the composition to be purified.

In this sense, purification does not require that the purified compound be homogeneous, e.g., 100% pure.

The terms "polypeptide," "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and non-naturally occurring amino acid polymer.

The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function similarly to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ -carboxyglutamate, and O-phosphoserine. Amino acid analogs refer to compounds that have the same basic chemical structure as a naturally occurring amino acid, e.g., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have modified R groups (e.g., norleucine) or modified peptide backbones, but retain some basic chemical structure as a naturally occurring amino acid. Amino acid mimetics refer to chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that function similarly to another amino acid.

Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variants" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG, and GCU each encode the amino acid alanine. Thus, at each position where an alanine is specified by a codon, the codon can be altered to another of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of

conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes silent variations of the nucleic acid. In certain contexts each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally similar molecule. Accordingly, a silent variation of a nucleic acid which encodes a polypeptide is implicit in a described sequence with respect to the expression product, but not necessarily with respect to actual probe sequences.

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known in the art. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention. Typically conservative substitutions include for one another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M) (see, e.g., Creighton, Proteins (1984)).

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. For a general discussion of this organization, see, e.g., Alberts, et al. (1994) Molecular Biology of the Cell (3rd ed.) and Cantor and Schimmel (1980) Biophysical Chemistry Part I: The Conformation of Biological Macromolecules. "Primary structure" refers to the amino acid sequence of a particular peptide. "Secondary structure" refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains. Domains are portions of a polypeptide that often form a compact unit of the polypeptide and are typically 25 to approximately 500 amino acids long. Typical domains are made up of sections of lesser organization such as stretches of β -sheet and α -helices. "Tertiary structure" refers to the complete three dimensional structure of a polypeptide monomer. "Quaternary structure" refers to the three dimensional structure formed, usually by the noncovalent association of independent tertiary units. Anisotropic terms are also known as energy terms.

“Nucleic acid” or “oligonucleotide” or “polynucleotide” or grammatical equivalents

used herein means at least two nucleotides covalently linked together. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50 or more nucleotides in length, up to about 100 nucleotides in length. Nucleic acids and polynucleotides are a polymers of any length, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, etc. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, nucleic acid analogs are included that may have at least one different linkage, e.g., phosphoramidate, phosphorothioate, phosphorodithioate, or O-methylphosphoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach Oxford University Press); and peptide nucleic acid backbones and linkages. Other analog nucleic acids include those with positive backbones; non-ionic backbones, and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, in Sanghui and Cook, eds. Carbohydrate Modifications in Antisense Research, ASC Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids. Modifications of the ribose-phosphate backbone may be done for a variety of reasons, e.g., to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T_m) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4° C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9° C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. As will be appreciated by those in the art, the depiction of a single strand also defines the sequence of the complementary

strand; thus the sequences described herein also provide the complement of the sequence.

The nucleic acid may be DNA, both genomic and cDNA, RNA, or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine

5 hypoxanthine, isocytosine, isoguanine, etc. "Transcript" typically refers to a naturally occurring RNA, e.g., a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus, e.g., the individual units of a peptide nucleic
10 acid, each containing a base, are referred to herein as a nucleoside.

A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, physiological, chemical, or other physical means. For example, useful labels include ^{32}P , fluorescent dyes, electron-dense reagents, enzymes (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins
15 or other entities which can be made detectable, e.g., by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the peptide. The labels may be incorporated into the cancer nucleic acids, proteins, and antibodies. Many methods known in the art for conjugating the antibody to the label may be employed, including those methods described by Hunter, et al. (1962) Nature 144:945; David, et al. (1974) Biochemistry
20 13:1014-1021; Pain, et al. (1981) J. Immunol. Meth., 40:219-230; and Nygren (1982) J. Histochem. and Cytochem. 30:407-412.

An "effector" or "effector moiety" or "effector component" is a molecule that is bound (or linked, or conjugated), either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to an antibody.
25 The "effector" can be a variety of molecules including, e.g., detection moieties including radioactive compounds, fluorescent compounds, an enzyme or substrate, tags such as epitope tags, a toxin; activatable moieties, a chemotherapeutic agent; a lipase; an antibiotic; or a radioisotope emitting "hard" e.g., beta radiation.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, either
30 covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, method

using high affinity interactions may achieve the same results where one of a pair of binding partners binds to the other, e.g., biotin, streptavidin.

As used herein a “nucleic acid probe or oligonucleotide” is a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, e.g., through hydrogen bond formation. As used herein, a probe may include natural (i.e., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, preferably one that does not functionally interfere with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. Probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably directly labeled, e.g., with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled, e.g., with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

The term “recombinant” when used with reference, e.g., to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, e.g., recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed or not expressed at all. By the term “recombinant nucleic acid” herein is meant nucleic acid, originally formed *in vitro*, in general, by the manipulation of nucleic acid, e.g., using polymerases and endonucleases, in a form not normally found in nature. In this manner, operably linkage of different sequences is achieved. Thus an isolated nucleic acid, in a linear form, or an expression vector formed *in vitro* by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, i.e., using the *in vivo* cellular machinery of the host cell rather than *in vitro* manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered

recombinant for the purposes of the invention. Similarly, a “recombinant protein” is a protein made using recombinant techniques, i.e., through the expression of a recombinant nucleic acid as depicted above.

The term “heterologous” when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not normally found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences, e.g., from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein will often refer to two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

A “promoter” is typically an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A “constitutive” promoter is a promoter that is active under most environmental and developmental conditions. An “inducible” promoter is a promoter that is active under environmental or developmental regulation. The term “operably linked” refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, e.g., wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

An “expression vector” is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed in operable linkage to a promoter.

The phrase “selectively (or specifically) hybridizes to” refers to the binding, duplexing, or hybridizing of a molecule selectively to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to essentially no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in "Overview of principles of hybridization and the strategy of nucleic acid assays" in Tijssen (1993) Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic Probes (vol. 24) Elsevier. Generally, stringent conditions are selected to be about 5-10° C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m , 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C for short probes (e.g., 10 to 50 nucleotides) and at least about 60° C for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is typically at least two times background, preferably 10 times background hybridization. Exemplary stringent hybridization conditions are often: 50% formamide, 5x SSC, and 1% SDS, incubating at 42° C, or, 5x SSC, 1% SDS, incubating at 65° C, with wash in 0.2x SSC, and 0.1% SDS at 65° C. For PCR, a temperature of about 36° C is typical for low stringency amplification, although annealing temperatures may vary between about 32° C and 48° C depending on primer length. For high stringency PCR amplification, a temperature of about 62° C is typical, although high stringency annealing temperatures can range from about 50° C to about 65° C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90° C - 95° C for 0.5 - 2 min., an annealing phase lasting 0.5 - 2 min., and an extension phase of about 72° C for 1 - 2 min. Protocols and guidelines for low and high stringency amplification reactions are provided, e.g., in Innis, et al.(1990) PCR Protocols, A Guide to Methods and Applications.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This

occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary “moderately stringent hybridization conditions” include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37° C, and a wash in 1X SSC at 45° C. A positive hybridization is at least twice background. Alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided in numerous reference, e.g., Ausubel, et al. (ed.) Current Protocols in Molecular Biology Lippincott.

The phrase “functional effects” in the context of assays for testing compounds that modulate activity of a lung cancer protein includes the determination of a parameter that is indirectly or directly under the influence of the lung cancer protein or nucleic acid, e.g., a physiological, enzymatic, functional, physical, or chemical effect, such as the ability to decrease lung cancer. It includes ligand binding activity; cell viability, cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis *in vivo*; mRNA and protein expression in cells undergoing metastasis, and other characteristics of lung cancer cells. “Functional effects” include *in vitro*, *in vivo*, and *ex vivo* activities.

By “determining the functional effect” is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of a lung cancer protein sequence, e.g., physiological, functional, enzymatic, physical, or chemical effects. Such functional effects can be measured by many means known to those skilled in the art, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the lung cancer protein; measuring binding activity or binding assays, e.g., binding to antibodies or other ligands, and measuring cellular proliferation. Determination of the functional effect of a compound on lung cancer can also be performed using lung cancer assays known to those of skill in the art such as an *in vitro* assays, e.g., cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis *in vivo*; mRNA and protein

expression in cells undergoing metastasis, and other characteristics of lung cancer cells. The functional effects can be evaluated by many means known to those skilled in the art, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of changes in RNA or protein levels for lung cancer-associated sequences, measurement of RNA stability, identification of downstream or reporter gene expression (CAT, luciferase, β -gal, GFP, and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

“Inhibitors”, “activators”, and “modulators” of lung cancer polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using *in vitro* and *in vivo* assays of lung cancer polynucleotide and polypeptide sequences. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of lung cancer proteins, e.g., antagonists. Antisense or inhibitory nucleic acids may seem to inhibit expression and subsequent function of the protein.

“Activators” are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate lung cancer protein activity. Inhibitors, activators, or modulators also include genetically modified versions of lung cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small chemical molecules and the like. Such assays for inhibitors and activators include, e.g., expressing the lung cancer protein *in vitro*, in cells, or cell membranes, applying putative modulator compounds, and then determining the functional effects on activity, as described above. Activators and inhibitors of lung cancer can also be identified by incubating lung cancer cells with the test compound and determining increases or decreases in the expression of 1 or more lung cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50 or more lung cancer proteins, such as lung cancer proteins encoded by the sequences set out in Tables 1A-16.

Samples or assays comprising lung cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably 50%, more preferably 25-0%. Activation of a lung cancer polypeptide is achieved when the activity value relative to the control (untreated with activators) is 110%, more preferably 150%, more

preferably 200-500% (i.e., two to five fold higher relative to the control), more preferably 1000-3000% higher.

The phrase “changes in cell growth” refers to any change in cell growth and proliferation characteristics *in vitro* or *in vivo*, such as cell viability, formation of foci, anchorage independence, semi-solid or soft agar growth, changes in contact inhibition and density limitation of growth, loss of growth factor or serum requirements, changes in cell morphology, gaining or losing immortalization, gaining or losing tumor specific markers, ability to form or suppress tumors when injected into suitable animal hosts, and/or immortalization of the cell. See, e.g., Freshney (1994) Culture of Animal Cells a Manual of Basic Technique pp. 231-241 (3rd ed.).

“Tumor cell” refers to precancerous, cancerous, and normal cells in a tumor.

“Cancer cells,” “transformed” cells, or “transformation” in tissue culture, refers to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene. Transformation is associated with phenotypic changes, such as immortalization of cells, aberrant growth control, nonmorphological changes, and/or malignancy (see, Freshney (1994) Culture of Animal Cells a Manual of Basic Technique (3rd ed.)).

“Antibody” refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD, and IgE, respectively. Typically, the antigen-binding region of an antibody or its functional equivalent will be most critical in specificity and affinity of binding. See Paul, Fundamental Immunology.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one “light” (about 25 kD) and one “heavy” chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible

for antigen recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an antibody below the disulfide linkages in the hinge region to produce $F(ab)'_2$, a dimer of Fab which itself is a light chain joined to V_H-C_H1 by a disulfide bond. The $F(ab)'_2$ may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the $F(ab)'_2$ dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region (see Paul (ed. 1999) Fundamental Immunology (4th ed.)). While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate that such fragments may be synthesized *de novo* either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized *de novo* using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries (see, e.g., McCafferty, et al. (1990) Nature 348:552-554).

For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies, many technique known in the art can be used (see, e.g., Kohler and Milstein (1975) Nature 256:495-497; Kozbor, et al. (1983) Immunology Today 4:72; Cole, et al. (1985), pp. 77-96 in Monoclonal Antibodies and Cancer Therapy; Coligan (1991 and supplements) Current Protocols in Immunology; Harlow and Lane (1988) Antibodies, A Laboratory Manual; and Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed.)). Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies. Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens (see, e.g., McCafferty, et al. (1990) Nature 348:552-554; Marks, et al. (1992) Biotechnology 10:779-783).

A "chimeric antibody" is an antibody molecule in which, e.g., (a) the constant region, or a portion thereof, is altered, replaced, or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function, and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the

variable region, or a portion thereof, is altered, replaced, or exchanged with a variable region having a different or altered antigen specificity.

Identification of lung cancer-associated sequences

5 In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a “fingerprint” of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is
10 characteristic of the state of the cell. That is, normal tissue may be distinguished from cancerous or metastatic cancerous tissue, or metastatic cancerous tissue can be compared with tissue from surviving cancer patients. By comparing expression profiles of tissue in known different lung cancer states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained.
15 Molecular profiling may distinguish subtypes of a currently collective disease designation, e.g., different forms of lung cancer (chronic disease, adenocarcinoma, etc.)

 The identification of sequences that are differentially expressed in lung cancer versus non-lung cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-
20 regulate lung cancer, and thus tumor growth or recurrence, in a particular patient. Alternatively, a treatment step may induce other markers which may be used as targets to destroy tumor cells. Similarly, diagnosis and treatment outcomes may be done or confirmed by comparing patient samples with the known expression profiles. Malignant disease may be compared to non-malignant conditions. Metastatic tissue can also be analyzed to determine
25 the stage of lung cancer in the tissue, or origin of primary tumor, e.g., metastasis from a remote primary site. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; e.g., screening can be done for drugs that suppress the lung cancer expression profile. This may be done by making biochips comprising sets of the important lung cancer genes,
30 which can then be used in these screens. PCR methods may be applied with selected primer pairs, and analysis may be of RNA or of genomic sequences. These methods can also be done on the protein basis; that is, protein expression levels of the lung cancer proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the lung cancer

nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the lung cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs or as protein or DNA vaccines.

5 Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in lung cancer relative to normal tissues and/or non-malignant lung disease, or in different types of lung disease, herein termed "lung cancer sequences." As outlined below, lung cancer sequences include those that are up-regulated (i.e., expressed at a higher level) in lung cancer, as well as those that are down-regulated (i.e., expressed at a lower level). In a preferred embodiment, the lung cancer sequences are from humans; however, as will be appreciated by those in the art, lung cancer sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other lung cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc.) and pets (dogs, cats, etc.). Lung cancer sequences from other organisms may be obtained using the techniques outlined below.

 Lung cancer sequences can include both nucleic acid and amino acid sequences. As will be appreciated by those in the art and is more fully outlined below, lung cancer nucleic acid sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; e.g., biochips comprising nucleic acid probes or PCR microtiter plates with selected probes to the lung cancer sequences can be generated.

 A lung cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the lung cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, e.g., using homology programs or hybridization conditions.

 For identifying lung cancer-associated sequences, the lung cancer screen typically includes comparing genes identified in different tissues, e.g., normal and cancerous tissues, cancer and non-malignant conditions, non-malignant conditions and normal tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue. Other suitable tissue comparisons include comparing lung cancer samples with metastatic cancer samples from other cancers, such as, breast, other gastrointestinal cancers, prostate, ovarian,

etc. Samples of, non metastatic disease tissue and tissue undergoing metastasis are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated as is known in the art for the preparation of mRNA. Suitable biochips are commercially available, e.g., from Affymetrix, Santa Clara, CA. Gene expression profiles as described herein are generated and the data analyzed.

In one embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, preferably normal lung, but also including, and not limited to colon, heart, brain, liver, breast, kidney, muscle, prostate, small intestine, large intestine, spleen, bone, and/or placenta. In a preferred embodiment, those genes identified during the lung cancer screen that are expressed in significant amounts in other tissues (e.g., essential organs) are removed from the profile, although in some embodiments, this is not necessary (e.g., where organs may be dispensible at a later stage of life). That is, when screening for drugs, it is usually preferable that the target expression be disease specific, to minimize possible side effects on other organs.

In a preferred embodiment, lung cancer sequences are those that are up-regulated in lung cancer; that is, the expression of these genes is higher in cancerous tissue than in normal lung or other tissue. "Up-regulation" as used herein means, when the ratio is presented as a number greater than one, that the ratio is greater than one, preferably 1.5 or greater, more preferably 2.0 or greater. Another embodiment is directed to sequences up-regulated in non-malignant conditions relative to normal. Unigene cluster identification numbers and accession numbers herein are for the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is known in the art, see, e.g., Benson, DA, et al (1998) *Nucleic Acids Research* 26:1-7 and <http://www.ncbi.nlm.nih.gov/>. Sequences are also available in other databases, e.g., European Molecular Biology Laboratory (EMBL) and DNA Database of Japan (DDBJ). Another embodiment is directed to sequences up-regulated in non-malignant conditions relative to normal. In some situations, the sequences may be derived from assembly of available sequences or be predicted from genomic DNA using exon prediction algorithms, such as FGENESH (Salamov and Solovyev (2000) *Genome Res.* 10:516-522). In other situations, sequences have been derived from cloning and sequencing of isolated nucleic acids.

In another preferred embodiment, lung cancer sequences are those that are down-regulated in the lung cancer; that is, the expression of these genes is lower in cancerous tissue

or normal lung or other tissue. "Down-regulation" as used herein means, when the ratio is presented as a number greater than one, that the ratio is greater than one, preferably 1.5 or greater, more preferably 2.0 or greater, or, when the ratio is presented as a number less than one, that the ratio is less than one, preferably 0.5 or less, more preferably 0.25 or less.

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Informatics

The ability to identify genes that are over or under expressed in lung cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure, biosensor development, and other related areas. For example, the expression profiles can be used in diagnostic or prognostic evaluation of patients with lung cancer. Or as another example, subcellular toxicological information can be generated to better direct drug structure and activity correlation (see Anderson (1998) Pharmaceutical Proteomics: Targets, Mechanism, and Function, paper presented at the IBC Proteomics conference, Coronado, CA (June 11-12, 1998)). Subcellular toxicological information can also be utilized in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable exposure thresholds (see U.S. Patent No. 5,811,231). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (e.g., nucleic acids, saccharides, lipids, drugs, and the like).

Thus, in another embodiment, the present invention provides a database that includes at least one set of assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in a form in which data can be maintained and transmitted, but is preferably an electronic database. The electronic database of the invention can be maintained on any electronic device allowing for the storage of and access to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the World Wide Web.

The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. It will be apparent to those of skill in the art that similar databases can be assembled for assay data acquired using an assay of the invention.

The compositions and methods for identifying and/or quantitating the relative and/or absolute abundance of a variety of molecular and macromolecular species from a biological sample representing lung cancer, i.e., the identification of lung cancer-associated sequences described herein, provide an abundance of information, which can be correlated with

pathological conditions, predisposition to disease, drug testing, therapeutic monitoring, gene-disease causal linkages, identification of correlates of immunity and physiological status, among others. Although the data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, data processing using high-speed computers is utilized.

An array of methods for indexing and retrieving biomolecular information is known in the art. For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein function hierarchies. U.S. Patent 5,953,727 discloses a relational database having sequence records containing information in a format that allows a collection of partial-length DNA sequences to be catalogued and searched according to association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S. Patent 5,926,818 discloses a multi-dimensional database comprising a functionality for multi-dimensional data analysis described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S. Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as the merger of two or more such tree structures.

See also Mount, et al. (2001) Bioinformatics; Durbin, et al. (eds., 1999) Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids (; Baxevasis and Oeullette (eds., 1998) Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins); Rashidi and Buehler (1999) Bioinformatics: Basic Applications in Biological Science and Medicine; Setubal, et al. (eds 1997) Introduction to Computational Molecular Biology; Misener and Krawetz (eds, 2000) Bioinformatics: Methods and Protocols; Higgins and Taylor (eds., 2000) Bioinformatics: Sequence, Structure, and Databanks: A Practical

Approach; Brown (2001) Bioinformatics: A Biologist's Guide to Biocomputing and the Internet; Han and Kamber (2000) Data Mining: Concepts and Techniques (2000); and Waterman (1995) Introduction to Computational Biology: Maps, Sequences, and Genomes.

The present invention provides a computer database comprising a computer and software for storing in computer-retrievable form assay data records cross-tabulated, e.g., with data specifying the source of the target-containing sample from which each sequence specificity record was obtained.

In an exemplary embodiment, at least one of the sources of target-containing sample is from a control tissue sample known to be free of pathological disorders. In a variation, at least one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another tissue specimen to be analyzed for lung cancer. In another variation, the assay records cross-tabulate one or more of the following parameters for each target species in a sample: (1) a unique identification code, which can include, e.g., a target molecular structure and/or characteristic separation coordinate (e.g., electrophoretic coordinates); (2) sample source; and (3) absolute and/or relative quantity of the target species present in the sample.

The invention also provides for the storage and retrieval of a collection of target data in a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble memory devices, and other data storage devices, including CPU registers and on-CPU data storage arrays. Typically, the target data records are stored as a bit pattern in an array of magnetic domains on a magnetizable medium or as an array of charge states or transistor gate states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and a charge storage area, which may be on the transistor). In one embodiment, the invention provides such storage devices, and computer systems built therewith, comprising a bit pattern encoding a protein expression fingerprint record comprising unique identifiers for at least 10 target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides a method for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in or retrieved from a computer storage device or database and at least one other sequence. The comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may

be of the relative amount of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

The invention also preferably provides a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux, SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or hard (fixed, Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

The invention also provides a network, comprising a plurality of computing devices linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line, wireless network, optical fiber, or other suitable signal transmission medium, whereby at least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells) composing a bit pattern encoding data acquired from an assay of the invention.

The invention also provides a method for transmitting assay data that includes generating an electronic signal on an electronic communications device, such as a modem, ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

In a preferred embodiment, the invention provides a computer system for comparing a query target to a database containing an array of data structures, such as an assay result obtained by the method of the invention, and ranking database targets based on the degree of identity and gap weight to the target data. A central processor is preferably initialized to load and execute the computer program for alignment and/or comparison of the assay results.

Data for a query target is entered into the central processor via an I/O device. Execution of the computer program results in the central processor retrieving the assay data from the data file, which comprises a binary description of an assay result.

The target data or record and the computer program can be transferred to secondary memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of the query target and results are output via an I/O device. For example, a central processor can be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC,

MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM, SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can be a terminal comprising a video display and a keyboard, a modem, an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O device.

The invention also preferably provides the use of a computer system, such as that described above, which comprises: (1) a computer; (2) a stored bit pattern encoding a collection of peptide sequence specificity records obtained by the methods of the invention, which may be stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values.

Characteristics of lung cancer-associated proteins

Lung cancer proteins of the present invention may be classified as secreted proteins, transmembrane proteins or intracellular proteins. In one embodiment, the lung cancer protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus. Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such proteins often results in unregulated or dysregulated cellular processes (see, e.g., Alberts (ed. 1994) Molecular Biology of the Cell (3d ed.)). For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more structural motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2

domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of amino acid sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate. One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains. Versions are available via the internet from Washington University in St. Louis, the Sanger Center in England, and the Karolinska Institute in Sweden (see, e.g., Bateman, et al (2000) *Nuc. Acids Res.* 28:263-266; Sonnhammer, et al. (1997) *Proteins* 28:405-420; Bateman, et al. (1999) *Nuc. Acids Res.* 27:260-262; and Sonnhammer, et al. (1998) *Nuc. Acids Res.* 26:320-322).

In another embodiment, the lung cancer sequences are transmembrane proteins. Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels, pumps, and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 17 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the

localization and number of transmembrane domains within the protein may be predicted (see, e.g., PSORT web site <http://psort.nibb.ac.jp/>).

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF, and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, hormones, neurotrophic factors and the like. Extracellular domains also bind to cell-associated molecules. In this respect, they may mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains may also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

Lung cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for extracellular immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities. Antibodies may be used to label such readily accessible proteins *in situ* or in histological analysis. Alternatively, antibodies can also label intracellular proteins, in which case analytical samples are typically permeablized to provide access to intracellular proteins. In addition, some membrane proteins can be processed to release a soluble protein, or to expose a residual fragment. Released soluble proteins may be useful diagnostic markers, processed residual protein fragments may be useful lung markers of disease.

It will also be appreciated by those in the art that a transmembrane protein can be made soluble by removing transmembrane sequences, e.g., through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

In another embodiment, the lung cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins may have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; e.g., if circulating, they often serve to transmit

signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor), an endocrine manner (acting on cells at a distance, e.g., secretion into the blood stream), or exocrine (secretion, e.g., through a duct or to adjacent epithelial surface as sweat glands, sebaceous glands, pancreatic ducts, lacrimal glands, mammary glands, wax producing glands of the ear, etc.). Thus secreted molecules often find use in modulating or altering numerous aspects of physiology. Lung cancer proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic markers, e.g., for blood, plasma, serum, or stool tests. Those which are enzymes may be antibody or small molecule targets. Others may be useful as vaccine targets, e.g., via CTL mechanisms.

Use of lung cancer nucleic acids

As described above, lung cancer sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology or linkage to the lung cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on the same molecule.

The lung cancer nucleic acid sequences of the invention, e.g., the sequences in Tables 1A-16, can be fragments of larger genes, i.e., they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein, extended sequences, in either direction, of the lung cancer genes can be obtained, using techniques well known in the art for cloning either longer sequences or the full length sequences; see Ausubel, et al., *supra*. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene (see, <http://www.ncbi.nlm.nih.gov/UniGene/>).

Once a lung cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire lung cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant lung cancer nucleic acid can be further-used as a probe to identify and isolate

other lung cancer nucleic acids, e.g., extended coding regions. It can also be used as a “precursor” nucleic acid to make modified or variant lung cancer nucleic acids and proteins.

The lung cancer nucleic acids of the present invention are used in several ways. In a first embodiment, nucleic acid probes to the lung cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, e.g., for gene therapy, RNAi, vaccine, and/or antisense applications. Alternatively, the lung cancer nucleic acids that include coding regions of lung cancer proteins can be put into expression vectors for the expression of lung cancer proteins, again for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to lung cancer nucleic acids (both the nucleic acid sequences outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the lung cancer nucleic acids, i.e., the target sequence (either the target sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by “substantially complementary” herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under appropriate reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long, with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being particularly preferred. That is, generally complements of ORFs or whole genes are not used. In some embodiments, nucleic acids of lengths up to hundreds of bases can be used.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a

particular target. The probes can be overlapping (i.e., have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By “immobilized” and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can typically be covalent or non-covalent. By “non-covalent binding” and grammatical equivalents herein is typically meant one or more of electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By “covalent binding” and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to a biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

The biochip comprises a suitable solid substrate. By “substrate” or “solid support” or other grammatical equivalents herein is meant a material that can be modified for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. Often the substrate may contain discrete individual sites appropriate for individual partitioning and identification. As will be appreciated by those in the art, the number of possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluoresce. A preferred substrate is described in US application entitled Reusable Low Fluorescent Plastic Biochip, U.S.

Application Serial No. 09/270,214, filed March 15, 1999, herein incorporated by reference in its entirety.

Generally the substrate is planar, although as will be appreciated by those in the art, other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g., the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g., using linkers as are known in the art; e.g., homo-or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, oligonucleotides are synthesized, and then attached to the surface of the solid support. Either the 5' or 3' terminus may be attached to the solid support, or attachment may be via linkage to an internal nucleoside.

In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface, as is known in the art. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized *in situ*, using known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affymetrix GeneChip™ technology.

Often, amplification-based assays are performed to measure the expression level of lung cancer-associated sequences. These assays are typically performed in conjunction with

reverse transcription. In such assays, a lung cancer-associated nucleic acid sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of lung cancer-associated RNA. Methods of quantitative amplification are well known to those of skill in the art. Detailed protocols for quantitative PCR are provided, e.g., in Innis, et al. (1990) PCR Protocols, A Guide to Methods and Applications.

In some embodiments, a TaqMan based assay is used to measure expression.

TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification (see, e.g., literature provided by Perkin-Elmer, e.g., www2.perkin-elmer.com).

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR) (see Wu and Wallace (1989) Genomics 4:560, Landegren, et al. (1988) Science 241:1077, and Barringer, et al. (1990) Gene 89:117), transcription amplification (Kwoh, et al. (1989) Proc. Natl. Acad. Sci. USA 86:1173), self-sustained sequence replication (Guatelli, et al. (1990) Proc. Nat. Acad. Sci. USA 87:1874), dot PCR, and linker adapter PCR, etc.

Expression of lung cancer proteins from nucleic acids

In a preferred embodiment, lung cancer nucleic acids, e.g., encoding lung cancer proteins, are used to make a variety of expression vectors to express lung cancer proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known to those of skill in the art (see, e.g., Ausubel, *supra*, and Fernandez and Hoeffler (eds 1999) Gene Expression Systems) and are used to express proteins. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the lung cancer protein. The term "control sequences" refers to DNA

sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g., include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

5 Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding
10 linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in
15 accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the lung cancer protein. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

In general, transcriptional and translational regulatory sequences may include, but are
20 not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences may be either constitutive or inducible promoters. The promoters
25 may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known in the art, and are useful in the present invention.

In addition, an expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two
30 organisms, e.g., in mammalian or insect cells for expression and in a prokaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector often contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating

vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are well known in the art (e.g., Fernandez and Hoeffler, *supra*).

In addition, in a preferred embodiment, the expression vector contains a selectable
5 marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

The lung cancer proteins of the present invention are usually produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding a lung cancer protein, under the appropriate conditions to induce or cause expression of the lung
10 cancer protein. Conditions appropriate for lung cancer protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation or optimization. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate
15 growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaeobacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are *Saccharomyces cerevisiae*
20 and other yeasts, *E. coli*, *Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line) and various other human cells and cell lines.

In a preferred embodiment, the lung cancer proteins are expressed in mammalian cells. Mammalian expression systems are also known in the art, and include retroviral and
25 adenoviral systems. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter (see, e.g., Fernandez and Hoeffler, *supra*). Typically, transcription termination and
30 polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived from SV40.

The methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, is well known in the art, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In a preferred embodiment, lung cancer proteins are expressed in bacterial systems. Promoters from bacteriophage may also be used and are known in the art. In addition, synthetic promoters and hybrid promoters are also useful; e.g., the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the lung cancer protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known in the art, and include vectors for *Bacillus subtilis*, *E. coli*, *Streptococcus cremoris*, and *Streptococcus lividans*, among others (e.g., Fernandez and Hoeffler, *supra*). The bacterial expression vectors are transformed into bacterial host cells using techniques well known in the art, such as calcium chloride treatment, electroporation, and others.

In one embodiment, lung cancer proteins are produced in insect cells. Expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors, are well known in the art.

In a preferred embodiment, lung cancer protein is produced in yeast cells. Yeast expression systems are well known in the art, and include expression vectors for *Saccharomyces cerevisiae*, *Candida albicans* and *C. maltosa*, *Hansenula polymorpha*,

Kluyveromyces fragilis and *K. lactis*, *Pichia guillermondii*, and *P. pastoris*, *Schizosaccharomyces pombe*, and *Yarrowia lipolytica*.

The lung cancer protein may also be made as a fusion protein, using techniques well known in the art. Thus, e.g., for the creation of monoclonal antibodies, if the desired epitope is small, the lung cancer protein may be fused to a carrier protein to form an immunogen. Alternatively, the lung cancer protein may be made as a fusion protein to increase expression for affinity purification purposes, or for other reasons. For example, when the lung cancer protein is a lung cancer peptide, the nucleic acid encoding the peptide may be linked to other nucleic acid for expression purposes.

In a preferred embodiment, the lung cancer protein is purified or isolated after expression. Lung cancer proteins may be isolated or purified in a variety of appropriate ways. Standard purification methods include electrophoretic, molecular, immunological and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the lung cancer protein may be purified using a standard anti-lung cancer protein antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. For general guidance in suitable purification techniques, see Scopes (1982) Protein Purification. The degree of purification necessary will vary depending on the use of the lung cancer protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the lung cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, therapeutic entities, for production of antibodies, as transcription or translation inhibitors, etc.

Variants of lung cancer proteins

In one embodiment, the lung cancer proteins are derivative or variant lung cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative lung cancer peptide will often contain at least one amino acid substitution, deletion or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion or deletion may occur at a particular residue within the lung cancer peptide.

Also included within one embodiment of lung cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three

classes: substitutional, insertional or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the lung cancer protein, using cassette or PCR mutagenesis or other techniques, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above.

5 However, variant lung cancer protein fragments having up to about 100-150 residues may be prepared by *in vitro* synthesis. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the lung cancer protein amino acid sequence. The variants typically exhibit a similar qualitative biological activity as the naturally occurring analogue, 10 although variants can also be selected which have modified characteristics as will be more fully outlined below.

While the site or region for introducing an amino acid sequence variation is often predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be 15 conducted at the target codon or region and the expressed lung cancer variants screened for the optimal combination of desired activity. Techniques exist for making substitution mutations at predetermined sites in DNA having a known sequence, e.g., M13 primer mutagenesis and PCR mutagenesis. Screening of mutants is often done using assays of lung cancer protein activities.

20 Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger insertions may be occasionally tolerated. Deletions generally range from about 1 to about 20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions or any combination thereof may be used to arrive 25 at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the molecule. Larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of a lung cancer protein are desired, substitutions are generally made in accordance with the amino acid substitution chart provided in the definition section.

30 Variants typically exhibit essentially the same qualitative biological activity and will elicit the same immune response as a naturally-occurring analog, although variants also are selected to modify the characteristics of lung cancer proteins as needed. Alternatively, the

variant may be designed or reorganized such that a biological activity of the lung cancer protein is altered. For example, glycosylation sites may be added, altered, or removed.

Covalent modifications of lung cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a lung cancer polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of a lung cancer polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking lung cancer polypeptides to a water-insoluble support matrix or surface for use in a method for purifying anti-lung cancer polypeptide antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-((p-azidophenyl)dithio)propioimide.

Other modifications include deamidation of glutaminyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of serinyl, threonyl or tyrosyl residues, methylation of the γ -amino groups of lysine, arginine, and histidine side chains (Creighton (1983) Proteins: Structure and Molecular Properties, pp. 79-86), acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the lung cancer polypeptide encompassed by this invention is an altered native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended herein to mean adding to or deleting one or more carbohydrate moieties of a native sequence lung cancer polypeptide. Glycosylation patterns can be altered in many ways. For example the use of different cell types to express lung cancer-associated sequences can result in different glycosylation patterns.

Addition of glycosylation sites to lung cancer polypeptides may also be accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence lung cancer polypeptide (for O-linked glycosylation sites). The lung cancer amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the lung cancer polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the lung cancer polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330, and in Aplin and Wriston (1981) CRC Crit. Rev. Biochem., pp. 259-306.

Removal of carbohydrate moieties present on the lung cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al. (1987) Arch. Biochem. Biophys., 259:52 and by Edge, et al. (1981) Anal. Biochem., 118:131.

Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases as described by Thotakura, et al. (1987) Meth. Enzymol., 138:350.

Another type of covalent modification of lung cancer comprises linking the lung cancer polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192, or 4,179,337.

Lung cancer polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising a lung cancer polypeptide fused to another, heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of a lung cancer polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxyl-terminus of the lung cancer polypeptide. The presence of such epitope-tagged forms of a lung cancer polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the lung cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a lung cancer polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are well known and examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; HIS6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field, et al. (1988) Mol. Cell. Biol. 8:2159-2165); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies

thereto (Evan, et al. (1985) Molecular and Cellular Biology 5:3610-3616); and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky, et al. (1990) Protein Engineering 3(6):547-553). Other tag polypeptides include the Flag-peptide (Hopp, et al. (1988) BioTechnology 6:1204-1210); the KT3 epitope peptide (Martin, et al. (1992) Science 255:192-194); tubulin epitope peptide (Skinner, et al. (1991) J. Biol. Chem. 266:15163-15166); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth, et al. (1990) Proc. Nat'l Acad. Sci. USA 87:6393-6397).

Also included are other lung cancer proteins of the lung cancer family, and lung cancer proteins from other organisms, which are cloned and expressed as outlined below.

Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related lung cancer proteins from primates or other organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include unique areas of the lung cancer nucleic acid sequence. As is generally known in the art, preferred PCR primers are from about 15 to about 35 nucleotides in length, with from about 20 to about 30 being preferred, and may contain inosine as needed. PCR reaction conditions are well known in the art (e.g., Innis, PCR Protocols, *supra*).

Antibodies to lung cancer proteins

In a preferred embodiment, when a lung cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the lung cancer protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller lung cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity.

Methods of preparing polyclonal antibodies are well known (e.g., Coligan, *supra*; and Harlow and Lane, *supra*). Polyclonal antibodies can be raised in a mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of Tables 1A-16 or fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal

being immunized. Immunogenic proteins include, e.g., keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Adjuvants include, e.g., Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art.

The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein (1975) Nature 256:495. In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of the tables, or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding (1986) Monoclonal Antibodies: Principles and Practice, pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovin, or primate origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are typically monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens or that have binding specificities for two epitopes on the same antigen. In one embodiment, one of the binding specificities is for a protein encoded by a nucleic acid of the tables or a fragment thereof, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.

In a preferred embodiment, the antibodies to lung cancer protein are capable of reducing or eliminating a biological function of a lung cancer protein, in a naked form or conjugated to an effector moiety. That is, the addition of anti-lung cancer protein antibodies (either polyclonal or preferably monoclonal) to lung cancer tissue (or cells containing lung cancer) may reduce or eliminate the lung cancer. Generally, at least a 25% decrease in activity, growth, size or the like is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

In a preferred embodiment the antibodies to the lung cancer proteins are humanized antibodies (e.g., Xenerex Biosciences, Medarex, Inc., Abgenix, Inc., Protein Design Labs, Inc.) Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of a human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. A humanized antibody optimally also will typically comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-329; and Presta (1992) Curr. Op. Struct. Biol. 2:593-596). Humanization can be performed following the method of Winter and co-workers (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-327; Verhoeven, et al. (1988) Science 239:1534-1536), by substituting rodent CDRs or CDR sequences for corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by corresponding sequence from a non-human species.

Human-like antibodies can also be produced using various techniques known in the art, including phage display libraries (Hoogenboom and Winter (1991) J. Mol. Biol. 227:381; Marks, et al. (1991) J. Mol. Biol. 222:581). The techniques of Cole, et al. and Boerner, et al. are also available for the preparation of human monoclonal antibodies (Cole, et al. (1985) Monoclonal Antibodies and Cancer Therapy, p. 77 and Boerner, et al. (1991) J. Immunol. 147(1):86-95). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in nearly all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, e.g., in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks, et al. (1992) Bio/Technology 10:779-783; Lonberg, et al. (1994) Nature 368:856-859; Morrison (1994) Nature 368:812-13; Fishwild, et al. (1996) Nature Biotechnology 14:845-51; Neuberger (1996) Nature Biotechnology 14:826; and Lonberg and Huszar (1995) Intern. Rev. Immunol. 13:65-93.

By immunotherapy is meant treatment of lung cancer with an antibody raised against a lung cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. The antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

In a preferred embodiment the lung cancer proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment, may bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted lung cancer protein.

In another preferred embodiment, the lung cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment may bind the extracellular domain of the lung cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The

antibody may cause down-regulation of the transmembrane lung cancer protein. The antibody may be a competitive, non-competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the lung cancer protein. The antibody may be an antagonist of the lung cancer protein or may prevent activation of a transmembrane lung cancer protein, or
5 may induce or suppress a particular cellular pathway. In some embodiments, when the antibody prevents the binding of other molecules to the lung cancer protein, the antibody prevents growth of the cell. The antibody may also be used to target or sensitize the cell to cytotoxic agents, including, but not limited to TNF- α , TNF- β , IL-1, INF- γ , and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate,
10 and the like. In some instances the antibody may belong to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, lung cancer may be treated by administering to a patient antibodies directed against the transmembrane lung cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, or otherwise provide
15 means to locally ablate cells.

In another preferred embodiment, the antibody is conjugated to an effector moiety. The effector moiety can be various molecules, including labeling moieties such as radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of a lung cancer protein. In another
20 aspect the therapeutic moiety may modulate an activity of molecules associated with or in close proximity to a lung cancer protein. The therapeutic moiety may inhibit enzymatic or signaling activity such as protease or collagenase activity associated with lung cancer.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to lung cancer tissue or cells results in a reduction
25 in the number of afflicted cells, thereby reducing symptoms associated with lung cancer. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin, saporin, auristatin, and the like. Cytotoxic agents also include
30 radiochemicals made by conjugating radioisotopes to antibodies raised against lung cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane lung cancer proteins not only serves to increase the local concentration of therapeutic moiety in the lung cancer

afflicted area, but also serves to reduce deleterious side effects that may be associated with the untargeted therapeutic moiety.

In another preferred embodiment, the lung cancer protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein or other entity which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the lung cancer protein can be targeted within a cell, i.e., the nucleus, an antibody theretomay contain a signal for that target localization, i.e., a nuclear localization signal.

The lung cancer antibodies of the invention specifically bind to lung cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a K_d of at least about 0.1 mM, more usually at least about 1 μ M, preferably at least about 0.1 μ M or better, and most preferably, 0.01 μ M or better. Selectivity of binding to the specific target and not to related other sequences is also important.

Detection of lung cancer sequence for diagnostic and therapeutic applications

In one aspect, the RNA expression levels of genes are determined for different cellular states in the lung cancer phenotype. Expression levels of genes in normal tissue (e.g., not undergoing lung cancer), in lung cancer tissue (and in some cases, for varying severities of lung cancer that relate to prognosis, as outlined below), or in non-malignant disease are evaluated to provide expression profiles. A gene expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state of the cell. While two states may have a particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or cancerous tissue. This will provide for molecular diagnosis of related conditions.

"Differential expression," or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and among cells and tissue. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, e.g.,

normal versus lung cancer tissue. Genes may be turned on or turned off in a particular state, relative to another state thus permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that expression is increased or decreased; i.e., gene expression is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays, Lockhart (1996) Nature Biotechnology 14:1675-1680, hereby expressly incorporated by reference. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, northern analysis and RNase protection. As outlined above, preferably the change in expression (i.e., upregulation or downregulation) is typically at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from 300 to at least 1000% being especially preferred.

Evaluation may be at the gene transcript or the protein level. The amount of gene expression may be monitored using nucleic acid probes to the RNA or DNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the lung cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to lung cancer genes, e.g., those identified as being important in a lung cancer or disease phenotype, can be evaluated in a lung cancer diagnostic test. In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes.

The lung cancer nucleic acid probes may be attached to biochips as outlined herein for the detection and quantification of lung cancer sequences in a particular cell. The assays are further described below in the example. PCR techniques can be used to provide greater sensitivity. Multiple protein expression monitoring can be performed as well. Similarly, these assays may be performed on an individual basis as well.

In a preferred embodiment nucleic acids encoding the lung cancer protein are detected. Although DNA or RNA encoding the lung cancer protein may be detected, of particular interest are methods wherein an mRNA encoding a lung cancer protein is detected.

Probes to detect mRNA can be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to, oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method detection of the mRNA is performed *in situ*. In this method permeabilized cells or tissue samples are contacted with a detectably labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxigenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a lung cancer protein is detected by binding the digoxigenin with an anti-digoxigenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing lung cancer sequences are used in diagnostic assays. This can be performed on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, lung cancer proteins, including intracellular, transmembrane, or secreted proteins, find use as markers of lung cancer, e.g., for prognostic or diagnostic purposes. Detection of these proteins in putative lung cancer tissue allows for detection, prognosis, or diagnosis of lung cancer or similar disease, and perhaps for selection of therapeutic strategy. In one embodiment, antibodies are used to detect lung cancer proteins. A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following separation of proteins, the lung cancer protein is detected, e.g., by immunoblotting with antibodies raised against the lung cancer protein. Methods of immunoblotting are well known to those of ordinary skill in the art.

In another preferred method, antibodies to the lung cancer protein find use in *in situ* imaging techniques, e.g., in histology (e.g., Asai (ed. 1993) Methods in Cell Biology:

Antibodies in Cell Biology, volume 37. In this method cells are contacted with from one to

many antibodies to the lung cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a detectable label, e.g., multicolor fluorescence or confocal imaging. In another method the primary antibody to the lung cancer protein(s) contains a detectable label, e.g., an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of lung cancer proteins. Many other histological imaging techniques are also provided by the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

In another preferred embodiment, antibodies find use in diagnosing lung cancer from blood, serum, plasma, stool, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of lung cancer proteins. Antibodies can be used to detect a lung cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (western blotting), immunoprecipitation, BIAcore technology and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous lung cancer protein or vaccine.

In a preferred embodiment, *in situ* hybridization of labeled lung cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including lung cancer tissue and/or normal tissue, are made. *In situ* hybridization (see, e.g., Ausubel, *supra*) is then performed. When comparing the fingerprints between an individual and a standard, the skilled artisan can make a diagnosis, a prognosis, or a prediction based on the findings. It is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

In a preferred embodiment, the lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing lung cancer sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to lung cancer, clinical, pathological, or other information, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. Single or multiple

genes may be useful in various combinations. As above, lung cancer probes may be attached to biochips for the detection and quantification of lung cancer sequences in a tissue or patient. The assays proceed as outlined above for diagnosis. PCR method may provide more sensitive and accurate quantification.

5

Assays for therapeutic compounds

In a preferred embodiment, the proteins, nucleic acids, and antibodies as described herein are used in drug screening assays. The lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing lung cancer sequences are used in drug screening
10 assays or by evaluating the effect of drug candidates on a “gene expression profile” or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent (e.g., Zlokarnik, et al. (1998) Science 279:84-8; Heid (1996) Genome Res. 6:986-94.

15 In a preferred embodiment, the lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified lung cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the lung cancer phenotype or an identified physiological function of a lung cancer protein. As above, this can be done on an individual gene level or
20 by evaluating the effect of drug candidates on a “gene expression profile”. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, *supra*.

Having identified differentially expressed genes herein, a variety of assays may be
25 performed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene with altered regulation in lung cancer, test compounds can be screened for the ability to modulate gene expression or for binding to the lung cancer protein. “Modulation” thus includes an increase or a decrease in gene expression. The preferred amount of modulation will depend on the original change of the
30 gene expression in normal versus tissue undergoing lung cancer, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in lung cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, a 10-fold decrease in lung

cancer tissue compared to normal tissue often provides a target value of a 10-fold increase in expression to be induced by the test compound.

The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be monitored, e.g., through the use of antibodies to the lung cancer protein and standard immunoassays. Proteomics and separation techniques may also allow quantification of expression.

In a preferred embodiment, gene or protein expression monitoring of a number of entities, i.e., an expression profile, is monitored simultaneously. Such profiles will typically involve a plurality of those entities described herein.

In this embodiment, the lung cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of lung cancer sequences in a particular cell. Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

Expression monitoring can be performed to identify compounds that modify the expression of one or more lung cancer-associated sequences, e.g., a polynucleotide sequence set out in the tables. Generally, in a preferred embodiment, a test compound is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate lung cancer, modulate lung cancer proteins, bind to a lung cancer protein, or interfere with the binding of a lung cancer protein and an antibody, substrate, or other binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical equivalents as used herein describes a molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the lung cancer phenotype or the expression of a lung cancer sequence, e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter expression profiles of nucleic acids or proteins provided herein. In one embodiment, the modulator suppresses a lung cancer phenotype, e.g., to a normal or non-malignant tissue fingerprint. In another embodiment, a modulator induces a lung cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, i.e., at zero concentration or below the level of detection.

In one aspect, a modulator will neutralize the effect of a lung cancer protein. By “neutralize” is meant that activity of a protein and the consequent effect on the cell is inhibited or blocked.

In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to a lung cancer polypeptide or to modulate activity. Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a “lead compound”) with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such “combinatorial chemical libraries” are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional “lead compounds” or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical “building blocks” such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (i.e., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks (Gallop, et al. (1994) J. Med. Chem. 37(9):1233-1251).

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent No. 5,010,175, Furka (1991) Pept. Prot. Res. 37:487-493, Houghton, et al. (1991) Nature, 354:84-88), peptoids (PCT Publication No WO 91/19735), encoded peptides (PCT Publication WO 93/20242), random bio-oligomers (PCT Publication WO 92/00091), benzodiazepines (U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs, et al. (1993) Proc. Nat. Acad. Sci. USA 90:6909-6913), vinylogous polypeptides (Hagihara, et al. (1992) J. Amer. Chem. Soc. 114:6568), nonpeptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann, et

al. (1992) J. Amer. Chem. Soc. 114:9217-9218), analogous organic syntheses of small compound libraries (Chen, et al. (1994) J. Amer. Chem. Soc. 116:2661), oligocarbamates (Cho, et al. (1993) Science 261:1303), and/or peptidyl phosphonates (Campbell, et al. (1994) J. Org. Chem. 59:658). See, generally, Gordon, et al. (1994) J. Med. Chem. 37:1385, nucleic acid libraries (see, e.g., Stratagene, Corp.), peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083), antibody libraries (see, e.g., Vaughn, et al. (1996) Nature Biotechnology 14(3):309-314, and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang, et al. (1996) Science 274:1520-1522, and U.S. Patent No. 5,593,853), and small organic molecule libraries (see, e.g., benzodiazepines, Baum (1993) C&EN, Jan 18, page 33; isoprenoids, U.S. Patent No. 5,569,588; thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pyrrolidines, U.S. Patent Nos. 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent No. 5,506,337; benzodiazepines, U.S. Patent No. 5,288,514; and the like).

Devices for the preparation of combinatorial libraries are commercially available (see, e.g., 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY, Symphony, Rainin, Woburn, MA, 433A Applied Biosystems, Foster City, CA, 9050 Plus, Millipore, Bedford, MA).

A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, Mass.; Orca, Hewlett-Packard, Palo Alto, Calif.), which mimic the manual synthetic operations performed by a chemist. The above devices, with appropriate modification, are suitable for use with the present invention. In addition, numerous combinatorial libraries are themselves commercially available (see, e.g., ComGenex, Princeton, N.J., Asinex, Moscow, Ru, Tripos, Inc., St. Louis, MO, ChemStar, Ltd, Moscow, RU, 3D Pharmaceuticals, Exton, PA, Martek Biosciences, Columbia, MD, etc.).

The assays to identify modulators are amenable to high throughput screening. Preferred assays thus detect modulation of lung cancer gene transcription, polypeptide expression, and polypeptide activity.

High throughput assays for evaluating the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known to those of skill in the art. Similarly, binding assays and reporter gene assays are similarly well known. Thus, e.g., U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins,

U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (i.e., in arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding.

In addition, high throughput screening systems are commercially available (see, e.g.,
5 Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA, etc.). These systems typically automate procedures, including sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a
10 high degree of flexibility and customization. The manufacturers of such systems provide detailed protocols for various high throughput systems. Thus, e.g., Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like.

In one embodiment, modulators are proteins, often naturally occurring proteins or
15 fragments of naturally occurring proteins. Thus, e.g., cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred. Particularly
20 useful test compound will be directed to the class of proteins to which the target belongs, e.g., substrates for enzymes or ligands and receptors.

In a preferred embodiment, modulators are peptides of from about 5 to about 30 amino acids, with from about 5 to about 20 amino acids being preferred, and from about 7 to about 15 being particularly preferred. The peptides may be digests of naturally occurring
25 proteins, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that the nucleic acid or peptide consists of essentially random sequences of nucleotides and amino acids, respectively. Since these random peptides (or nucleic acids, discussed below) are often chemically synthesized, they may incorporate a nucleotide or amino acid at any position. The synthetic process can be designed to generate
30 randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. In a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, 5 sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines or histidines for phosphorylation sites, etc.

Modulators of lung cancer can also be nucleic acids, as defined above.

10 As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. Digests of procaryotic or eucaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

15 After a candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence is analyzed. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example, an *in vitro* transcription 20 with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, 25 alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin 30 is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

Nucleic acid assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos.

5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246 and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allow formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration, pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be used as appropriate, depending on the sample preparation methods and purity of the target.

The assay data are analyzed to determine the expression levels, and changes in expression levels as between states, of individual genes, forming a gene expression profile.

Screens are performed to identify modulators of the lung cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another embodiment, e.g., for diagnostic applications, having identified differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially expressed gene. Again, having identified the importance of a gene in a particular state,

screens are performed to identify agents that bind and/or modulate the biological activity of the gene product, or evaluate genetic polymorphisms.

Genes can be screened for those that are induced in response to a candidate agent. After identifying a modulator based upon its ability to suppress a lung cancer expression pattern leading to a normal expression pattern, or to modulate a single lung cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated lung cancer tissue reveals genes that are not expressed in normal tissue or lung cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be identified and used by methods described herein for lung cancer genes or proteins. In particular these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated lung cancer tissue sample.

Thus, in one embodiment, a test compound is administered to a population of lung cancer cells, that have an associated lung cancer expression profile. By “administration” or “contacting” herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (i.e., a peptide) may be put into a viral construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used.

Once a test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

Thus, e.g., lung cancer or non-malignant tissue may be screened for agents that modulate, e.g., induce or suppress a lung cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on lung cancer activity. By defining such a signature for the lung cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

Measure of lung cancer polypeptide activity, or of lung cancer or the lung cancer phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the metastatic polypeptides can be measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of lung cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian lung cancer polypeptide is typically used, e.g., mouse, preferably human.

Assays to identify compounds with modulating activity can be performed *in vitro*. For example, a lung cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5 to 48 hours. In one embodiment, the lung cancer polypeptide levels are determined *in vitro* by measuring the level of protein or mRNA. The level of protein is typically measured using immunoassays such as western blotting, ELISA and the like with an antibody that selectively binds to the lung cancer polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNase protection, dot blotting, are preferred. The level of protein or mRNA is typically detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or enzymatically labeled antibodies, and the like, as described herein.

Alternatively, a reporter gene system can be devised using a lung cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or β -gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques known to those of skill in the art.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or the gene product itself can be done. The gene products of differentially expressed

genes are sometimes referred to herein as "lung cancer proteins." The lung cancer protein may be a fragment, or alternatively, be the full length protein to a fragment shown herein.

In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another
5 embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

In a preferred embodiment, binding assays are done. In general, purified or isolated
10 gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the lung cancer proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining a lung cancer
15 protein and a candidate compound, and determining the binding of the compound to the lung cancer protein. Preferred embodiments utilize the human lung cancer protein, although other mammalian proteins may also be used, e.g., for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative lung cancer proteins may be used.

Generally, in a preferred embodiment of the methods herein, the lung cancer protein
20 or the candidate agent is non-diffusably bound to an insoluble support, preferably having isolated sample receiving areas (e.g., a microtiter plate, an array, etc.). The insoluble supports may be made of a composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of
25 screening. The surface of such supports may be solid or porous and of a convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents
30 and samples. The particular manner of binding of the composition is typically not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition, and is nondiffusable. Preferred methods of binding include the use of antibodies (which do not sterically block either the ligand binding site or activation

sequence when the protein is bound to the support), direct binding to “sticky” or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

In a preferred embodiment, the lung cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the lung cancer protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled *in vitro* protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

The determination of the binding of the test modulating compound to the lung cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all or a portion of the lung cancer protein to a solid support, adding a labeled candidate agent (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as appropriate.

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one component can be labeled with different labels, e.g., ^{125}I for the proteins and a fluorophor for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor may be a binding moiety known to bind to the target molecule (i.e., a lung cancer protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically between 4 and 40° C. Incubation periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically

between 0.1 and 1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

In a preferred embodiment, the competitor is added first, followed by a test compound. Displacement of the competitor is an indication that the test compound is binding to the lung cancer protein and thus is capable of binding to, and potentially modulating, the activity of the lung cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the lung cancer protein with a higher affinity. Thus, if the test compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is capable of binding to the lung cancer protein.

In a preferred embodiment, the methods comprise differential screening to identify agents that are capable of modulating the activity of the lung cancer proteins. In one embodiment, the methods comprise combining a lung cancer protein and a competitor in a first sample. A second sample comprises a test compound, a lung cancer protein, and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the lung cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the lung cancer protein.

Alternatively, differential screening is used to identify drug candidates that bind to the native lung cancer protein, but cannot bind to modified lung cancer proteins. The structure of the lung cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of a lung cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results.

Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in an order that provides for the requisite binding.

In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of a lung cancer protein. The methods comprise adding a test compound, as defined above, to a cell comprising lung cancer proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes a lung cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g., hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including chemotherapeutics, radiation, carcinogenics, or other cells (e.g., cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

In this way, compounds that modulate lung cancer agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the lung cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the compound.

In one embodiment, a method of inhibiting lung cancer cell division is provided. The method comprises administration of a lung cancer inhibitor. In another embodiment, a method of inhibiting lung cancer is provided. The method may comprise administration of a lung cancer inhibitor. In a further embodiment, methods of treating cells or individuals with lung cancer are provided, e.g., comprising administration of a lung cancer inhibitor.

In one embodiment, a lung cancer inhibitor is an antibody as discussed above. In another embodiment, the lung cancer inhibitor is an antisense molecule.

A variety of cell growth, proliferation, viability, and metastasis assays are known to those of skill in the art, as described below.

Soft agar growth or colony formation in suspension

5 Normal cells require a solid substrate to attach and grow. When the cells are transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and
10 grow. Soft agar growth or colony formation in suspension assays can be used to identify modulators of lung cancer sequences, which when expressed in host cells, inhibit abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

15 Techniques for soft agar growth or colony formation in suspension assays are described in Freshney (1994) Culture of Animal Cells a Manual of Basic Technique (3rd ed.), herein incorporated by reference. See also, the methods section of Garkavtsev, et al. (1996), *supra*, herein incorporated by reference.

20 *Contact inhibition and density limitation of growth*

 Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a
25 higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells. Alternatively, labeling index with (³H)-thymidine at saturation density can be used to measure density limitation of growth. See Freshney (1994), *supra*. The transformed cells, when transfected with tumor suppressor genes, regenerate a
30 normal phenotype and become contact inhibited and would grow to a lower density.

 In this assay, labeling index with (³H)-thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with a lung cancer-associated sequence and are grown for 24 hours at saturation density in

non-limiting medium conditions. The percentage of cells labeling with (^3H)-thymidine is determined autoradiographically. See, Freshney (1994), *supra*.

Growth factor or serum dependence

Transformed cells typically have a lower serum dependence than their normal counterparts (see, e.g., Temin (1966) J. Natl. Cancer Inst. 37:167-175; Eagle, et al. (1970) J. Exp. Med. 131:836-879); Freshney, *supra*. This is in part due to release of various growth factors by the transformed cells. Growth factor or serum dependence of transformed host cells can be compared with that of control.

Tumor specific markers levels

Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released from human glioma at a higher level than from normal brain cells (see, e.g., Gullino, "Angiogenesis, tumor vascularization, and potential interference with tumor growth" in Mihich (ed. 1985) Biological Responses in Cancer, pp. 178-184). Similarly, Tumor angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal counterparts. See, e.g., Folkman (1992) "Angiogenesis and Cancer" in Sem Cancer Biol.

Various techniques which measure the release of these factors are described in Freshney (1994), *supra*. Also, see, Unkeless, et al. (1974) J. Biol. Chem. 249:4295-4305; Strickland and Beers (1976) J. Biol. Chem. 251:5694-5702; Whur, et al. (1980) Br. J. Cancer 42:305-312; Gullino, "Angiogenesis, tumor vascularization, and potential interference with tumor growth" in Mihich (ed. 1985) Biological Responses in Cancer, pp. 178-184; Freshney Anticancer Res. 5:111-130 (1985).

Invasiveness into Matrigel

The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate lung cancer-associated sequences. Tumor cells exhibit a good correlation between malignancy and invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

Techniques described in Freshney (1994), *supra*, can be used. Briefly, the level of invasion of host cells can be measured by using filters coated with Matrigel or some other extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance

5 moved, or by prelabeling the cells with ^{125}I and counting the radioactivity on the distal side of the filter or bottom of the dish. See, e.g., Freshney (1984), *supra*.

Tumor growth in vivo

Effects of lung cancer-associated sequences on cell growth can be tested in transgenic
10 or immune-suppressed mice. Knock-out transgenic mice can be made, in which the lung cancer gene is disrupted or in which a lung cancer gene is inserted. Knock-out transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous lung cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous lung cancer gene with a mutated
15 version of the lung cancer gene, or by mutating the endogenous lung cancer gene, e.g., by exposure to carcinogens.

A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice
20 that possess germ cells partially derived from the mutant cell line. Therefore, by breeding the chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion (see, e.g., Capecchi, et al. (1989) Science 244:1288). Chimeric targeted mice can be derived according to Hogan, et al. (1988) Manipulating the Mouse Embryo: A Laboratory Manual, Cold Spring Harbor Laboratory and Robertson (ed. 1987) Teratocarcinomas and
25 Embryonic Stem Cells: A Practical Approach, IRL Press, Washington, D.C.

Alternatively, various immune-suppressed or immune-deficient host animals can be used. For example, genetically athymic “nude” mouse (see, e.g., Giovanella, et al. (1974) J. Natl. Cancer Inst. 52:921), a SCID mouse, a thymectomized mouse, or an irradiated mouse (see, e.g., Bradley, et al. (1978) Br. J. Cancer 38:263; Selby, et al. (1980) Br. J. Cancer 41:52)
30 can be used as a host. Transplantable tumor cells (typically about 10^6 cells) injected into isogenic hosts will produce invasive tumors in a high proportions of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing a lung cancer-associated sequences are injected subcutaneously. After a suitable length of time,

preferably 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control. Tumors that have statistically significant reduction (using, e.g., Student's T test) are said to have inhibited growth.

5 Polynucleotide modulators of lung cancer

Antisense and RNAi Polynucleotides

In certain embodiments, the activity of a lung cancer-associated protein is downregulated, or entirely inhibited, by the use of antisense or an inhibitory polynucleotide, i.e., a nucleic acid complementary to, and which can preferably hybridize specifically to, a
10 coding mRNA nucleic acid sequence, e.g., a lung cancer protein mRNA, or a subsequence thereof. Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturally-occurring nucleotides, or synthetic species formed from naturally-occurring subunits or their
15 close homologs. Antisense polynucleotides may also have altered sugar moieties or inter-sugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species which are known for use in the art. Analogs are comprehended by this invention so long as they function effectively to hybridize with the lung cancer protein mRNA. See, e.g., Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

20 Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized *in vitro*. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known to those of skill in the art.

Antisense molecules as used herein include antisense or sense oligonucleotides.
25 Sense oligonucleotides can, e.g., be employed to block transcription by binding to the anti-sense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for lung cancer molecules. A preferred antisense molecule is for a lung cancer sequence in the tables, or for a ligand or activator thereof. Antisense or sense
30 oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein

is described in, e.g., Stein and Cohen (1988) Cancer Res. 48:2659 and van der Krol, et al. (1988) BioTechniques 6:958).

RNA interference is a mechanism to suppress gene expression in a sequence specific manner. See, e.g., Brumelkamp, et al. (2002) Sciencexpress (21March2002); Sharp (1999) Genes Dev. 13:139-141; and Cathew (2001) Curr. Op. Cell Biol. 13:244-248. In mammalian cells, short, e.g., 21 nt, double stranded small interfering RNAs (siRNA) have been shown to be effective at inducing an RNAi response. See, e.g., Elbashir, et al. (2001) Nature 411:494-498. The mechanism may be used to downregulate expression levels of identified genes, e.g., treatment of or validation of relevance to disease.

Ribozymes

In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of lung cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes (see, e.g., Castanotto, et al. (1994) Adv. in Pharmacology 25: 289-317 for a general review of the properties of different ribozymes).

The general features of hairpin ribozymes are described, e.g., in Hampel, et al. (1990) Nucl. Acids Res. 18:299-304; European Patent Publication No. 0 360 257; U.S. Patent No. 5,254,678. Methods of preparing are well known to those of skill in the art (see, e.g., WO 94/26877; Ojwang, et al. (1993) Proc. Natl. Acad. Sci. USA 90:6340-6344; Yamada, et al. (1994) Human Gene Therapy 1:39-45; Leavitt, et al. (1995) Proc. Natl. Acad. Sci. USA 92:699-703; Leavitt, et al. (19994) Human Gene Therapy 5:1151-120; and Yamada, et al. (1994) Virology 205: 121-126).

Polynucleotide modulators of lung cancer may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of lung cancer may be introduced into a cell containing the target nucleic acid sequence, e.g., by

formation of an polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

Thus, in one embodiment, methods of modulating lung cancer in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-lung cancer antibody that reduces or eliminates the biological activity of an endogenous lung cancer protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic acid encoding a lung cancer protein. This may be accomplished in any number of ways. In a preferred embodiment, e.g., when the lung cancer sequence is down-regulated in lung cancer, such state may be reversed by increasing the amount of lung cancer gene product in the cell. This can be accomplished, e.g., by overexpressing the endogenous lung cancer gene or administering a gene encoding the lung cancer sequence, using known gene-therapy techniques. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), e.g., as described in PCT/US93/03868, hereby incorporated by reference in its entirety. Alternatively, e.g., when the lung cancer sequence is up-regulated in lung cancer, the activity of the endogenous lung cancer gene is decreased, e.g., by the administration of a lung cancer antisense or RNAi nucleic acid.

In one embodiment, the lung cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to lung cancer proteins. Similarly, the lung cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify lung cancer antibodies useful for production, diagnostic, or therapeutic purposes. In a preferred embodiment, the antibodies are generated to epitopes unique to a lung cancer protein; that is, the antibodies show little or no cross-reactivity to other proteins. The lung cancer antibodies may be coupled to standard affinity chromatography columns and used to purify lung cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the lung cancer protein.

Methods of identifying variant lung cancer-associated sequences

Without being bound by theory, expression of various lung cancer sequences is correlated with lung cancer. Accordingly, disorders based on mutant or variant lung cancer genes may be determined. In one embodiment, the invention provides methods for

identifying cells containing variant lung cancer genes, e.g., determining all or part of the sequence of at least one endogenous lung cancer genes in a cell. In a preferred embodiment, the invention provides methods of identifying the lung cancer genotype of an individual, e.g., determining all or part of the sequence of at least one lung cancer gene of the individual.

- 5 This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced lung cancer gene to a known lung cancer gene, i.e., a wild-type gene.

10 The sequence of all or part of the lung cancer gene can then be compared to the sequence of a known lung cancer gene to determine if any differences exist. This can be done using known homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the lung cancer gene of the patient and the known lung cancer gene correlates with a disease state or a propensity for a disease state, as outlined herein.

- 15 In a preferred embodiment, the lung cancer genes are used as probes to determine the number of copies of the lung cancer gene in the genome.

In another preferred embodiment, the lung cancer genes are used as probes to determine the chromosomal localization of the lung cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when
20 chromosomal abnormalities such as translocations, and the like are identified in the lung cancer gene locus.

Administration of pharmaceutical and vaccine compositions

- 25 In one embodiment, a therapeutically effective dose of a lung cancer protein or modulator thereof, is administered to a patient. By “therapeutically effective dose” herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques (e.g., Ansel, et al. (1992) Pharmaceutical Dosage Forms and Drug Delivery; Lieberman, Pharmaceutical Dosage Forms (vols. 1-3), Dekker, ISBN 0824770846,
30 082476918X, 0824712692, 0824716981; Lloyd (1999) The Art, Science and Technology of Pharmaceutical Compounding; and Pickar (1999) Dosage Calculations). Adjustments for lung cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration,

drug interaction and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art.

A “patient” for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

The administration of the lung cancer proteins and modulators thereof of the present invention can be done in a variety of ways, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the lung cancer proteins and modulators may be directly applied as a solution or spray.

The pharmaceutical compositions of the present invention comprise a lung cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. “Pharmaceutically acceptable acid addition salt” refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid and the like. “Pharmaceutically acceptable base addition salts” include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose,

lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms
5 suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules and lozenges. It is recognized that lung cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, etc.) when administered orally, should be protected from digestion. This is typically accomplished either by complexing the
10 molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier. Means of protecting agents from digestion are well known in the art.

The compositions for administration will commonly comprise a lung cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions
15 are sterile and generally free of undesirable matter. These compositions may be sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate
20 and the like. The concentration of active agent in these formulations can vary widely, and will be selected primarily based on fluid volumes, viscosities, body weight and the like in accordance with the particular mode of administration selected and the patient's needs (e.g., Remington's Pharmaceutical Science (15th ed., 1980) and Hardman, et al. (eds. 1996) Goodman and Gilman: The Pharmacological Basis of Therapeutics).

Thus, a typical pharmaceutical composition for intravenous administration would be
25 about 0.1 to 10 mg per patient per day. Dosages from 0.1 up to about 100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally
30 administrable compositions will be known or apparent to those skilled in the art, e.g., Remington's Pharmaceutical Science and Goodman and Gilman, The Pharmacological Basis of Therapeutics, *supra*.

The compositions containing modulators of lung cancer proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications, compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and its complications. An amount adequate to accomplish this is defined as a “therapeutically effective dose.” Amounts effective for this use will depend upon the severity of the disease and the general state of the patient’s health. Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. In any event, the composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a mammal is referred to as a “prophylactically effective dose.” The particular dose required for a prophylactic treatment will depend upon the medical condition and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender, administration route, efficiency, etc. Such prophylactic treatments may be used, e.g., in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer based, at least in part, upon gene expression profiles. Vaccine strategies may be used, in either a DNA vaccine form, or protein vaccine.

It will be appreciated that the present lung cancer protein-modulating compounds can be administered alone or in combination with additional lung cancer modulating compounds or with other therapeutic agent, e.g., other anti-cancer agents or treatments.

In numerous embodiments, one or more nucleic acids, e.g., polynucleotides comprising nucleic acid sequences set forth in the tables, such as antisense or RNAi polynucleotides or ribozymes, will be introduced into cells, *in vitro* or *in vivo*. The present invention provides methods, reagents, vectors, and cells useful for expression of lung cancer-associated polypeptides and nucleic acids using *in vitro* (cell-free), *ex vivo*, or *in vivo* (cell or organism-based) recombinant expression systems.

The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors and other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (see, e.g.,

Berger and Kimmel, Guide to Molecular Cloning Techniques, Methods in Enzymology volume 152 (Berger), Ausubel, et al. (eds. 1999) Current Protocols (supplemented through 1999), and Sambrook, et al. (1989) Molecular Cloning - A Laboratory Manual (2nd ed., Vol. 1-3).

5 In a preferred embodiment, lung cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, lung cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the lung cancer coding regions) can be administered in a gene therapy application. These lung cancer genes can include antisense or inhibitory applications, e.g., as inhibitory RNA or gene
10 therapy (e.g., for incorporation into the genome) or as antisense compositions.

Lung cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL, and antibody responses.. Such vaccine compositions can include, e.g., lipidated peptides (see, e.g., Vitiello, et al. (1995) J. Clin. Invest. 95:341), peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres
15 (see, e.g., Eldridge, et al. (1991) Molec. Immunol. 28:287-294; Alonso, et al. (1994) Vaccine 12:299-306; Jones, et al. (1995) Vaccine 13:675-681), peptide compositions contained in immune stimulating complexes (ISCOMS) (see, e.g., Takahashi, et al. (1990) Nature 344:873-875; Hu, et al. (1998) Clin Exp Immunol. 113:235-243), multiple antigen peptide systems (MAPs) (see, e.g., Tam (1988) Proc. Natl. Acad. Sci. U.S.A. 85:5409-5413; Tam
20 (1996) J. Immunol. Methods 196:17-32), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, et al., p. 379 In: Kaufmann (ed. 1996) Concepts in vaccine development; Chakrabarti, et al. (1986) Nature 320:535; Hu, et al. (1986) Nature 320:537; Kieny, et al. (1986) AIDS Bio/Technology 4:790; Top, et al. (1971) J. Infect. Dis. 124:148; Chanda, et al.
25 (1990) Virology 175:535), particles of viral or synthetic origin (see, e.g., Kofler, et al. (1996) J. Immunol. Methods 192:25; Eldridge, et al. (1993) Sem. Hematol. 30:16; Falo, et al. (1995) Nature Med. 7:649), adjuvants (Warren, et al. (1986) Annu. Rev. Immunol. 4:369; Gupta, et al. (1993) Vaccine 11:293), liposomes (Reddy, et al. (1992) J. Immunol. 148:1585; Rock (1996) Immunol. Today 17:131), or, naked or particle absorbed cDNA (Ulmer, et al. (1993)
30 Science 259:1745; Robinson, et al. (1993) Vaccine 11:957; Shiver, et al., p. 423 In: Kaufmann (ed. 1996) Concepts in vaccine development; Cease and Berzofsky (1994) Annu. Rev. Immunol. 12:923 and Eldridge, et al. (1993) Sem. Hematol. 30:16). Toxin-targeted

delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

Vaccine compositions often include adjuvants. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Vaccines can be administered as nucleic acid compositions wherein DNA or RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient. This approach is described, for instance, in Wolff, et. al. (1990) Science 247:1465 as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivacaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (see, e.g., U.S. Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, e.g., as a vector to express nucleotide sequences that encode lung cancer polypeptides or polypeptide fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover, et al. (1991) Nature 351:456-460. A wide variety of other vectors useful for therapeutic administration or immunization e.g., adeno and adeno-associated virus vectors, retroviral vectors, *Salmonella typhi* vectors, detoxified anthrax toxin vectors, and the

like, will be apparent to those skilled in the art from the description herein (see, e.g., Shata, et al. (2000) Mol Med Today 6:66-71; Shedlock, et al. (2000) J. Leukoc. Biol. 68:793-806; Hipp, et al. (2000) In Vivo 14:571-85).

Methods for the use of genes as DNA vaccines are well known, and include placing a lung cancer gene or portion of a lung cancer gene under the control of a regulatable promoter or a tissue-specific promoter for expression in a lung cancer patient. The lung cancer gene used for DNA vaccines can encode full-length lung cancer proteins, but more preferably encodes portions of the lung cancer proteins including peptides derived from the lung cancer protein. In one embodiment, a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from a lung cancer gene. For example, lung cancer-associated genes or sequence encoding subfragments of a lung cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular epitopes.

In a preferred embodiment, DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the lung cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

In another preferred embodiment lung cancer genes find use in generating animal models of lung cancer. When the lung cancer gene identified is repressed or diminished in metastatic tissue, gene therapy technology, e.g., wherein antisense or inhibitory RNA directed to the lung cancer gene will also diminish or repress expression of the gene. Animal models of lung cancer find use in screening for modulators of a lung cancer-associated sequence or modulators of lung cancer. Similarly, transgenic animal technology including gene knockout technology, e.g., as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the lung cancer protein. When desired, tissue-specific expression or knockout of the lung cancer protein may be necessary.

It is also possible that the lung cancer protein is overexpressed in lung cancer. As such, transgenic animals can be generated that overexpress the lung cancer protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene.

Animals generated by such methods will find use as animal models of lung cancer and are additionally useful in screening for modulators to treat lung cancer.

Kits for Use in Diagnostic and/or Prognostic Applications

5 For use in diagnostic, research, and therapeutic applications suggested above, kits are also provided by the invention. In diagnostic and research applications such kits may include at least one of the following: assay reagents, buffers, lung cancer-specific nucleic acids or antibodies, hybridization probes and/or primers, antisense polynucleotides, ribozymes, RNAi, dominant negative lung cancer polypeptides or polynucleotides, small molecule inhibitors of
10 lung cancer-associated sequences, etc. A therapeutic product may include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

 In addition, the kits may include instructional materials containing instructions (e.g., protocols) for the practice of the methods of this invention. While the instructional materials typically comprise written or printed materials they are not limited to such. A medium
15 capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such media may include addresses to internet sites that provide such instructional materials.

 The present invention also provides for kits for screening for modulators of lung
20 cancer-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: a lung cancer-associated polypeptide or polynucleotide, reaction tubes, and instructions for testing lung cancer-associated activity. Optionally, the kit contains biologically active lung cancer protein. A wide variety of kits and components can be prepared according to the present
25 invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes typically will be selected based on correlations with important parameters in disease which may be identified in historical or outcome data.

EXAMPLES

Example 1: Gene Chip Analysis

5 Molecular profiles of various normal and cancerous tissues were determined and analyzed using gene chips. RNA was isolated and gene chip analysis was performed as described (Glynne, et al. (2000) Nature 403:672-676; Zhao, et al. (2000) Genes Dev. 14:981-993).

Tables 1A and 1B were previously filed on April 18, 2001 in USSN 60/284,770 (18501-001500US) and on November 29, 2001 in USSN 60/334,370 (18501-001520US)

5	Table 1A					
	Pkey	ExAccn	UnigenelD	Unigene Title	70% chron/90% NL	70% SQAD/90% NL
	100134	D13264	Hs.49	macrophage scavenger receptor 1	1.61	0.74
	100780	HG3731-HT4001		***Immunoglobulin Heavy Chain, Vdjr Reg	2.68	3.28
	100971	J02874	Hs.83213	fatty acid binding protein 4; adipocyte	1.96	0.14
10	101088	L05568	Hs.553	solute carrier family 6 (neurotransmitte	0.79	0.07
	101102	L07594	Hs.79059	transforming growth factor; beta recepto	2.55	1
	101168	L15388	Hs.211569	G protein-coupled receptor kinase 5	0.88	0.27
	101277	L38486	Hs.118223	microfibrillar-associated protein 4	0.89	0.26
	101330	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do	0.59	0.29
15	101336	L49169	Hs.75678	FBJ murine osteosarcoma viral oncogene h	1.15	0.41
	101345	L76380	Hs.152175	calcitonin receptor-like	0.81	0.31
	101678	M62505	Hs.2161	complement component 5 receptor 1 (C5a l	1.31	0.77
	101764	M80563	Hs.81256	S100 calcium-binding protein A4 (calcium	1.44	0.82
	101771	M81750	Hs.153837	myeloid cell nuclear differentiation ant	0.96	0.45
20	101842	M93221	Hs.75182	mannose receptor; C type 1	1.27	0.37
	102283	U31384	Hs.83381	guanine nucleotide binding protein 11	1.04	0.3
	102363	U39447	Hs.198241	amine oxidase; copper containing 3 (vasc	0.96	0.26
	102507	U52154	Hs.193044	potassium inwardly-rectifying channel; s	2.81	3.45
	102698	U75272	Hs.1867	progastricin (pepsinogen C)	0.95	0.23
25	103025	X54131	Hs.123641	protein tyrosine phosphatase; receptor t	1.62	0.21
	103280	X79981	Hs.76206	cadherin 5; VE-cadherin (vascular epithe	0.9	0.41
	103496	Y09267	Hs.132821	flavin containing monooxygenase 2	1.27	0.49
	103541	Z11697	Hs.79197	CD83 antigen (activated B lymphocytes; i	1.86	1
	103554	Z18951	Hs.74034	caveolin 1; caveolae protein; 22kD	1.27	0.47
30	104212	AB002298	Hs.173035	KIAA0300 protein	1.17	0.16
	104691	AA011176	Hs.37744	ESTs	1.08	0.35
	104825	AA035613	Hs.141883	ESTs	0.75	0.27
	104857	AA043219	Hs.19058	ESTs	2.6	3.3
	104865	AA045136	Hs.22575	ESTs	1.23	0.49
35	104989	AA102098	Hs.118615	ESTs	0.63	0.32
	105729	AA292694	Hs.3807	ESTs; Weakly similar to PHOSPHOLEMMAN PR	0.86	0.34
	105847	AA398606	Hs.32241	ESTs	1.32	0.4
	105894	AA400979	Hs.25691	calcitonin receptor-like receptor activi	0.78	0.28
	106490	AA451861	Hs.115537	ESTs; Weakly similar to dipeptidase prec	1.2	0.47
40	106536	AA453997	Hs.23804	ESTs	0.82	0.15
	106605	AA457718	Hs.21103	Homo sapiens mRNA; cDNA DKFp564B076 (fr	0.99	0.07
	106667	AA461086	Hs.16578	ESTs	1.17	0.4
	106773	AA478109	Hs.188833	ESTs	1.46	0.43
	106797	AA478962	Hs.169943	ESTs	1.18	0.32
45	106844	AA485055	Hs.158213	sperm associated antigen 6	0.98	0.51
	106870	AA487576	Hs.26530	serum deprivation response (phosphatidyl	1.05	0.14
	106954	AA496980	Hs.204038	ESTs	1.25	0.33
	107054	AA600150	Hs.14366	ESTs	1.11	0.4
50	107292	T30407	Hs.4789	ESTs; Weakly similar to oxidative-stress	1.07	2.58
	107994	AA036811	Hs.165030	ESTs	0.7	0.21
	107997	AA037388	Hs.82223	Human DNA sequence from clone 141H5 on c	1.02	0.48
	108041	AA041552	Hs.61957	ESTs	1.44	0.51
	108087	AA045709	Hs.40545	ESTs	1.98	1
55	108382	AA074885	Hs.67726	macrophage receptor with collagenous str	1.52	0.72
	108435	AA078787	Hs.194101	ESTs	2.53	1.53
	108480	AA081093	Hs.68055	ESTs	1.56	0.48
	109252	AA194830	Hs.85944	ESTs	2.69	3.18
	109550	F01534	Hs.26981	ESTs	1.19	0.65
60	109613	F03031	Hs.27519	ESTs	1.01	0.29
	109837	H00656	Hs.29792	ESTs	0.81	0.15
	109893	H04768	Hs.30484	ESTs	1.44	0.32
	109984	H09594	Hs.10299	ESTs	0.62	0.14
	110099	H16568	Hs.23748	ESTs	1.01	0.28
65	110837	N30796	Hs.17424	ESTs; Weakly similar to semaphorin F [H.	1.1	0.22
	111247	N69825	Hs.16762	Homo sapiens mRNA; cDNA DKFp564B2062 (f	1.26	0.26
	111341	N80935	Hs.22483	ESTs	1.57	0.52
	111510	R07856	Hs.16355	ESTs	3.96	1
	111737	R25410	Hs.9218	ESTs	0.97	0.24
70	113195	T57112		***yc20g11.s1 Stratagene lung (#937210)	1.22	0.35
	113238	T62979	Hs.189813	ESTs	2.27	0.45
	113540	T90496	Hs.16757	ESTs	1.06	0.22
	113552	T90889	Hs.16026	ESTs	1.16	0.42
	113606	T93093	Hs.17125	ESTs	1.48	0.7
75	113695	T98965	Hs.17948	ESTs	1.54	0.28
	113946	W84753	Hs.37896	ESTs	1.79	0.72
	114251	Z39898	Hs.21948	ESTs	1.95	0.25
	114359	Z41589	Hs.153483	ESTs; Moderately similar to H1 chloride	1.42	0.13
	115230	AA278300	Hs.182980	ESTs	2.62	0.42
80	115279	AA279760	Hs.63671	ESTs	1.79	0.91
	115566	AA398083	Hs.43977	ESTs	0.86	0.2
	115965	AA446661	Hs.173233	ESTs	0.79	0.04
	116166	AA461556	Hs.202949	KIAA1102 protein	2.29	0.68
	116279	AA486073	Hs.57362	ESTs	2.27	0.78
	117023	H88157	Hs.41105	ESTs	1.36	0.16

	117209	H99959	Hs.42768	ESTs	1.46	0.48
	118901	N90719	Hs.94445	ESTs	1.51	1
	118981	N93839	Hs.39288	ESTs	1.34	0.48
5	119073	R32894	Hs.45514	v-els avian erythroblastosis virus E26 o	1.14	0.27
	119221	R98105		***yr30g11.s1 Soares fetal liver spleen	1.32	0.63
	119824	W74536	Hs.184	advanced glycosylation end product-speci	1	0.19
	119861	W80715		ESTs; Moderately similar to !!!! ALU SUB	1.83	0.45
	120041	W92775	Hs.59368	ESTs	1.23	0.55
10	120132	Z38839	Hs.125019	ESTs; Highly similar to KIAA0886 protein	0.91	0.37
	120467	AA251579	Hs.187628	ESTs	1.87	1.91
	121314	AA402799	Hs.182538	ESTs	1.3	0.31
	121643	AA417078	Hs.193767	ESTs	2.31	0.68
	121690	AA418074	Hs.110286	ESTs	1.47	0.51
15	122633	AA454080	Hs.34853	inhibitor of DNA binding 4; dominant neg	1.31	0.63
	123978	C20653	Hs.170278	ESTs	1.52	0.32
	124214	H58608	Hs.151323	ESTs	0.93	0.35
	124357	N22401		***yw37g07.s1 Morton Fetal Cochlea Homo	1.29	1
	124438	N40188	Hs.102550	ESTs	1.36	0.7
20	125167	W45560	Hs.102541	ESTs	1.46	0.69
	125174	W51835	Hs.231082	EST	3.07	3.76
	125422	AA903229	Hs.153717	ESTs	1.34	0.3
	125561	AA117667	Hs.22978	ESTs	1.89	0.63
	125831	D60988		***HUM145B09B Clontech human fetal brain	0.94	0.36
25	127002	R35380	Hs.24979	ESTs	3.02	4.06
	127307	AA369367	Hs.126712	ESTs; Weakly similar to pIL2 hypothetica	1.01	0.69
	127609	AA622559	Hs.150318	ESTs	1.21	0.32
	127959	AI302471	Hs.124292	ESTs	2.5	1
	128458	D52193	Hs.56340	ESTs	1.13	0.33
30	128624	AA479209	Hs.102647	ESTs	1.45	0.58
	128789	AA486567	Hs.105695	ESTs	1.1	0.34
	128798	AF014958	Hs.105938	chemokine (C-C motif) receptor-like 2	1.16	0.55
	128952	R51076	Hs.107361	ESTs; Highly similar to Rap2 interacting	2.04	2.4
	129057	X62466	Hs.214742	CDW52 antigen (CAMPATH-1 antigen)	1.77	0.73
35	129210	AA401654	Hs.202949	KIAA1102 protein	1.11	0.36
	129240	W24360	Hs.237868	interleukin 7 receptor	0.91	0.41
	129402	T63781		***yc21g01.s1 Stratagene lung (#937210)	1.36	0.43
	129565	X77777	Hs.198726	vasoactive intestinal peptide receptor 1	0.67	0.08
40	129593	AA487015	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	1.3	0.42
	129626	AA447410	Hs.11712	ESTs; Weakly similar to !!!! ALU SUBFAM1	1.28	0.46
	129699	AA458578	Hs.12017	KIAA0439 protein; homolog of yeast ubliq	1.58	1
	129898	N48595	Hs.13256	ESTs	1.13	0.53
	129958	L20591	Hs.1378	annexin A3	0.81	0.31
45	130273	U59914	Hs.153863	MAD (mothers against decapentaplegic; Dr	0.59	0.22
	130655	N92934	Hs.17409	cysteine-rich protein 1 (intestinal)	1.44	0.76
	130657	T94452	Hs.201591	ESTs	0.96	0.42
	131061	N64328	Hs.22567	ESTs; Moderately similar to HYPOTHETICAL	1.51	0.45
	131066	F09006	Hs.22588	ESTs	0.97	0.37
	131263	R38334	Hs.24950	regulator of G-protein signalling 5	2.34	2.82
50	131589	U52100	Hs.29191	epithelial membrane protein 2	1.2	0.62
	131686	AA157428	Hs.30687	Grb2-associated binder 2	0.95	0.38
	131751	H18335	Hs.31562	ESTs	1.47	0.52
	132430	T23630	Hs.258675	EST	1.86	2.09
55	132476	N67192	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	1.73	0.58
	132836	F09557	Hs.79299	slit (Drosophila) homolog 3	0.91	0.29
	133120	X64559	Hs.65424	telranectin (plasminogen-binding protein	0.82	0.2
	133488	D45370	Hs.74120	adipose specific 2	1.29	0.48
	133565	H57056	Hs.204831	ESTs	2.25	0.57
60	133651	U97105	Hs.173381	dihydropyrimidinase-like 2	1.65	0.62
	133835	AA059489	Hs.76640	ESTs; Highly similar to RGC-32 [R.norveg	1.16	0.34
	133978	W73859	Hs.78061	transcription factor 21	0.79	0.27
	133985	L34657	Hs.78146	platelet/endothelial cell adhesion molec	0.99	0.28
	134299	AA487558	Hs.8135	ESTs	1.02	0.46
	134300	U81984	Hs.166082	endothelial PAS domain protein 1	0.86	0.42
65	134323	AA028976	Hs.8175	Homo sapiens mRNA; cDNA DKFZp564M0763 (f	1.19	0.27
	134343	D50683	Hs.82028	transforming growth factor; beta recepto	1.21	0.67
	134417	D87969	Hs.82921	solute carrier family 35 (CMP-sialic aci	1.28	1
	134561	U76421	Hs.85302	adenosine deaminase; RNA-specific; B1 (h	2.12	0.55
	134624	W67147	Hs.8700	deleted in liver cancer 1	2.35	2.74
70	134696	H88354	Hs.8861	ESTs	1.35	0.33
	134749	L10955	Hs.89485	carbonic anhydrase IV	0.89	0.2
	134786	L06139	Hs.89640	TEK tyrosine kinase; endothelial (venous	0.48	0.21
	134869	T35288	Hs.90421	ESTs; Moderately similar to !!!! ALU SUB	2.14	2.64
	135346	M21056	Hs.992	phospholipase A2; group IB (pancreas)	0.63	0.13
75	100113	D00591	Hs.84746	Chromosome condensation 1	1	2.15
	100147	D13666	Hs.136348	Homo sapiens mRNA for osteoblast specifi	0.5	2
	100280	D42085	Hs.155314	KIAA0095 gene product	1.02	1.39
	100335	D63391	Hs.6793	platelet-activating factor acetylhydrola	1	5.58
	100360	D78335	Hs.75939	Uridine monophosphate kinase	0.91	2.04
80	100372	D79997	Hs.184339	KIAA0175 gene product	0.75	2.03
	100486	HG1112-HT1112		TIGR: ras-like protein TC4	1.09	1.93
	100559	HG2197-HT2267		*collagen, type VII, alpha 1*	0.97	3.6
	100576	HG2290-HT2386		*calcitonin/alpha-CGRP, alt. transcript	1	1
	100668	HG2981-HT3938		*TIGR: CD44 (epican, alt. transcript 12	0.85	1.9
	100906	HG4716-HT5158		Guanosine 5'-Monophosphate Synthase	1.18	2.29
85	100930	HG721-HT4827		*TIGR: placental protein 14, endometrial	1	1.45

	100960	J00124	Hs.117729	keratin 14 (epidermolysis bullosa simple	0.84	2.6
	101031	J05070	Hs.151738	"Matrix metalloproteinase 9 (gelatinase	0.77	1.52
	101111	L08424	Hs.1619	Achaete-scute complex (Drosophila) homol	1	1
5	101124	L10343	Hs.112341	"Protease inhibitor 3, skin-derived (SKA	0.62	2.67
	101175	L18920	Hs.36980	"Melanoma antigen, family A, 2"	1	1
	101204	L24203	Hs.82237	Ataxia-telangiectasia group D-associated	0.74	4.1
	101431	M19888	Hs.1076	Small proline-rich protein 1B (cornifin)	0.85	2.51
	101448	M21389	Hs.195850	keratin 5 (epidermolysis bullosa simplex	0.61	8.83
10	101511	M27826	Hs.267319	Endogenous retroviral protease	1.03	1.13
	101526	M29540	Hs.220529	Carcinoembryonic antigen-related cell ad	1.07	4.61
	101548	M31328	Hs.71642	"Guanine nucleotide binding protein (G p	0.97	1.13
	101625	M57293		"Human parathyroid hormone-related pepti	1	1
	101649	M60047	Hs.1690	Heparin-binding growth factor binding pr	1	2.7
15	101724	M69225	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	1	8.98
	101748	M76482	Hs.1925	Desmoglein 3 (pemphigus vulgaris antigen	1	2.78
	101759	M80244	Hs.184601	"Solute carrier family 7 (cationic amino	1.07	2.45
	101804	M86699	Hs.169840	TTK protein kinase	1	1
	101806	M86757	Hs.112408	S100 calcium-binding protein A7 (psorias	0.74	1.76
20	101809	M86849		"Homo sapiens connexin 26 (GJB2) mRNA, c	1	7
	101845	M93426	Hs.78867	"Protein tyrosine phosphatase, receptor-	1	1
	101851	M94250	Hs.82045	Midkine (neurite growth-promoting factor	1.13	2.6
	102083	U10323	Hs.75117	"Interleukin enhancer binding factor 2,	1.03	1.61
	102154	U17760	Hs.75517	"Laminin, beta 3 (nicein (125kD), kalini	0.94	3.62
25	102193	U20758	Hs.313	secreted phosphoprotein 1 (osteopontin;	0.34	4.59
	102305	U33286	Hs.90073	chromosome segregation 1 (yeast homolog)	1.45	2.97
	102348	U37519	Hs.87539	Aldehyde dehydrogenase 8	0.52	2.25
	102581	U61145	Hs.77256	Enhancer of zeste (Drosophila) homolog 2	0.91	2.46
	102610	U65011	Hs.30743	Preferentially expressed antigen in mela	1	3.88
30	102623	U66083	Hs.37110	"Melanoma antigen, family A, 9 (MAGE-9)"	1	1
	102669	U71207	Hs.29279	Eyes absent (Drosophila) homolog 2	1	1
	102696	U74612	Hs.239	Forkhead box M1	1.06	2.77
	102829	U91618	Hs.80962	Neurotensin	1	1
35	102888	X04741	Hs.76118	Ubiquitin carboxyl-terminal esterase L1	1.13	2.59
	102913	X07696	Hs.80342	keratin 15	0.7	4.72
	102915	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stromolysin	1.15	3.35
	102963	X15943	Hs.37058	"Calcitonin/calcitonin-related polypepti	1	1
	103021	X53587	Hs.85266	"Integrin, beta 4"	1.38	2.34
40	103036	X54925	Hs.83169	Matrix metalloprotease 1 (interstitial c	1	14.93
	103058	X57348	Hs.184510	Stratifin	1.25	4.17
	103060	X57766	Hs.155324	matrix metalloproteinase 11 (stromelysin	1	1.72
	103119	X63629	Hs.2877	"Cadherin 3, P-cadherin (placental)"	1.16	7.38
	103206	X72755	Hs.77367	monokine induced by gamma interferon	0.71	1.48
	103242	X76342	Hs.389	"Alcohol dehydrogenase 7 (class IV), mu	1	1
45	103312	X82693	Hs.3185	"Lymphocyte antigen 6 complex, locus D;	0.92	1.28
	103478	Y07755	Hs.38991	S100 calcium-binding protein A2	1.05	5.81
	103558	Z19574	Hs.2785	keratin 17	0.65	6.68
	103576	Z26317	Hs.2631	Desmoglein 2	0.79	1.73
	103587	Z29083	Hs.82128	5T4 Oncofetal antigen	1	3.93
50	103594	Z31560	Hs.816	"SRY (sex determining region Y)-box 2, p	0.71	7.23
	103768	AA089997		"ESTs, Highly similar to integral membra	0.99	1.8
	104158	AA454908	Hs.8127	KIAA0144 gene product	0.96	1.29
	104558	R56678	Hs.88959	Human DNA sequence from clone 967N21 on	1.23	7.23
	104689	AA010665		ESTs	0.96	2.11
55	104733	AA019498	Hs.23071	ESTs	1.18	1.88
	104906	AA055809	Hs.26802	Protein kinase domains containing protei	1.11	3.15
	104978	AA088458	Hs.19322	ESTs; Weakly similar to !!! ALU SUBFAMI	1.64	2.89
	105012	AA116036	Hs.9329	"Homo sapiens mRNA for fls353, complete	1.19	3.91
	105175	AA186804	Hs.25740	ESTs; Weakly similar to unknown [S.cerev	0.9	4.63
60	105263	AA227926	Hs.6682	ESTs	0.95	2.87
	105298	AA233459	Hs.26369	ESTs	1	1.13
	105312	AA233854	Hs.23348	S-phase kinase-associated protein 2 (p45	1.32	3.01
	105719	AA291644	Hs.36793	Hypothetical protein FLJ23188	1.28	2.31
	105743	AA293300	Hs.9598	ESTs	1	1
65	106012	AA411621	Hs.8895	ESTs; same as BFH6?	0.94	2.04
	106231	AA429571	Hs.38002	KIAA1355 protein	1.04	1.5
	106540	AA454607	Hs.38114	Hypothetical protein FLJ11100	1.26	2.26
	106575	AA456039	Hs.105421	ESTs	1	2
70	106632	AA459897	Hs.11950	GPI-anchored metastasis-associated prote	0.87	1.32
	106727	AA465342	Hs.34045	Hypothetical protein FLJ20764	0.87	1.59
	106906	AA490237	Hs.222024	Transcription factor BMAL2 (cycle-like f	0.61	1.6
	107059	AA608545	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	0.48	2.67
	107104	AA609786	Hs.15243	Nucleolar protein 1 (120kD)	1.01	1.44
	107151	AA621169	Hs.8687	ESTs; procollagen I-N proteinase	0.97	2.89
75	107284	S74039	Hs.291904	Accessory proteins BAP31/BAP29	1.15	3.65
	107901	AA026418	Hs.91539	ESTs	0.72	3.44
	107922	AA028028	Hs.61460	Ig superfamily receptor LNIR precursor	1	2.48
	107932	AA029317	Hs.18878	Hypothetical protein FLJ21620	1	1
	108695	AA121315	Hs.70823	KIAA1077 protein	0.91	3.53
80	108857	AA133250	Hs.62180	ESTs	1	1
	108860	AA133334	Hs.129911	ESTs	0.73	7.3
	108990	AA152296	Hs.72045	ESTs	1	1
	109166	AA179845	Hs.73625	"RAB6 interacting, kinesin-like (rabkine	1	4.55
	109424	AA227919	Hs.85962	Hyaluronan synthase 3	1	1.28
85	109665	F05012	Hs.27027	Hypothetical protein DKFZp762H1311	1.42	2
	109970	H09281	Hs.13234	ESTs	1.13	2.16

	110015	H10998	Hs.7164	A disintegrin and metalloproteinase doma	0.84	1.95
	110156	H18957	Hs.4213	ESTs	0.94	1.41
	110561	H59617	Hs.5199	HSPC150 protein similar to ubiquitin-con	0.91	3.18
5	111223	N68921	Hs.34806	ESTs; Weakly similar to neogenin [H.sapi	0.91	3.13
	111345	N89820	Hs.14559	Hypothetical protein FLJ10540	1	1.25
	111876	R38239	Hs.293246	*ESTs, Weakly similar to putative p150 [0.83	1.27
	111902	R39191	Hs.109445	KIAA1020 protein	0.91	0.91
	112244	R51309	Hs.70823	KIAA1077 protein	0.77	3.01
10	112973	T17271		*cDNA FLJ13308 fis, clone OVARC1001436,	1	1
	112989	T23482	Hs.89981	"Diacylglycerol kinase, zeta (104kD)"	0.55	1.03
	113047	T25867	Hs.7549	ESTs	0.87	2
	113095	T40920	Hs.126733	ESTs	1	1
	113531	T90345	Hs.16740	Hypothetical protein FLJ11036	0.42	1.44
15	113970	W86748	Hs.8109	ESTs	1.17	1.73
	114346	Z41450	Hs.130489	*ATPase, aminophospholipid transporter-I	0.86	0.82
	114407	AA010188	Hs.103305	ESTs	0.8	1.88
	114471	AA028074	Hs.104613	RP42 homolog	1.06	1.34
	114509	AA043551	Hs.101799	KIAA1350 protein	1.82	2.32
20	115060	AA253214	Hs.198249	*Gap junction protein, beta 5 (connexin	0.79	1.49
	115091	AA255900	Hs.184523	KIAA0965 protein	0.72	1.92
	115123	AA256642	Hs.236894	*ESTs, High sim to LRP1_hu low density l	0.59	1.97
	115291	AA279943	Hs.122579	ESTs	1	1.25
	115506	AA292537	Hs.45207	Hypothetical protein KIAA1335	1.15	1.48
25	115522	AA331393	Hs.47378	ESTs	0.5	3.29
	115536	AA347193	Hs.62180	ESTs	1	1
	115697	AA411502	Hs.63325	Homo sapiens type II membrane serine pro	1	6.53
	115909	AA436666	Hs.59761	ESTs	1	6.98
	115978	AA447522	Hs.69517	Differentially expressed in Fanconi anem	1	2.31
30	116028	AA452112	Hs.42644	thioredoxin-like	0.99	1.68
	116107	AA456968	Hs.92030	ESTs	1.14	1.8
	116134	AA460246	Hs.50441	CGI-04 protein	1.11	1.86
	116157	AA461063	Hs.44298	Hypothetical protein	0.99	1.9
	116158	AA461187	Hs.61762	Hypoxia-inducible protein 2	0.44	0.86
35	116335	AA495830	Hs.87013	*Homo sapiens cDNA FLJ10238 fis, clone H	0.62	3.89
	116483	C14092	Hs.76118	Ubiquitin carboxyl-terminal esterase L1	1.04	2.36
	117320	N23239	Hs.211092	LUNX protein; PLUNC(palate lung & nasal	0.51	0.64
	117557	N33920	Hs.44532	Diubiquitin	1.11	2.63
	117693	N40939	Hs.112110	PTD007 protein	0.98	1.79
40	117881	N50073	Hs.260622	Butyrate-induced transcript 1	1	1.43
	118368	N64339	Hs.48956	ESTs	0.67	2.86
	118566	N68558	Hs.42824	Hypothetical protein FLJ10718	1.21	0.83
	118695	N71781	Hs.50081	KIAA1199 see CVA7.doc	0.88	1.63
	119780	W72967	Hs.191381	ESTs; Weakly similar to hypothetical pro	1	1
45	119845	W79920	Hs.58561	G protein-coupled receptor 87	1	1
	120102	W95428	Hs.132927	*ESTs, Moderately similar to p53 regulat	1	1
	120104	W95477	Hs.180479	ESTs	0.69	3.07
	120486	AA253400	Hs.137569	Tumor protein 63 kDa with strong homolog	1.08	12.05
50	120859	AA350158	Hs.1619	Achaete-scute complex (Drosophila) homol	1	1
	120880	AA360240	Hs.97019	EST	1	1
	120948	AA397822	Hs.104650	Hypothetical protein FLJ10292	1.04	2.15
	120983	AA398209	Hs.97587	EST	1	1
	121362	AA405500	Hs.97932	Chondromodulin I precursor	1	1
	121369	AA405657	Hs.128791	CGI-09 protein	1	1.8
55	121791	AA423978	Hs.293317	*ESTs, Weakly similar to JM27 [H.sapiens	1	1
	123005	AA479726	Hs.105577	ESTs	1	1
	123044	AA481549	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro	0.95	1.88
	123160	AA488687	Hs.284235	ESTs	1.59	4.98
60	123479	AA599469	Hs.135056	clone RP5-850E9 on chromosome 20	1.19	1.64
	123571	AA608956	Hs.112619	*ESTs, Weakly similar to PQ0109 Purkinje	1.03	1.14
	123829	AA620697	Hs.112208	XAGE-1 protein	1.39	2.2
	124006	D60302	Hs.108977	ESTs	1	4.85
	124059	F13673	Hs.99769	ESTs	1.49	8.62
	124960	T15386	Hs.194766	Seizure related gene 6 (mouse)-like	0.76	0.77
65	125218	W73561	Hs.110024	NADH:ubiquinone oxidoreductase MLRQ subu	1.33	1.77
	125453	R06041	Hs.18048	*Melanoma antigen, family A, 10"	0.8	1.42
	125759	AA425587	Hs.82226	Glycoprotein (transmembrane) nmb	1.52	2.26
	125972	AA434562	Hs.35406	*ESTs, Highly similar to unnamed protein	1.05	2.48
	125994	H55782	Hs.270799	EST	1	1.95
70	126395	N70192	Hs.278956	Hypothetical protein FLJ12929	1	1.35
	126645	AI167942	Hs.61635	STEAP1 (Homo sapiens BAC clone RG041D11	1	2.23
	127221	AI354332	Hs.72365	ESTs	0.73	3.27
	127479	AA513722	Hs.179729	collagen; type X; alpha 1 (Schmid metaph	0.51	1.94
	128192	AI204246		KIAA1085 protein	1.8	3.16
75	128610	L38608	Hs.10247	activated leucocyte cell adhesion molecu	0.89	0.97
	128777	U46006	Hs.10526	Cysteine and glycine-rich protein 2	1	1
	128924	AA234962	Hs.26557	Plakophilin 3	1.3	2.97
	129041	H58873	Hs.169902	*Solute carrier family 2 (facilitated gl	0.84	2.04
	129099	H50398	Hs.108660	*ATP-binding cassette, sub-family C (CFT	0.87	1.04
80	129404	AA172056	Hs.111128	ESTs	1	1
	129466	L42583		*Genbank Homo sapiens keratin 16 isoform	0.72	12.67
	129605	S72493	Hs.115947	Keratin 16 (focal non-epidermolytic palm	0.92	1.5
	129628	U26727	Hs.1174	*Cyclin-dependent kinase inhibitor 2A (m	0.85	1.93
	130023	X13461	Hs.239600	Calmodulin-like 3	0.84	1.22
	130080	X14850	Hs.147097	*H2A histone family, member X"	0.98	1.96
85	130385	AA126474	Hs.155223	stanniocalcin 2	1	1

	130410	V01514	Hs.155421	Alpha-fetoprotein	0.63	0.63
	130441	U35835	Hs.301387	"Human DNA-PK mRNA, partial cds"	1.15	3.65
	130482	L32866	Hs.1578	Baculoviral IAP repeat-containing 5 (sur	1	1.88
5	130553	AA430032	Hs.252587	Pituitary tumor-transforming 1	0.92	1.96
	130577	M35410	Hs.162	Insulin-like growth factor binding prote	1.17	4.7
	130627	L23808	Hs.1695	Matrix metalloproteinase 12 (macrophage	0.69	4.05
	130800	AA223386	Hs.19574	ESTs; Weakly similar to katanin p80 subu	1.13	2.41
	130939	AA598689	Hs.21400	ESTs	0.8	0.89
10	131046	X02530	Hs.2248	INTERFERON-GAMMA INDUCED PROTEIN PRECURS	0.8	1.15
	131244	D38076	Hs.24763	RAN binding protein 1	1.13	1.85
	131877	J04088	Hs.156346	Topoisomerase (DNA) II alpha (170kD)	1	1
	131927	AA461549	Hs.34780	"Doublecortin; lissencephaly, X-linked (0.81	0.62
	131965	W90146	Hs.35962	ESTs	0.74	3.27
15	131978	D80008	Hs.36232	KIAA0186 gene product	1	1
	132354	L05187	Hs.211913	Small proline-rich protein 1A	0.69	1.43
	132543	AA417152	Hs.5101	ESTs; Highly similar to protein regulati	0.79	4.27
	132632	N59764	Hs.5398	guanine-monophosphate synthetase	1	1.08
	132653	U31201	Hs.54451	"laminin gamma2 chain gene (LAMC2), exon	1	1
20	132659	Z75190	Hs.54481	"Low density lipoprotein receptor-relate	0.89	0.89
	132710	W93726	Hs.55279	"Serine (or cysteine) proteinase inhibit	0.64	4.41
	132758	W52432	Hs.56105	"ESTs, Weakly similar to WDNM RAT WDNM1	1.55	2.08
	132767	L05188	Hs.231622	Small proline-rich protein 2B	0.83	1.66
	132816	M74542	Hs.575	Aldehyde dehydrogenase 3	0.55	0.55
25	132990	AA458761	Hs.18387	transcription factor AP-2 alpha (activat	1	3.53
	133070	U69611	Hs.64311	"A disintegrin and metalloproteinase dom	1.16	2
	133282	U52960	Hs.286145	"SRB7 (suppressor of RNA polymerase B, y	1	2.7
	133317	AA215299	Hs.70830	U6 snRNA-associated Sm-like protein LSm7	0.95	1.42
	133370	AA156897	Hs.72157	Homo sapiens mRNA; cDNA DKFZp564I1922	1.12	2.55
30	133391	X57579	Hs.727	H.sapiens activin beta-A subunit (exon 2	1.65	1.76
	133832	H03387	Hs.241305	estrogen-responsive B box protein (EBBP)	1.02	1.39
	134032	Z81326	Hs.78589	"Serine (or cysteine) proteinase inhibit	1	1
	134168	AA398908	Hs.181634	"Homo sapiens cDNA: FLJ23602 fis, clone	0.95	1.53
	134218	AA227480	Hs.80205	Pim-2 oncogene	1.36	2.48
35	134405	R67275	Hs.82772	""collagen, type XI, alpha 1""	0.76	2.86
	134453	X70683	Hs.83484	SRY (sex determining region Y)-box 4	1.89	3.78
	134470	X54942	Hs.83758	CDC28 protein kinase 2	1.82	4.11
	134645	U87459	Hs.167379	"Cancer/testis antigen (NY-ESO-1, CTAG1,	0.82	0.83
	134781	M17183	Hs.89626	Parathyroid hormone-like hormone	1	1
40	135002	U19147	Hs.272484	G antigen 6	1	1
	100040	M97935		AFFX control: STAT1	0.92	1.25
	101201	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin;	2.92	8.5
	101664	M60752	Hs.121017	H2A histone family; member A	1	1
	102025	U03911	Hs.78934	mutS (E. coli) homolog 2 (colon cancer;	0.8	1.61
45	102031	U04898	Hs.2156	RAR-related orphan receptor A	1	1
	102221	U24576		LIM domain only 4	1	1
	102270	U30255	Hs.75688	phosphogluconate dehydrogenase	1.08	1.43
	102339	U37022	Hs.95577	cyclin-dependent kinase 4	0.88	1.32
	102391	U41668	Hs.77494	deoxyguanosine kinase	1.07	1.58
50	103000	X51956	Hs.146580	enolase 2; (gamma; neuronal)	0.91	1.49
	103395	X94754	Hs.119503	methionine-tRNA synthetase	0.89	1.32
	105638	AA281599	Hs.20418	Homo sapiens mRNA for histone H2B; c	0.91	1.25
	105726	AA292328	Hs.9754	activating transcription factor 5	0.94	1.48
	114841	AA234722	Hs.55408	ESTs; Moderately similar to CALCIUM-DEPE	0.78	1.56
55	115206	AA262491	Hs.186572	ESTs	1	1
	115906	AA436616	Hs.82302	ESTs	0.74	2.52
	119132	R49046	Hs.107911	ATP-binding cassette; sub-family B (MDR/	1.1	1.51
	124163	H30539	Hs.189838	ESTs	1	1
	126487	AA482505	Hs.184601	solute carrier family 7 (cationic amino	1.01	1.46
60	127141	AA307960	Hs.75478	KIAA0956 protein	0.85	1.4
	128034	AA905754	Hs.75103	tyrosine 3-monooxygenase/tryptophan 5-mo	1	1.18
	128609	AA234365	Hs.102456	survival of motor neuron protein Interac	1	1.5
	128895	R37753	Hs.106985	ESTs	1.7	2
	130199	Z48579	Hs.172028	a disintegrin and metalloprotease domain	1	1
65	130524	U89995	Hs.159234	forkhead box E1	1	1
	133000	U24152	Hs.62402	p21/Cdc42/Rac1-activated kinase 1 (yeast	1	1
	133658	M25756	Hs.75426	secretogranin II (chromogranin C)	1	1
	135047	AA460466	Hs.93597	ESTs	1	1
70	100053	M27830		AFFX control: 28S ribosomal RNA	0.88	1.53
	100114	D00596	Hs.82962	thymidylate synthetase	0.68	1.86
	100128	D11094	Hs.61153	proteasome (prosome; macropain) 26S subu	1.29	2.03
	100154	D14657	Hs.81892	KIAA0101 gene product	0.71	4.26
	100161	D14694	Hs.77329	phosphatidylserine synthase 1	1.02	1.56
	100168	D14874	Hs.394	adrenomedullin	0.46	1.17
75	100187	D17793	Hs.78183	aldo-keto reductase family 1; member C3	1	1
	100188	D21063	Hs.57101	minichromosome maintenance deficient (S.	0.97	1.4
	100217	D26600	Hs.89545	proteasome (prosome; macropain) subunit;	1.13	1.9
	100220	D28364		""Human mRNA for annexin II, 5'UTR (seq	1.11	1.53
	100287	D43950	Hs.1600	chaperonin containing TCP1; subunit 5 (e	1.13	2.09
80	100297	D49489	Hs.182429	protein disulfide isomerase-related prot	0.92	1.78
	100330	D55716	Hs.77152	minichromosome maintenance deficient (S.	1.07	1.61
	100355	D78129		""Homo sapiens mRNA for squalene epoxid	0.96	1.87
	100364	D78586	Hs.154868	carbamoyl-phosphate synthetase 2; aspart	1.49	2.46
	100368	D79987	Hs.153479	extra spindle poles; S. cerevisiae; homo	0.59	1.32
	100398	D84557	Hs.155462	minichromosome maintenance deficient (mi	1.08	1.9
85	100438	D87448	Hs.91417	topoisomerase (DNA) II binding protein	1	2.15

	100455	D87953	Hs.75789	N-myc downstream regulated	0.91	1.48
	100491	HG1153-HT1153		Nucleoside Diphosphate Kinase Nm23-H2s	0.99	1.41
	100518	HG174-HT174		Desmoplakin I	1.28	3.17
5	100528	HG1828-HT1857		***Nexin, Glia-Derived***	0.68	1.9
	100661	HG2874-HT3018		Ribosomal Protein L39 Homolog	1.1	5.44
	100667	HG2981-HT3127		***Epican, Alt. Splice 11***	0.8	1.97
	100830	HG4074-HT4344		Rad2	1.01	2.12
	101061	K03515	Hs.944	glucose phosphate isomerase	0.91	1.79
10	101131	L10838	Hs.167460	splicing factor; arginine/serine-rich 3	1.23	1.87
	101162	L14595	Hs.174203	solute carrier family 1 (glutamate/neutral)	1.35	2.73
	101181	L19686	Hs.73798	macrophage migration inhibitory factor (1.03	1.78
	101183	L19779	Hs.795	H2A histone family; member O	0.57	1.3
	101216	L25876	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	0.7	2.2
15	101228	L27706	Hs.82916	chaperonin containing TCP1; subunit 6A (0.99	1.99
	101233	L29008	Hs.878	sorbitol dehydrogenase	0.82	2.11
	101247	L33801	Hs.78802	glycogen synthase kinase 3 beta	1.2	1.91
	101332	L47276		***Homo sapiens (cell line HL-6) alpha t	0.69	2.78
	101342	L76191	Hs.182018	interleukin-1 receptor-associated kinase	1.04	1.84
20	101396	M15796	Hs.78996	proliferating cell nuclear antigen	0.95	3.55
	101423	M18391	Hs.89839	EphA1	1	1.5
	101445	M21259	Hs.1066	small nuclear ribonucleoprotein polypept	1.21	1.96
	101505	M27396	Hs.75692	asparagine synthetase	0.93	1.6
	101525	M29536	Hs.12163	eukaryotic translation initiation factor	1.19	1.93
25	101535	M30448	Hs.251669	casein kinase 2; beta polypeptide	0.96	1.42
	101607	M38690	Hs.1244	CD9 antigen (p24)	1.11	1.25
	101624	M55998		***Human alpha-1 collagen type I gene, 3	1.17	1.98
	101758	M77836	Hs.79217	pyrroline-5-carboxylate reductase 1	1.77	3.45
	101839	M93036	Hs.692	membrane component; chromosomal 4; surfa	0.71	1.45
30	101853	M94362	Hs.76084	lamin B2	0.84	1.19
	101977	S83364		***putative Rab5-interacting protein [c]	0.89	1.9
	101992	U01038	Hs.77597	polo (Drosophila)-like kinase	0.66	1.46
	102009	U02680	Hs.82643	protein tyrosine kinase 9	1.23	3.35
	102012	U03057	Hs.118400	singed (Drosophila)-like (sea urchin fas	0.85	1.88
35	102039	U05861	Hs.201967	aldo-keto reductase family 1; member C1	0.93	2.32
	102123	U14518	Hs.1594	centromere protein A (17kD)	1	4.28
	102130	U15009	Hs.1575	small nuclear ribonucleoprotein D3 polyp	0.89	1.42
	102148	U16954	Hs.75823	ALL1-fused gene from chromosome 1q	0.8	2.95
	102210	U23028	Hs.2437	eukaryotic translation initiation factor	1.01	1.34
40	102220	U24389	Hs.65436	lysyl oxidase-like 1	1.15	2.34
	102260	U28386	Hs.159557	karyopherin alpha 2 (RAG cohort 1; impor	1.14	2.69
	102330	U35451	Hs.77254	chromobox homolog 1 (Drosophila HP1 beta	1.05	1.7
	102423	U44754	Hs.179312	small nuclear RNA activating complex; po	1.14	2.99
	102455	U48705	Hs.75562	discoidin domain receptor family; member	1.05	2.01
45	102499	U51478	Hs.76941	ATPase; Na+/K+ transporting; beta 3 poly	1.27	1.92
	102522	U53347	Hs.183556	solute carrier family 1 (neutral amino a	0.84	1.31
	102590	U62136		***Homo sapiens enterocyte differentiati	1.11	1.6
	102676	U72514	Hs.12045	putative protein	1.04	2.17
	102687	U73379	Hs.93002	ubiquitin carrier protein E2-C	0.86	2.28
50	102704	U76638	Hs.54089	BRCA1 associated RING domain 1	1.12	1.63
	102781	U83843		***Human HIV-1 Nef interacting protein (0.9	1.39
	102784	U85658	Hs.61796	transcription factor AP-2 gamma (activat	0.98	2.16
	102827	U91327	Hs.6456	chaperonin containing TCP1; subunit 2 (b	0.96	1.62
	102935	X13482	Hs.80506	small nuclear ribonucleoprotein polypept	1.21	4.2
55	102972	X16662	Hs.87268	annexin A8	1.25	2.32
	102983	X17620	Hs.118638	non-metastatic cells 1; protein (NM23A)	1.03	1.83
	103023	X53793	Hs.117950	multifunctional polypeptide similar to S	1.58	5.44
	103038	X54941	Hs.77550	CDC28 protein kinase 1	1.32	3.79
	103075	X59543	Hs.2934	ribonucleotide reductase M1 polypeptide	1.11	2.58
60	103168	X68314	Hs.2704	glutathione peroxidase 2 (gastrointestin	0.75	3.05
	103185	X69910	Hs.74368	transmembrane protein (63kD); endoplasm	1.01	1.97
	103212	X73874	Hs.2393	phosphorylase kinase; alpha 1 (muscle)	0.95	1.72
	103223	X74801	Hs.1708	chaperonin containing TCP1; subunit 3 (g	0.97	1.77
	103260	X78416	Hs.3155	casein; alpha	1	1
65	103262	X78565	Hs.204133	hexabrachion (tenascin C; cytactin)	1.23	3.09
	103330	X85373	Hs.77496	small nuclear ribonucleoprotein polypept	1.12	2.25
	103364	X90872	Hs.75854	SULT1C sulfotransferase	2.85	4.62
	103375	X91868	Hs.54416	sine oculis homeobox (Drosophila) homolo	1	2.48
	103391	X94453	Hs.114366	pyrroline-5-carboxylate synthetase (glut	1	1.53
70	103404	X95586	Hs.78596	proteasome (prosome; macropain) subunit;	0.92	1.53
	103437	X98260	Hs.82254	M-phase phosphoprotein 11	0.92	1.54
	103448	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	0.55	0.96
	103605	Z35402	Hs.194657	cadherin 1; E-cadherin (epithelial)	1.32	2.51
	103646	Z68228	Hs.2340	junction plakoglobin	0.88	1.28
75	103658	Z74615	Hs.172928	collagen; type I; alpha 1	1.06	2.98
	103774	AA092898	Hs.92918	ESTs; Weakly similar to R07G3.8 [C.elega	1.88	4.66
	104261	AF008442	Hs.5409	RNA polymerase I subunit	0.87	2.17
	104276	C02193	Hs.85222	ESTs; Weakly similar to R27090_2 [H.sapi	1.4	2.49
	104289	C16281	Hs.75478	KIAA0956 protein	1.15	1.68
80	104434	L02870	Hs.1640	collagen; type VII; alpha 1 (epidermolys	1.04	1.49
	104453	M19169	Hs.123114	cystatin SN	0.38	0.76
	104611	R98280	Hs.125845	ribose-5-phosphate-3-epimerase	1.08	2.25
	104758	AA024661	Hs.7010	ESTs; Weakly similar to ACYL-COA DEHYDRO	1.14	1.65
	105114	AA156532	Hs.11801	adenosine A2b receptor pseudogene	0.91	1.38
85	105132	AA159501	Hs.247280	HBV associated factor	1.08	1.7
	105174	AA186613	Hs.34744	ESTs	0.95	2.05

	105280	AA232215	Hs.14600	ESTs	1	1.4
	105344	AA235303	Hs.8645	ESTs	0.72	2.02
	105516	AA257971	Hs.21214	ESTs	1.35	3.56
5	105621	AA280865	Hs.6375	Homo sapiens mRNA; cDNA DKFZp564K0222 (f	1.23	1.82
	105698	AA287393	Hs.15202	ESTs; Weakly similar to oligodendrocyte-	0.98	1.28
	105705	AA290767	Hs.101282	Homo sapiens mRNA; cDNA DKFZp434B102 (fr	0.92	1.32
	105724	AA292098	Hs.22934	ESTs; Weakly similar to ZINC FINGER PROT	0.99	1.41
	105782	AA350215	Hs.21580	ESTs	1	1
10	105799	AA372018	Hs.24743	ESTs	1.08	1.78
	105807	AA393803	Hs.16869	ESTs; Moderately similar to COLLAGEN ALP	0.95	1.34
	105891	AA400768	Hs.26662	ESTs; Weakly similar to tumor necrosis f	0.87	2.25
	105936	AA404338		ESTs	1.14	1.46
	106069	AA417741	Hs.29899	ESTs; Weakly similar to ZINC FINGER PROT	1	1
	106103	AA421104	Hs.12094	ESTs	1.04	1.44
15	106140	AA424524	Hs.14912	KIAA0286 protein	1.23	2.11
	106149	AA424881	Hs.256301	ESTs	0.83	1.48
	106154	AA425304	Hs.6994	ESTs	0.77	2.05
	106182	AA426609	Hs.10862	ESTs	0.74	2.23
20	106220	AA428582	Hs.32196	ESTs; Moderately similar to metargidin p	0.97	1.99
	106228	AA429290	Hs.17719	ESTs	0.99	1.54
	106318	AA436570	Hs.9605	pre-mRNA cleavage factor Im (25kD)	0.95	2.09
	106341	AA441798	Hs.5243	ESTs; Moderately similar to pL2 hypothe	0.98	2.66
	106432	AA448850	Hs.17138	ESTs	0.95	1.93
25	106474	AA450212	Hs.42484	Homo sapiens mRNA; cDNA DKFZp564C053 (fr	1	1
	106483	AA451676	Hs.30299	IGF-II mRNA-binding protein 2	1.4	2.29
	106599	AA457235	Hs.12842	ESTs; Moderately similar to non-function	1	1.82
	106611	AA458904	Hs.26267	ESTs; Weakly similar to torsinA [H.sapie	1.49	2.78
	106654	AA460449	Hs.3784	ESTs; Highly similar to phosphoserine am	1	1.4
30	107076	AA609145	Hs.21143	ESTs; Weakly similar to fos39554_1 [H.sa	1.11	1.49
	107115	AA610108	Hs.27693	ESTs; Highly similar to CGI-124 protein	1	1.03
	107129	AA620553	Hs.4756	flap structure-specific endonuclease 1	1.13	3.63
	107159	AA621340	Hs.10600	ESTs; Weakly similar to ORF YKR081c [S.c	1.05	2.09
	107444	W28391	Hs.5181	proliferation-associated 2G4; 38kD	1.18	1.9
35	107481	W58247	Hs.27437	Homo sapiens kinesin superfamily motor K	0.99	2.74
	107516	X56597	Hs.99853	fibrillarin	0.94	1.77
	107529	Y12065	Hs.5092	nucleolar protein (KKE/D repeat)	1.05	2.29
	107531	Y13936	Hs.17883	protein phosphatase 1G (formerly 2C); ma	1.06	1.62
	107801	AA019433	Hs.173100	ESTs	1.03	1.4
40	107957	AA031948	Hs.57548	ESTs	0.95	1.46
	108565	AA085342	Hs.1526	ATPase; Ca++ transporting; cardiac muscl	0.59	1.35
	108780	AA128561	Hs.117938	collagen; type XVII; alpha 1	1	7.63
	108828	AA131584	Hs.71435	DKFZP564O0463 protein	1.33	2.56
	109060	AA160879	Hs.241551	chloride channel; calcium activated; fam	0.67	1.42
45	109112	AA169379	Hs.72865	ESTs	1.03	2.31
	109344	AA213696	Hs.86559	poly(A)-binding protein-like 1	0.97	1.55
	109412	AA227145	Hs.209473	ESTs; Weakly similar to REGULATOR OF MIT	0.76	1.87
	110780	N23174	Hs.22891	solute carrier family 7 (cationic amino	0.9	0.95
	110958	N50550	Hs.24587	signal transduction protein (SH3 contain	1.17	2.26
50	111018	N54067	Hs.3628	mitogen-activated protein kinase kinase	1.21	1.85
	111337	N79612	Hs.16607	ESTs; Highly similar to Myosin heavy cha	1	1.45
	112305	R54822	Hs.26244	ESTs	1	1
	112401	R61279	Hs.237536	ESTs; Weakly similar to F25B5.3 [C.elega	1.24	1.64
	112853	T02843	Hs.4351	EST	1.56	1.96
55	112869	T03313	Hs.4747	dyskeratosis congenita 1; dyskerin	1.03	1.57
	112992	T23513	Hs.7147	ESTs	1	1
	113048	T25895	Hs.184008	ESTs; Weakly similar to RNA-binding prot	1.37	2.26
	113063	T32438	Hs.5027	ESTs	1	1
	113179	T55182	Hs.152571	ESTs; Highly similar to IGF-II mRNA-bind	1.33	2.7
60	113573	T91166	Hs.15990	ESTs	0.76	1.47
	113811	W44928	Hs.4878	ESTs	0.79	1.51
	114086	Z38266	Hs.12770	Homo sapiens PAC clone DJ0777O23 from 7p	0.9	1.34
	114587	AA070827	Hs.180320	ESTs; Weakly similar to GOLGI 4-TRANSMEM	1.02	1.76
	114846	AA234929	Hs.44343	ESTs	1.32	2.36
65	114964	AA243873	Hs.82184	ring finger protein 3	1.1	1.84
	115047	AA252627	Hs.22554	homeo box B5	1.01	2.36
	115166	AA258409	Hs.198907	myelin protein zero-like 1	1.05	2.31
	115167	AA258421	Hs.43728	hypothetical protein	1.52	2.52
	115239	AA278650	Hs.73291	ESTs; Weakly similar to similar to the b	0.7	2.57
70	115278	AA279757	Hs.67466	ESTs; Weakly similar to BACN32G11.d [D.m	1.14	2.12
	115652	AA405098	Hs.38178	ESTs	0.82	4.67
	115875	AA433943	Hs.43946	ESTs; Weakly similar to Weak similarity	1.2	1.98
	116004	AA449122	Hs.76086	ESTs; Highly similar to small zinc finge	0.96	1.31
	116121	AA459254	Hs.48855	ESTs	0.97	1.55
75	116129	AA459956	Hs.49163	ESTs; Highly similar to putative ribonuc	1.08	2.73
	116190	AA464963	Hs.67776	ESTs	0.8	1.57
	116312	AA490494	Hs.65403	ESTs	1.37	2.65
	116732	F13779	Hs.165909	ESTs	0.92	1.8
	117602	N35020	Hs.44685	ESTs; Weakly similar to GOLIATH PROTEIN	1.15	1.84
80	117950	N51394	Hs.75478	KIAA0956 protein	1.04	2.36
	117992	N52000	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586B0222 (f	0.62	1.29
	118785	N75386	Hs.111867	GLI-Kruppel family member GLI2	1	1
	119717	W69134	Hs.57987	ESTs	1	1.4
	119814	W74069	Hs.58350	ESTs	0.78	1.77
	120128	Z38499	Hs.91448	MKP-1 like protein tyrosine phosphatase	0.86	1.46
85	120242	Z98443	Hs.86366	ESTs	0.83	2.01

	120483	AA252994	Hs.1578	apoptosis inhibitor 4 (survivin)	0.74	1.64
	121054	AA398604	Hs.97387	ESTs	1.05	1.93
	121326	AA404246	Hs.97031	ESTs; Weakly similar to Similar to phyto	0.98	1.3
5	121376	AA405699	Hs.166232	ESTs; Moderately similar to SODIUM- AND	0.91	1.83
	121457	AA411448	Hs.208985	ESTs	0.91	1.59
	121780	AA422086	Hs.124660	ESTs	0.46	0.55
	121781	AA422150	Hs.98370	cytochrome P540 family member predicted	1.07	1.54
	121844	AA425732	Hs.98485	gap junction protein; beta 2; 26kD (conn	0.94	1.4
10	122059	AA431737	Hs.98749	EST	1.93	2.33
	122338	AA443311	Hs.98998	ESTs	1	1
	122354	AA443772	Hs.186692	ESTs	0.88	1.39
	122591	AA453265	Hs.99311	ESTs; Weakly similar to MRJ [H.sapiens]	2.28	2.93
	122790	AA460156	Hs.99556	ESTs	0.88	1.3
15	123398	AA521265	Hs.105514	ESTs	1	1.93
	123518	AA608531	Hs.170313	ESTs	1	1
	123673	AA609471	Hs.112712	ESTs	1	1.15
	124000	D57317	Hs.74861	activated RNA polymerase II transcriptio	0.74	1.12
	124367	N24006	Hs.99348	distal-less homeo box 5	0.67	1.1
20	124447	N48000	Hs.140945	Homo sapiens mRNA; cDNA DKFZp586L141 (fr	1.19	1.7
	125756	W25498	Hs.81634	ATP synthase; H+ transporting; mitochond	0.93	1.59
	125769	A1382972	Hs.82128	5T4 oncofetal trophoblast glycoprotein	1.65	6.76
	125852	H09290	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	0.72	2.26
	125924	AA526849	Hs.82109	syndecan 1	1.22	2.25
25	126037	M85772	Hs.6066	KIAA1112 protein	1.36	1.63
	126214	N29455	Hs.74316	desmoplakin (DPI; DPII)	1.93	3.55
	126414	N78770	Hs.223439	ESTs	1.21	1.66
	126737	AA488132	Hs.62741	ESTs	1	1
	126743	AA179253	Hs.172182	poly(A)-binding protein; cytoplasmic 1	1.3	2.16
30	126926	AA179546	Hs.832	ESTs; Highly similar to INTEGRIN BETA-8	2.53	2.8
	127432	AA501734	Hs.170311	heterogeneous nuclear ribonucleoprotein	1.57	2.12
	128218	H02682	Hs.99189	ESTs; Moderately similar to recombination	1.24	2.09
	128527	M31523	Hs.101047	transcription factor 3 (E2A immunoglobul	1.08	1.78
	128568	X60673	Hs.247568	adenylate kinase 3	1.23	3.48
35	128584	M11433	Hs.101850	retinol-binding protein 1; cellular	0.87	2.42
	128628	C14037	Hs.251978	EST	1.22	1.9
	128691	W27939	Hs.103834	ESTs	1.1	1.73
	128714	V00599	Hs.179661	Homo sapiens clone 24703 beta-tubulin mR	0.92	1.17
40	128733	AA328993	Hs.104558	ESTs	1.34	1.94
	128781	X85372	Hs.105465	small nuclear ribonucleoprotein polypept	0.9	1.34
	129052	AA496297	Hs.182740	ribosomal protein S11	2.59	3.19
	129095	L12350	Hs.108623	thrombospondin 2	1.04	3.2
	129241	AA435665	Hs.109706	ESTs; Moderately similar to HN1 [M.muscu	0.95	1.61
	129665	M88458	Hs.118778	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	1.28	2.63
45	129703	AA401348	Hs.179999	ESTs	0.97	1.63
	129720	AA476582	Hs.12152	ESTs; Moderately similar to SIGNAL RECOG	1.09	1.79
	129850	N20593	Hs.56845	GDP dissociation inhibitor 2	0.74	1.68
	129896	AA043021	Hs.13225	UDP-Gal:betaGlcNAc beta 1,4- galactosylt	1.43	4.19
	130069	AA055896	Hs.146428	collagen; type V; alpha 1	1.17	1.98
50	130405	H88359	Hs.155396	nuclear factor (erythroid-derived 2)-lik	1.26	1.79
	130541	X05608	Hs.211584	neurofilament; light polypeptide (68kD)	1	1
	130599	M91670	Hs.174070	ubiquitin carrier protein	1.07	1.66
	130867	J04093	Hs.2056	UDP glycosyltransferase 1	1	4.8
	131009	AA063596	Hs.22142	ESTs; Weakly similar to NADH-CYTOCHROME	0.93	1.05
55	131028	U20240	Hs.2227	CCAAT/enhancer binding protein (C/EBP);	1	1.23
	131083	U66661	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	1.1	1.8
	131091	T35341	Hs.22880	ESTs; Highly similar to dipeptidyl pepti	1.28	1.98
	131144	C14412	Hs.23528	ESTs; Highly similar to HSPC038 protein	1.43	2.06
	131148	C00038	Hs.23579	ESTs	0.88	3.38
60	131164	Y00503	Hs.182265	keratin 19	1.19	2.77
	131185	M25753	Hs.23960	cyclin B1	0.86	3.84
	131219	C00476	Hs.24395	small inducible cytokine subfamily B (Cy	0.66	2.96
	131454	AA455896	Hs.2699	glypican 1	0.99	1.54
	131687	L11066	Hs.3069	heat shock 70kD protein 9B (mortalin-2)	1	1.18
65	131689	AA599653	Hs.30696	transcription factor-like 5 (basic helix	1	1.95
	131692	D50914	Hs.30736	KIAA0124 protein	1.55	2.39
	131786	AA135554	Hs.32125	ESTs	1	1.33
	131843	AA195893	Hs.184062	ESTs; Moderately similar to putative Rab	0.83	1.63
	131860	U02082	Hs.334	Oncogene TIM	1.08	2.2
70	131884	H90124	Hs.3463	ribosomal protein S23	1.23	1.24
	131903	AA481723	Hs.3436	deleted in oral cancer (mouse; homolog)	0.91	1.18
	131945	M87339	Hs.35120	replication factor C (activator 1) 4 (37	1	2.8
	131958	AA093998	Hs.3566	ESTs; Highly similar to phosphorylation	0.87	1.36
	131964	W42508	Hs.3593	ESTs	1	1.25
75	132001	J00277	Hs.37003	v-Ha-ras Harvey rat sarcoma viral onco	1.12	1.43
	132040	AA146843	Hs.172894	BH3 interacting domain death agonist	1	1.55
	132065	D82226	Hs.211594	proteasome (prosome; macropain) 26S subu	0.89	1.27
	132109	AA599801	Hs.40098	ESTs	1	1.05
	132112	AA150661	Hs.40154	jumonji (mouse) homolog	0.99	1.44
80	132123	AA447123	Hs.250705	ESTs	1.06	2.46
	132162	H89551	Hs.41241	ESTs	1.08	2.46
	132180	AA405569	Hs.418	fibroblast activation protein; alpha; se	1.02	4.56
	132309	AA460917	Hs.2780	jun D proto-oncogene	1.16	1.8
	132371	AA235448	Hs.46677	ESTs	0.8	1.26
85	132618	AA253330	Hs.5344	adaptor-related protein complex 1; gamma	0.5	1.49
	132736	U68019	Hs.211578	MAD (mothers against decapentaplegic; Dr	1.21	1.81

	132771	AA488432	Hs.56407	phosphoserine phosphatase	1	1.3
	132833	U78525	Hs.57783	eukaryotic translation initiation factor	0.91	1.43
	132922	T23641	Hs.6066	KIAA1112 protein	1.16	1.53
5	132959	AA028103	Hs.61472	ESTs; Weakly similar to unknown [S.cerev	1.02	1.88
	132994	AA051133	Hs.7594	solute carrier family 2 (facilitated glu	0.72	2.97
	133005	C21400	Hs.103329	KIAA0970 protein	0.88	1.34
	133065	X62535	Hs.172690	diacylglycerol kinase; alpha (80kD)	0.93	1.23
	133083	N70633	Hs.6456	chaperonin containing TCP1; subunit 2 (b	1.14	1.76
10	133086	L17131	Hs.139800	high-mobility group (nonhistone chromoso	0.97	1.43
	133134	T89703	Hs.65648	RNA binding motif protein 8	1.1	1.8
	133195	AA350744	Hs.181409	KIAA1007 protein	2.29	2.69
	133313	AA249427	Hs.70704	ESTs	1.07	1.68
	133331	T62039	Hs.158675	ribosomal protein L14	0.85	1.18
15	133438	D13370	Hs.73722	APEX nuclease (multifunctional DNA repai	0.91	1.45
	133445	T99303	Hs.73797	guanine nucleotide binding protein (G pr	0.94	1.68
	133483	X52426	Hs.74070	keratin 13	0.85	1.14
	133492	L40397	Hs.74137	transmembrane trafficking protein	1.1	1.69
	133504	W95070	Hs.74316	desmoplakin (DPI; DP11)	0.7	6.21
20	133517	X52947	Hs.74471	gap junction protein; alpha 1; 43kD (con	0.95	1.3
	133540	D78151	Hs.74619	proteasome (prosome; macropain) 26S subu	0.91	1.25
	133594	L07758	Hs.172589	nuclear phosphoprotein similar to S. cer	0.84	1.29
	133627	U09587	Hs.75280	glycyl-tRNA synthetase	1.09	1.99
	133671	T25747	Hs.75471	zinc finger protein 146	1.02	1.5
25	133859	U86782	Hs.178761	26S proteasome-associated pad1 homolog	1.11	3.33
	133865	F09315	Hs.170290	discs; large (Drosophila) homolog 5	1.84	6.7
	133913	W84712	Hs.7753	calumenin	1.15	1.86
	133963	L34587	Hs.184693	transcription elongation factor B (SIII)	1.3	1.91
	133982	U47621	Hs.207251	nucleolar autoantigen (55kD) similar to	1.3	1.99
30	134100	L07540	Hs.171075	replication factor C (activator 1) 5 (36	0.72	1.65
	134110	U41060	Hs.79136	LIV-1 protein; estrogen regulated	1.04	1.62
	134158	U15174	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	1	1.55
	134161	U97188	Hs.79440	IGF-II mRNA-binding protein 3	0.82	1.95
	134193	F09570	Hs.7980	ESTs	0.98	1.48
35	134367	X54199	Hs.82285	phosphoribosylglycinamide formyltransfer	1	2.8
	134402	U25165	Hs.82712	fragile X mental retardation; autosomal	1.26	2
	134457	D86963	Hs.174044	dishevelled 3 (homologous to Drosophila	1	1.47
	134469	X17567	Hs.83753	small nuclear ribonucleoprotein polypept	0.94	1.57
	134498	M63180	Hs.84131	threonyl-tRNA synthetase	1.2	2.64
40	134501	W84870	Hs.211568	eukaryotic translation initiation factor	0.84	1.36
	134507	M63488	Hs.84318	replication protein A1 (70kD)	1.7	2.93
	134548	U41515	Hs.85215	Deleted in split-hand/split-foot 1 regio	1.46	2.73
	134599	X99226	Hs.86297	Fanconi anemia; complementation group A	1.36	2.22
	134692	R73567	Hs.8850	a disintegrin and metalloproteinase doma	0.77	1.64
45	134693	N70361	Hs.8854	ESTs	1.09	1.82
	134806	Z49099	Hs.89718	spermine synthase	0.98	1.35
	134821	Z34974	Hs.198382	plakophilin 1 (ectodermal dysplasia/skin	0.99	1.4
	134864	Y08999	Hs.90370	actin related protein 2/3 complex; subun	0.95	1.42
	134914	U29615	Hs.91093	chitinase 1 (chitotriosidase)	1.16	1.29
50	134953	L10678	Hs.91747	profilin 2	0.95	1.76
	134993	AA282343	Hs.9242	purine-rich element binding protein B	0.98	1.73
	135051	C15324	Hs.93668	ESTs	1.35	2.11
	135158	U51711		Human desmocollin-2 mRNA; 3' UTR	0.86	1.16

Table 1B shows the accession numbers for those keys in Table 1A lacking unigenelD's. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the Accession column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT	Accessions
65	100661 23182_1	BE623001 L05096 AA383604 AW966416 N53295 AA460213 AW571519 AA603655
	100667 26401_3	L05424 X56794 S66400 X55150 W60071 AW351820 X55938 M83326 BE005289 BE070059 M83324 BE005248 BE069717 BE181648 BE069700 AW606203 BE069721 AW382138 AW803776 BE463954 BE005334 BE005274 T27386 AA932714 AA972695 AW377728 AI632506 T29066 AI783934 AW377727 BE163715 AL047291 AA279047 AA523003 BE008048 BE440141 W23614 BE090519 BE092193 N29181 N20358 N44153 BE546944 T69231 AW377441 AA907406 H50799 AW051416 AI420712 BE620922 AI279161 AA992549 W47198 BE005241 AI342696 H50700 AI969974 AI863855 AA374490 AW130675 AI950633 AA146687 H99482 X55150 BE005414 BE005339 N28294 AI673068 AI887890 AW804171 AI675961 AW804172 AA778841 AL048050 AI127757 AI095568 AW204965 AW468978 W31898 AI052595 AI278771 BE464018 AI081503 AI824196 AA513211 AA411062 AW084376 N48752 AA703209 N35580 AW059918 AA054563 AI280942 T27619 BE621435 N66010 AW589527 AI160414 AA283090 AA962536 H82726 W52115 W45432 W60433 AA577548 AA146714 BE150994 AA054615 AW796025 AW382768 BE565671 C00444 AA054555
75	100668 26401_3	L05424 X56794 S66400 X55150 W60071 AW351820 X55938 M83326 BE005289 BE070059 M83324 BE005248 BE069717 BE181648 BE069700 AW606203 BE069721 AW382138 AW803776 BE463954 BE005334 BE005274 T27386 AA932714 AA972695 AW377728 AI632506 T29066 AI783934 AW377727 BE163715 AL047291 AA279047 AA523003 BE008048 BE440141 W23614 BE090519 BE092193 N29181 N20358 N44153 BE546944 T69231 AW377441 AA907406 H50799 AW051416 AI420712 BE620922 AI279161 AA992549 W47198 BE005241 AI342696 H50700 AI969974 AI863855 AA374490 AW130675 AI950633 AA146687 H99482 X55150 BE005414 BE005339 N28294 AI673068 AI887890 AW804171 AI675961 AW804172 AA778841 AL048050 AI127757 AI095568 AW204965 AW468978 W31898 AI052595 AI278771 BE464018 AI081503 AI824196 AA513211 AA411062 AW084376 N48752 AA703209 N35580 AW059918 AA054563 AI280942 T27619 BE621435 N66010 AW589527 AI160414 AA283090 AA962536 H82726 W52115 W45432 W60433 AA577548 AA146714 BE150994 AA054615 AW796025 AW382768 BE565671 C00444 AA054555
80		J04088 NM_001067 AF071747 AJ011741 N85424 AL042407 AA218572 BE296748 BE083981 AL040877 AW499918 AW675045 H17813
85	101332 25130_1	BE081283 AA670403 AW504327 BE094229 AA104024 AI471482 AI970337 AA737616 AI827444 AW003286 AI742333 AI344044 AI765634

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AW674920 N57176 AA026480 AW576767 H93284 AA026863 AW177787 AA026654 AW177786 BE092134 BE092137 BE092136 AW177784
AI022862 BE091653 AW376811 AW848592 AA040018 BE185331 BE182164 AA368564 AW951576 T29918 AA131077 W95048 W25458
AW205789 H90899 N29754 W32490 R20904 BE167181 BE167165 N84767 H27408 H30146 AI190590 C03378 AI554403 AI205263 AA128470
AI392926 AF139065 AW370813 AW370827 AW798417 AW798780 AW798883 AW798569 R33557 AA149190 C03029 AW177783 AA088866
AW370829 AA247685 BE002273 AI760816 AI439101 AW879451 AI700963 AA451923 AI340326 AI590975 T48793 AI568096 AI142882 AA039975
AI470146 AA946936 BE067737 BE067786 W19287 AA644381 AA702424 AI417612 AI305554 AI686869 AI568892 AW190555 AI571075 AI220573
AA056527 AI471874 AI304772 AW517828 AI915596 AI627383 AI270345 AW021347 AW166807 AW105614 AI346078 AA552300 W95070
AI494069 AI911702 AA149191 AA026864 AI830049 AI887258 AW780435 AI910434 AI819984 AI858282 AI078449 AI025932 AI860584 AI635878
AA026047 AA703232 D12062 AW192085 AA658154 AW514597 AW591892 T87181 AA782066 AW243815 AW150038 AW268383 AW004633
AI927207 AA782109 AW473233 AI804485 AW169216 AI572669 AA602182 AW015480 AW771865 AI270027 AA961816 AA283207 AI076952
AI498487 AI348053 AI783914 H44405 AW799118 AA128330 AA515500 AA918281 W02156 AI905927 AA022701 W38382 R20795 T77861
AW860878
100528 45979_1 BE386801 AU077299 AA143755 BE302747 AA853375 U30162 BE274163 BE277479 BE408180 BE274874 C15000 AA047476 N27099 AI359165
AI638794 AI151283 AI863925 AW444977 AI207392 AA931263 AA443112 R40138 AW068538 AA351008 AA676972 R62503 AA916492 AW001865
H42334 H38280 AA121497 AA114137 AI750938 M17783 AA383786 BE274462 AI753182 C05975 AA347404 AW069298 AI754351 AI754044
AA188808 AA186879 AA565243 AL040655 AA456177 AI750722 AA045756 AA213580 C16936 AW578747 AW753731 H41632 N44761 R58560
R61260 AA039902 N59721 AW992543 R68380 AA149686 T29017 H03739 BE383822 BE387105 BE408251 BE410425 H41560 AA247591
BE389677 AI752233 AI566195 AA868004 AI424523 AW753720 AA852159 BE386803
100559 2260_1 NM_000094 L02870 D13694 S51236 M96984 AW946290 M65158 AI285422 D29523 AL119886 AW630655 L06862 AI884355 AW168737 T29085
AW797005 AW801340 AI355504 AW079048 AW801337 AI690455 AI972063 AW268565 W68588 AA587326 AA883498 AI033523 AW510356
AW591998 H98463 AL043852 AI150055 AI566239 AI624803 AA844717 H40670 AA922334 AI864424 AW615094 AW451233 AI302203 F31221
AI872170 W68589 AA904478 AI917631 AW014208 AW450759 AA847625 AI284033 AA848176 AA598507
100576 9986_1 X00356 NM_001741 M26095 X03662 M12667 X02330 X02330 AA716058 AW296074 X04861 AI695720 AA719597
124357 genbank_N22401 N22401
101624 entrez_M55998 M55998
101625 entrez_M57293 M57293
135158 57963_1 AL037551 AI804716 AW439811 AI569470 AA075299 AI738572 AI270388 AI816783 AW263026 AI633951 AI655285 AI990572 AI950425
AW241533 AA916883 AA576693 AA160156 AA613783 AW078884 AI888282 AI275241 AI133467 AA164921

Tables 2A-8C were previously filed on November 9, 2001 in USSN 60/339,245 (18501-004100US)

Table 2A shows 504 genes down-regulated in lung tumors relative to normal lung and chronically diseased lung. Chronically diseased lung samples represent chronic non-malignant lung diseases such as fibrosis, emphysema, and bronchitis. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: 90th percentile of AI for normal lung samples divided by the 80th percentile of AI for adenocarcinoma and squamous cell carcinoma lung tumor samples.
 R2: median of AI for normal lung samples divided by 90th percentile of AI for adenocarcinoma and squamous cell carcinoma lung tumor samples.
 R3: median of AI for normal lung samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples divided by the 90th percentile of AI for adenocarcinoma and squamous cell carcinoma lung tumor samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples.
 R4: average of AI for normal lung samples divided by average AI for squamous cell carcinoma and adenocarcinoma lung tumors.
 R5: median of AI for normal lung samples divided by the 90th percentile of AI for adenocarcinomas.
 R6: median of AI for normal lung samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples divided by the 90th percentile of AI for adenocarcinomas minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples.
 R7: average of AI for normal lung samples divided by the 90th percentile of AI for squamous cell carcinomas.
 R8: median of AI for normal lung samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples divided by the 90th percentile of AI for squamous cell carcinomas minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples.

Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2	R3	R4	R5	R6	R7	R8
100095	Z97171	Hs.78454	myocilin; trabecular meshwork inducible	40.20							
100115	NM_002084	Hs.336920	glutathione peroxidase 3 (plasma)								3.46
100138	U83508	Hs.2463	angiotensin 1			2.30					
100299	D49493	Hs.2171	growth differentiation factor 10		11.00						
100306	U86749	Hs.80598	transcription elongation factor A (SII);						3.06		
100447	NM_014767	Hs.74583	KIAA0275 gene product								3.16
100458	S74019	Hs.247979	Vpre-B	42.40							
100862	AA005247	Hs.285754	Hepatocyte Growth Factor Receptor						4.13		
100959	AA359129	Hs.118127	actin; alpha; cardiac muscle				125.60				
101032	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	36.40							
101081	AF047347	Hs.4880	amyloid beta (A4) precursor protein-bind				34.60				
101088	X70697	Hs.553	solute carrier family 6 (neurotransmitter)				193.20				
101125	AJ250562	Hs.82749	transmembrane 4 superfamily member 2						3.10		
101180	U11874	Hs.846	interleukin 8 receptor; beta				54.86				
101308	L41390		"Homo sapiens core 2 beta-1,6-N-acetylgl	33.20							
101330	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do				36.40				
101345	NM_005795	Hs.152175	Calcitonin receptor-like			2.29					
101346	A1738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N				70.55				
101397	M26380	Hs.180878	lipoprotein lipase								3.54
101414	NM_000066	Hs.38069	complement component 8; beta polypeptide							3.81	
101435	NM_001100	Hs.1288	actin; alpha 1; skeletal muscle				34.60				
101507	X16896	Hs.82112	interleukin 1 receptor; type I				37.60				
101530	M29874	Hs.1360	cytochrome P450; subfamily IIB (phenobar								4.25
101537	A1469059	Hs.184915	zinc finger protein; Y-linked			2.54					
101542	NM_000102	Hs.1363	cytochrome P450; subfamily XVII (steroid		5.50						
101545	BE246154	Hs.154210	EDG1; endothelial differentiation, sphin	39.40							
101554	BE207611	Hs.123078	thyroid stimulating hormone receptor		13.00						
101560	AW958272	Hs.83733	Intercellular adhesion molecule 2, exon								3.38
101574	M34182	Hs.158029	protein kinase; cAMP-dependent; catalyti						4.37		
101805	M37984	Hs.118845	troponin C; slow								3.80
101621	BE391804	Hs.82661	guanylate binding protein 1; interferon-	30.20							
101680	AA299330	Hs.1042	Sjogren syndrome antigen A1 (52kD; ribon							2.75	
101829	AW452398	Hs.129763	solute carrier family 8 (sodium/calcium						3.37		
101842	M93221	Hs.75182	mannose receptor; C type 1				38.20				
101961	AW004056	Hs.168357	"Hs-TBX2=T-box gene (T-box region) [huma			2.32					
101994	T92248	Hs.2240	uteroglobin								6.85
102020	AU077315	Hs.154970	transcription factor CP2			2.45					
102091	BE280901	Hs.83155	aldehyde dehydrogenase 7								6.75
102112	AW025430	Hs.155591	forkhead box F1	54.60							
102190	AA723157	Hs.73769	folate receptor 1 (adult)								3.98
102202	NM_000507	Hs.574	fructose-bisphosphatase 1								3.62
102241	NM_007351	Hs.268107	Multimerin			2.32					
102310	U33839		Accession not listed in Genbank		7.00						
102397	U41898		"Human sodium cotransporter RKST1 mRNA,	29.40							
102571	U60115	Hs.239069	"Homo sapiens skeletal muscle LIM-protei								3.75
102620	AA976427	Hs.121513	Human clone W2-6 mRNA from chromosome X						3.07		
102636	U67092		"Human ataxia-telangiectasia locus prote			2.40					
102667	U70867	Hs.83974	solute carrier family 21 (prostaglandin			3.15					
102675	U72512	Hs.7771	"Human B-cell receptor associated protei						3.56		
102698	M18667	Hs.1867	progastricin (papsinogen C)								4.51
102727	U79251	Hs.99902	opioid-binding protein/cell adhesion mol					12.00			
102852	V00571	Hs.75294	corticotropin releasing hormone	37.40							
103026	X54162	Hs.79386	thyroid and eye muscle autoantigen D1 (6					13.00			
103028	X54380	Hs.74094	pregnancy-zone protein	28.80							
103098	M86361		Human mRNA for T cell receptor; clone IG					10.00			
103117	X63578	Hs.295449	parvalbumin		6.00						
103241	X76223		H.sapiens MAL gene exon 4			2.47					
103280	U84722	Hs.76206	Cadherin 5, VE-cadherin (vascular epithe			2.69					
103360	Y16791	Hs.73082	keratin; hair; acidic; 5							2.16	

	103496	Y09267	Hs.132821	flavin containing monooxygenase 2					5.97
	103508	Y10141		"H.sapiens DAT1 gene, partial, VNTR"				3.27	
	103561	NM_001843	Hs.143434	contactin 1	2.40				
	103569	NM_005512	Hs.151641	glycoprotein A repetitions predominant	2.99				
5	103575	Z26256		"H.sapiens isoform 1 gene for L-type cal				4.18	
	103627	Z48513		H.sapiens XG mRNA (clone PEP6)				3.44	
	103767	BE244667	Hs.296155	CGI-100 protein					2.25
	103850	AA187101	Hs.213194	Hypothetical protein MGC10895; sim to SR		46.55			
10	104078	AA402801	Hs.303276	ESTs				3.05	
	104326	AW732858	Hs.143067	ESTs				3.54	
	104352	BE219898	Hs.173135	dual-specificity tyrosine-(Y)-phosphoryl				3.16	
	104398	AI423930	Hs.36790	ESTs; Weakly similar to putative p150 [H	64.80				
	104473	AI904823	Hs.31297	ESTs					3.38
15	104493	AW960427	Hs.79059	ESTs; Moderately similar to TGF-BETA REC		2.47			
	104495	AW975687	Hs.292979	ESTs	28.60				
	104595	AI799603	Hs.271568	ESTs				3.42	
	104597	AI364504	Hs.93967	ESTs; Weakly similar to Slit-1 protein [6.00			
	104659	AW969769	Hs.105201	ESTs	34.00				
20	104686	AA010539	Hs.18912	ESTs		11.00			
	104691	U29690	Hs.37744	ESTs; Beta-1-adrenergic receptor	56.80				
	104764	AI039243	Hs.278585	ESTs			60.40		
	104776	AA026349		ESTs	34.20				
	104825	AA035613	Hs.141883	ESTs		3.03			
25	104865	T79340	Hs.22575	Homo sapiens cDNA: FLJ21042 fis, clone C	41.20				
	104942	NM_016348	Hs.10235	ESTs					3.27
	104989	R65998	Hs.285243	ESTs			40.00		
	105062	AW954355	Hs.36529	ESTs					3.20
	105101	H63202	Hs.38163	ESTs	34.20				
30	105173	U54617	Hs.8364	ESTs					4.17
	105194	R06780	Hs.19800	ESTs		16.00			
	105226	R58958	Hs.26608	ESTs			2.34		
	105256	AA430650	Hs.16529	transmembrane 4 superfamily member (tet			2.72		
	105394	BE245812	Hs.8941	ESTs			2.61		
35	105647	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	33.60				
	105789	AF106941	Hs.18142	arrestin; beta 2					3.59
	105817	AA397825		synaptopodin				4.46	
	105847	AW964490	Hs.32241	ESTs			35.40		
	105894	AI904740	Hs.25691	calcitonin receptor-like receptor activi		3.43			
40	105999	BE268786	Hs.21543	ESTs		7.00			
	106075	AA045290	Hs.25930	ESTs			42.60		
	106178	AL049935	Hs.301763	KIAA0554 protein	34.80				
	106381	AB040916	Hs.24106	ESTs			12.00		
	106467	AA450040	Hs.154162	ADP-ribosylation factor-like 2				3.69	
45	106536	AA329648	Hs.23804	ESTs			96.40		
	106569	R20909	Hs.300741	sorcin			47.20		
	106605	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr			220.40		
	106842	AF124251	Hs.26054	novel SH2-containing protein 3		2.55			
	106844	AA485055	Hs.158213	sperm associated antigen 6	39.20				
50	106870	AI983730	Hs.26530	serum deprivation response (phosphatidyl		2.28			
	106943	AW888222	Hs.9973	ESTs					4.28
	106954	AF128847	Hs.204038	ESTs					4.32
	107106	AA862496	Hs.28482	ESTs			10.45		
	107163	AF233588	Hs.27018	ESTs		2.57			
55	107201	D20378	Hs.30731	EST				3.84	
	107238	D59362	Hs.330777	EST		8.00			
	107376	U90545	Hs.327179	solute carrier family 17 (sodium phospho		10.67			
	107530	Y13622	Hs.85087	latent transforming growth factor beta b		2.32			
	107688	AW082221	Hs.60536	ESTs			34.60		
60	107706	AA015579	Hs.29276	ESTs	28.40				
	107723	AA015967		EST				3.29	
	107727	AA149707	Hs.173091	DKFZP434K151 protein			80.80		
	107750	AA017291	Hs.60781	ESTs			51.40		
	107751	AA017301	Hs.235390	ESTs				3.14	
65	107873	AK000520	Hs.143811	ESTs		9.00			
	107899	BE019261	Hs.83869	ESTs; Weakly similar to !!!! ALU SUBFAM				3.65	
	107994	AA036811	Hs.48469	ESTs			44.60		
	107997	AL049176	Hs.82223	Human DNA sequence from clone 141H5 on c			32.00		
	108041	AW204712	Hs.61957	ESTs			30.80		
70	108048	AI797341	Hs.165195	ESTs					4.75
	108338	AA070773		"zm53g11.s1 Stratagene fibroblast (#9372		2.33			
	108434	AA078899		"zm94b1.s1 Stratagene colon HT29 (#93722					2.92
	108447	AA079126		"zm92a11.s1 Stratagene ovarian cancer (#				3.06	
	108480	AL133092	Hs.68055	ESTs			34.00		
75	108499	AA083103		"zn1b12.s1 Stratagene hNT neuron (#93723					3.36
	108535	R13949	Hs.226440	Homo sapiens clone 24881 mRNA sequence			19.00		
	108550	AA084867		"zn11f6.s1 Stratagene hNT neuron (#93723			12.00		
	108604	AA934589	Hs.49696	ESTs		2.33			
	108625	AW972330	Hs.283022	ESTs					5.82
80	108629	AA102425		"zn24c6.s1 Stratagene neuroepithelium NT				3.42	
	108655	AA099960		"zm65c6.s1 Stratagene fibroblast (#93721		7.00			
	108756	AA127221	Hs.117037	Homo sapiens mRNA; cDNA DKFZp564N1164 (f		6.05			
	108864	AI733852	Hs.199957	ESTs	28.80				
	108895	AL138272	Hs.62713	ESTs	32.80				
	108921	AI568801	Hs.71721	ESTs			57.80		
85	108967	AA142989	Hs.71730	ESTs	28.80				

5	109001	AI056548	Hs.72116	ESTs, Moderately similar to hedgehog-int	2.57				
	109003	AA147497	Hs.71825	ESTs				2.11	
	109004	AA156235	Hs.139077	EST	5.60				
	109065	AA161125	Hs.252739	EST			10.00		
	109250	H83784	Hs.62113	ESTs; Weakly similar to PHOSPHATIDYLETHA				3.44	
10	109490	AA233416	Hs.139202	ESTs				2.92	
	109510	AI798863	Hs.87191	ESTs	2.40				
	109578	F02208	Hs.27214	ESTs	10.00				
	109601	F02695	Hs.311662	EST			40.80		
	109613	H47315	Hs.27519	ESTs			54.40		
15	109650	R31770	Hs.23540	ESTs	31.20				
	109682	H18017	Hs.22869	ESTs	8.40				
	109724	D59899	Hs.127842	ESTs			29.40		
	109782	AB020644	Hs.14945	long fatty acyl-CoA synthetase 2 gene			8.00		
	109833	R79864	Hs.29889	ESTs	10.00				
20	109837	H00656	Hs.29792	ESTs		6.49			
	109977	T64183	Hs.282982	ESTs				2.75	
	109984	AI796320	Hs.10299	ESTs			107.00		
	110146	H41324	Hs.31581	ESTs; Moderately similar to SYNTAXIN 1B				2.22	
	110271	H28985	Hs.31330	ESTs				3.48	
25	110280	AW874263	Hs.32468	ESTs	44.20				
	110420	R93141	Hs.184261	ESTs			32.00		
	110578	T62507	Hs.11038	ESTs	28.40				
	110634	R98905	Hs.35992	ESTs			20.00		
	110726	AW961818	Hs.24379	potassium voltage-gated channel; shaker-				4.15	
30	110837	H03109	Hs.108920	ESTs; Weakly similar to semaphorin F [H.			56.80		
	110875	N35070	Hs.26401	tumor necrosis factor (ligand) superfam		3.13			
	110894	R92356	Hs.66881	ESTs; Moderately similar to cytoplasmic	5.33				
	110971	AI760098	Hs.21411	ESTs			44.60		
	111023	AV655386	Hs.7645	ESTs	32.40				
35	111057	T79639	Hs.14629	ESTs			17.14		
	111247	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f				4.58	
	111330	BE247767	Hs.18166	KIAA0870 protein				3.42	
	111374	BE250726	Hs.283724	ESTs; Moderately similar to HYA22 [H.sap				3.91	
	111442	AW449573	Hs.181003	ESTs			33.20		
40	111737	H04607	Hs.9218	ESTs			53.00		
	111747	AI741471	Hs.23666	ESTs	46.20				
	111807	R33508	Hs.18827	ESTs	16.00				
	111862	R37472	Hs.21559	EST				3.91	
	112045	AI372588	Hs.8022	TU3A protein				2.74	
45	112057	R43713	Hs.22945	EST				4.92	
	112214	AW148652	Hs.167398	ESTs			13.00		
	112263	R52393	Hs.25917	ESTs		2.43			
	112314	AW206093	Hs.748	ESTs	9.00				
	112324	R55965	Hs.26479	limbic system-associated membrane protei			14.00		
50	112362	AW300887	Hs.26638	ESTs; Weakly similar to CD20 receptor [H		2.49			
	112380	H63010	Hs.5740	ESTs		2.34			
	112425	AA324998	Hs.321677	ESTs; Weakly similar to !!!! ALU SUBFAM	8.00			4.53	
	112473	R65993	Hs.279798	pregnancy specific beta-1-glycoprotein 9				3.62	
	112492	N51620	Hs.28694	ESTs			29.80		
55	112541	AF038392	Hs.116674	ESTs					
	112620	R80552	Hs.29040	ESTs		2.37			
	112623	AW373104	Hs.25094	ESTs		2.26			
	112867	T03254	Hs.167393	ESTs			12.00		
	112894	T08188	Hs.3770	ESTs	6.50				
60	112954	AA928953	Hs.6655	ESTs	7.00				
	113029	AW081710	Hs.7369	ESTs; Weakly similar to !!!! ALU SUBFAM				4.39	
	113086	AA346839	Hs.209100	DKFZP434C171 protein				4.47	
	113140	T50405	Hs.175967	ESTs			10.00		
	113252	NM_004469	Hs.11392	c-fos induced growth factor (vascular en	14.00				
65	113257	AI821378	Hs.159367	ESTs				3.72	
	113394	T81473	Hs.177894	ESTs				3.60	
	113437	T85349	Hs.15923	EST	35.00				
	113454	AI022166	Hs.16188	ESTs	6.00				
	113502	T89130	Hs.16026	ESTs	39.60				
70	113552	AI654223	Hs.333181	ESTs				2.58	
	113645	T95358	Hs.17932	EST			38.20		
	113691	T96935	Hs.269192	ESTs				3.09	
	113706	AA004693	Hs.11958	oxidative 3 alpha hydroxysteroid dehydro		2.31			
	113883	U89281	Hs.170056	Homo sapiens mRNA; cDNA DKFZp586B0220 (f	30.40				
75	113924	BE178285	Hs.269181	ESTs			13.00		
	114035	W92798	Hs.114727	ESTs					
	114058	AK002016	Hs.12248	ESTs			40.60		
	114084	AA708035	Hs.25425	ESTs		2.31			
	114121	H05785	Hs.125019	Human lymphoid nuclear protein (LAF-4)	7.00				
80	114124	W57554	Hs.306117	interleukin 13 receptor; alpha 1	6.00				
	114275	AW515443	Hs.173091	DKFZP434K151 protein			48.80		
	114297	AA149707	Hs.33532	ESTs; Highly similar to Miz-1 protein [H				3.45	
	114427	AA017176	Hs.243010	*ze63b11.s1 Soares retina N2b4HR Homo sa			10.00		
	114449	AA020736		ESTs, Moderately similar to RTC0_HUMAN G	14.00			3.13	
85	114452	AI369275		*zm97a5.s1 Stratagene colon HT29 (#93722					
	114609	AA079505		*zn25b3.s1 Stratagene neuroepithelium NT			35.40		
	114648	AA101056	Hs.155651	Homo sapiens HNF-3beta mRNA for hepatocy				3.42	
	114731	BE094291	Hs.288464	ESTs	33.00				
	114762	AA146979							

	114776	AA151719	Hs.95834	ESTs	34.40				
	115009	AA251561	Hs.48689	ESTs	30.20				
	115272	AW015947		ESTs; Weakly similar to hypothetical L1	32.60				
5	115279	AW964897	Hs.290825	ESTs		6.00			
	115302	AL109719	Hs.47578	ESTs			12.00		
	115365	AW976252	Hs.268391	ESTs				3.32	
	115559	AL079707	Hs.207443	ESTs				48.00	
	115566	AI142336	Hs.43977	ESTs				56.20	
10	115683	AF255910	Hs.54650	ESTs, Weakly similar to (define not ava	31.40				
	115744	AA418538	Hs.43945	ESTs; Highly similar to dJ1178H5.3 [H.sa				33.60	
	115819	AA486620	Hs.41135	Endomucin 2				74.40	
	115949	AI478427	Hs.43125	ESTs		3.18			
	115965	AA001732	Hs.173233	ESTs				388.80	
15	116035	AA621405	Hs.184664	ESTs				33.20	
	116049	AA454033	Hs.41644	ESTs				45.80	
	116081	AI190071	Hs.55278	ESTs					3.57
	116082	AB029496	Hs.59729	ESTs		3.06			
	116213	AA292105	Hs.326740	leucine rich repeat (in FLII) interactin	50.60				
20	116228	AI767947	Hs.50841	ESTs; Weakly similar to tuftelin [M.musc		3.85			
	116250	N76712	Hs.44829	ESTs		6.00			
	116419	AI613480	Hs.47152	ESTs; Weakly similar to testicular tekti				30.00	
	116617	D80761	Hs.45220	EST		2.27			
	116784	AB007979	Hs.301281	tenascin R (restrictin; janusin)	47.20				
25	116835	N39230	Hs.38218	ESTs				41.20	
	116970	AB023179	Hs.9059	KIAA0962 protein				11.00	
	117023	AW070211	Hs.102415	ESTs				91.00	
	117027	AW085208	Hs.130093	ESTs	49.40			32.60	
	117036	H88908	Hs.41192	EST					
30	117110	AA160079	Hs.172932	ESTs		8.67			
	117209	W03011	Hs.306881	ESTs				30.60	
	117325	N23599	Hs.43396	ESTs				9.29	
	117454	N29569	Hs.44055	ESTs					3.19
	117475	N30205	Hs.93740	ESTs	44.00				
35	117543	BE219453	Hs.42722	ESTs		16.00			
	117567	AW444761	Hs.44565	ESTs				12.00	
	117570	N48649	Hs.44583	ESTs				11.00	
	117600	N34963	Hs.44676	EST					3.74
	117730	N45513	Hs.46608	ESTs		6.00			
40	117791	N48325	Hs.93956	EST		9.00			
	117929	N51075	Hs.47191	ESTs				29.20	
	117990	AA446167	Hs.47385	ESTs		8.00			
	118224	N62275	Hs.48503	EST	31.40				
	118244	N62516	Hs.48556	ESTs	32.80				
45	118357	AL109667	Hs.124154	Homo sapiens mRNA full length insert cDN		2.40			
	118446	N66361	Hs.269121	ESTs		2.28			
	118447	N66399	Hs.49193	EST	30.80				
	118530	N67900	Hs.118446	ESTs					3.10
	118549	N68163	Hs.322954	EST					3.41
50	118823	W03754	Hs.50813	ESTs; Weakly similar to long chain fatty		3.94			
	118862	W17065	Hs.54522	ESTs					3.58
	118935	AI979247	Hs.247043	KIAA0525 protein				33.00	
	118944	AI734233	Hs.226142	ESTs; Weakly similar to !!!! ALU SUBFAM				11.43	
	118995	N94591	Hs.323056	ESTs		14.00			
55	119073	BE245360	Hs.279477	ERG-2/ERG-1; V-ets avian erythroblastosi				52.60	
	119268	T16335	Hs.65325	EST	31.40				
	119514	W37937		Accession not listed in Genbank					3.50
	119824	W74536	Hs.184	advanced glycosylation end product-speci		2.75			
	119831	AL117664	Hs.58419	DKFZP586L2024 protein					3.21
60	119861	W78816	Hs.49943	ESTs; Moderately similar to !!!! ALU SUB				33.80	
	119889	W84346	Hs.58671	ESTs				30.03	
	119921	W86192	Hs.58815	ESTs	29.00				
	120082	H80286	Hs.40111	ESTs					3.80
	120094	AA811339	Hs.124049	ESTs		6.00			
65	120132	W57554	Hs.125019	Human lymphoid nuclear protein (LAF-4)				36.60	
	120378	AA223249	Hs.285728	ESTs		12.00			
	120404	AB023230	Hs.96427	KIAA1013 protein	39.40				
	120504	AA256837		ESTs				8.00	
	120512	N55761	Hs.194718	ESTs	33.00				
70	120667	AA287740	Hs.78335	microtubule-associated protein; RP/EB fa					4.18
	120777	AA287702	Hs.10031	KIAA0955 protein				46.60	
	121082	AA398722		ESTs				39.00	
	121191	AA400205	Hs.104447	ESTs	41.60				
	121248	AA400914	Hs.97827	EST					5.08
75	121363	AI287280	Hs.97933	ESTs				12.00	
	121366	AI743515		ESTs				20.00	
	121483	AI660332	Hs.25274	ESTs; Moderately similar to putative sev					3.32
	121518	AA412155		ESTs				30.20	
	121545	AA412442	Hs.98132	ESTs		2.29			
80	121622	AA416931	Hs.126065	ESTs		9.00			
	121665	AA416556	Hs.98234	ESTs				34.80	
	121709	AI338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	34.80				
	121730	AI140683	Hs.98328	ESTs	38.80				
	121740	AA421138	Hs.98334	EST		7.00			
85	121772	AI590770	Hs.110347	Homo sapiens mRNA for alpha integrin bin	36.20				
	121821	AL040235	Hs.3346	ESTs					3.61

	121835	AB033030	Hs.300670	ESTs		2.34			
	121841	AA427794	Hs.104864	ESTs		2.61			
	121885	AA934883	Hs.98467	ESTs				2.25	
	121888	AA426429	Hs.98463	ESTs				2.92	
5	121938	AA428659	Hs.98610	ESTs			46.80		
	121950	AA429515		EST			31.40		
	122030	AA431310	Hs.98724	ESTs	34.40				
	122054	AA431725	Hs.98746	EST				3.58	
10	122211	AA300900	Hs.98849	ESTs; Moderately similar to bithoraxoid-	49.40				
	122233	AA436455	Hs.98872	EST	29.80				
	122247	AA436676	Hs.98890	EST			39.80		
	122253	AA436703	Hs.104936	ESTs; Weakly similar to hypothetical pro	9.00				
	122266	AA436840	Hs.98907	EST				3.60	
15	122285	AA436981	Hs.121602	EST				3.14	
	122409	AA446830	Hs.99081	ESTs	30.80				
	122485	AA524547	Hs.160318	phospholemma		2.65			
	122697	AA420683	Hs.98321	Homo sapiens cDNA FLJ14103 fis, clone MA	15.00				
	122772	AW117452	Hs.99489	ESTs	6.67				
20	122831	AI857570	Hs.5120	ESTs				3.37	
	122913	AI638774	Hs.105328	ESTs			32.20		
	123049	BE047680	Hs.211869	ESTs			41.80		
	123076	AI345569	Hs.190046	ESTs	35.80				
	123136	AW451999	Hs.194024	ESTs				2.58	
25	123309	N52937	Hs.102679	ESTs			19.00		
	123455	AA353113	Hs.112497	ESTs			82.80		
	123691	AA609579	Hs.112724	ESTs				3.95	
	123756	AA609971	Hs.112795	EST	35.40				
	123802	AA620448		Homo sapiens clone 24760 mRNA sequence	58.00				
30	123837	AI807243	Hs.112893	ESTs			32.40		
	123844	AA938905	Hs.120017	olfactory receptor; family 7; subfamily		2.63			
	123936	NM_004673	Hs.241519	ESTs	29.00				
	123987	C21171	Hs.95497	ESTs; Weakly similar to GLUCOSE TRANSPOR			70.60		
	124013	AI521936	Hs.107149	ESTs; Weakly similar to PTB-ASSOCIATED S	28.40				
35	124160	R40290	Hs.124685	ESTs			13.00		
	124205	H77570	Hs.108135	ESTs				4.74	
	124226	AA618527	Hs.190266	ESTs		2.35			
	124246	H67680	Hs.270962	ESTs			29.40		
40	124348	AI796320	Hs.10299	ESTs	17.00				
	124358	AW070211	Hs.102415	"yw35g11.s1 Morton Fetal Cochlea Homo sa		3.07			
	124409	AI814166	Hs.107197	ESTs				3.14	
	124442	AW663632	Hs.285625	TATA box binding protein (TBP)-associate		2.48			
	124468	N51413	Hs.109284	ESTs			30.80		
	124479	AB011130	Hs.127436	calcium channel; voltage-dependent; alph					6.03
45	124519	AI670056	Hs.137274	ESTs; Weakly similar to SPLICEOSOME ASSO		2.50			
	124711	NM_004657	Hs.26530	serum deprivation response (phosphatidyl	59.20				
	124866	AI768289	Hs.304389	ESTs	8.00				
	124874	BE550182	Hs.127826	ESTs			37.60		
	125097	AW576389	Hs.335774	ESTs			10.00		
50	125179	AW206468	Hs.103118	ESTs				3.12	
	125200	AW836591	Hs.103156	ESTs					2.79
	125299	T32982	Hs.102720	ESTs			34.20		
	125400	AL110151	Hs.128797	DKFZP586D0824 protein	29.00				
55	125810	H00083		aryl hydrocarbon receptor-interacting pr	32.20				
	126176	BE242256	Hs.2441	KIAA0022 gene product		12.00			
	126303	D78841		HUM525A05B Human placenta polyA+ (TFuji			33.60		
	126403	AW629054	Hs.125976	ESTs; Weakly similar to metalloprotease/	35.80				
	126507	AL040137	Hs.23964	ESTs; Weakly similar to HC1 ORF [M.muscu			29.80		
60	126773	AA648284	Hs.187584	ESTs	39.60				
	127307	AW962712	Hs.126712	ESTs; Weakly similar to pIL2 hypothetica	28.80				
	127462	AA760776	Hs.293977	aa59b04.s1 NCI_CGAP_GCB1 Homo sapiens c			34.40		
	127486	AW002846	Hs.105468	ESTs	9.00				
	127572	AA594027	Hs.191788	ESTs		2.36			
	127609	X80031	Hs.530	ESTs			29.40		
65	127832	AW976035	Hs.292396	ESTs			37.20		
	127898	AA774725	Hs.128970	ESTs				4.42	
	128073	AW340720	Hs.125983	ESTs			38.40		
	128101	AA905730	Hs.128254	ESTs	7.33				
70	128149	NM_012214	Hs.177576	mannosyl (alpha-1;3-)-glycoprotein beta-				2.58	
	128212	W27411	Hs.336920	glutathione peroxidase 3 (plasma)		3.09			
	128333	W68800	Hs.12126	ESTs; Weakly similar to LR8 [H.sapiens]			34.40		
	128364	N76462	Hs.269152	ESTs; Weakly similar to ZINC FINGER PROT	10.00				
	128426	AI265784	Hs.145197	ESTs				4.31	
	128598	AA305407	Hs.102308	potassium inwardly-rectifying channel; s	31.20				
75	128634	AA464918		ESTs; Moderately similar to !!!! ALU SUB			41.60		
	128687	AW271273	Hs.23767	ESTs			87.00		
	128726	AI311238	Hs.104476	ESTs				4.02	
	128773	NM_004131	Hs.1051	granzyme B (granzyme 2; cytotoxic T-lymp			9.00		
	128833	W26667	Hs.184581	ESTs				3.76	
80	128870	H39537	Hs.75309	eukaryotic translation elongation factor	2.66				
	128878	R25513	Hs.10683	ESTs				3.10	
	128885	AF134803	Hs.180141	cofilin 2 (muscle)			11.00		
	128998	W04245	Hs.107761	ESTs; Weakly similar to PUTATIVE RHO/RAC				3.21	
	129000	AA744902	Hs.107767	ESTs; Moderately similar to CaM-KII inh					3.68
	129038	AW156903	Hs.108124	ribosomal protein L41				3.17	
85	129098	AW580945	Hs.330466	ESTs	34.60				

	129210	AL039940	Hs.202949	KIAA1102 protein					4.09
	129240	AA361258	Hs.237868	interleukin 7 receptor	2.29				
	129262	BE222198	Hs.109843	ESTs			3.30		
5	129301	AF182277	Hs.330780	Human cytochrome P450-IIB (hIIB3) mRNA;					4.05
	129331	AW167668	Hs.279772	ESTs; Highly similar to CGI-38 protein [4.09
	129381	AW245805	Hs.110903	claudin 5 (transmembrane protein deleted	2.93				
	129565	X77777	Hs.198726	vasoactive intestinal peptide receptor 1		160.80			
	129595	U09550	Hs.1154	oviductal glycoprotein 1; 120kD			10.00		
10	129613	AW978517	Hs.172847	ESTs; Weakly similar to collagen alpha 1				3.40	
	129782	AW016932	Hs.104105	EST	9.00				
	129950	F07783	Hs.1369	decay accelerating factor for complement		87.80			
	129958	R27496	Hs.1378	annexin A3		44.60			
	129959	AL036554	Hs.274463	defensin; alpha 1; myeloid-related seque	2.72				
15	130160	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1;3-galactosyltr		42.20			
	130259	NM_000328	Hs.153614	retinitis pigmentosa GTPase regulator	2.54				
	130273	AW972422	Hs.153863	MAD (mothers against decapentaplegic; Dr		51.60			
	130312	AF056195	Hs.15430	DKFZP586G1219 protein				3.16	
	130436	NM_001928	Hs.155597	D component of complement (adipsin)					4.11
20	130523	AA999702	Hs.214507	ESTs				4.77	
	130799	AB028945	Hs.12696	ESTs	6.00				
	130885	NM_005883	Hs.20912	adenomatous polyposis coli like				3.54	
	131002	AL050295	Hs.22039	KIAA0758 protein					3.50
	131012	AL039940	Hs.202949	KIAA1102 protein	20.00				
25	131031	NM_001650	Hs.288650	aquaporin 4	41.20				
	131061	N64328	Hs.268744	ESTs; Moderately similar to KIAA0273 [H.		31.40			
	131066	AW169287	Hs.22588	ESTs		29.60			
	131082	AI091121	Hs.246218	ESTs; Weakly similar to zinc finger prot			9.00		
	131087	AF147709	Hs.22824	ESTs; Weakly similar to p160 myb-binding					3.86
30	131161	AF033382	Hs.23735	potassium voltage-gated channel; subfami				3.14	
	131179	AA171388	Hs.184482	DKFZP586D0624 protein				3.80	
	131182	AI824144	Hs.23912	ESTs					3.67
	131205	NM_003102	Hs.2420	superoxide dismutase 3; extracellular	2.98				
	131277	AA131466	Hs.23767	ESTs	3.15				
35	131281	AA251716	Hs.25227	ESTs		32.20			
	131282	X03350	Hs.4	alcohol dehydrogenase 3 (class I); gamma					3.44
	131285	AI567943	Hs.25274	ESTs; Moderately similar to putative sev				6.40	
	131355	R52804	Hs.25956	DKFZP564D206 protein	8.00				
	131391	AW085781	Hs.26270	ESTs	10.00				
40	131461	AA992841	Hs.27263	butyrate response factor 2 (EGF-response	28.80				
	131487	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1763 (f					4.03
	131517	AB037789	Hs.263395	ESTs; Highly similar to semaphorin VIa [39.00				
	131545	AL137432	Hs.28564	ESTs			11.00		
	131583	AK000383	Hs.323092	ESTs; Weakly similar to dual specificity			10.00		
45	131647	AA359615	Hs.30089	ESTs	2.47				
	131675	H15205	Hs.30509	ESTs				3.06	
	131676	AI126821	Hs.30514	ESTs	45.80				
	131708	S60415	Hs.30941	calcium channel; voltage-dependent; beta	2.28				
	131717	X94630	Hs.3107	CD97 antigen					3.78
50	131756	AA443966	Hs.31595	ESTs		40.60			
	131762	AA744902	Hs.107767	ESTs; Moderately similar to CaM-KII inhi					3.67
	131821	AA017247	Hs.164577	ESTs	2.87				
	131839	AB014533	Hs.33010	KIAA0633 protein				3.48	
	131861	AL096858	Hs.184245	KIAA0929 protein Msx2 interacting nuclea	54.00				
55	132015	AI418006	Hs.3731	ESTs		49.20			
	132070	BE622641	Hs.38489	ESTs		34.80			
	132242	AA332697	Hs.42721	ESTs	2.68				
	132334	AW080704	Hs.45033	lacrima proline rich protein	4.66				
	132476	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	34.20				
60	132490	NM_001290	Hs.4980	LIM binding domain 2		2.66			
	132533	AI922988	Hs.172510	ESTs	13.00				
	132598	X80031	Hs.530	collagen; type IV; alpha 3 (Goodpasture		30.60			
	132619	H28855	Hs.53447	ESTs; Moderately similar to kinesin Iigh				4.02	
	132652	N41739	Hs.61260	ESTs				3.18	
65	132726	N52298	Hs.55608	ESTs; Weakly similar to cDNA EST yk484g1			11.43		
	133028	R51604	Hs.300842	ESTs	2.37				
	133071	BE384932	Hs.64313	ESTs	2.27				
	133120	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein	2.63				
70	133129	AA428580	Hs.65551	ESTs					5.49
	133147	AA026533	Hs.66	interleukin 1 receptor-like 1	6.20				
	133151	NM_014051	Hs.94896	ESTs				3.69	
	133213	AA903424	Hs.6786	ESTs		31.40			
	133276	AW978439	Hs.69504	ESTs			9.00		
75	133377	AJ131245	Hs.7239	SEC24 (S. cerevisiae) related gene famil	41.20				
	133407	AF017987	Hs.7306	secreted frizzled-related protein 1	50.20				
	133535	AL134030	Hs.284180	protocadherin 2 (cadherin-like 2)				3.72	
	133537	U41518	Hs.74602	aquaporin 1 (channel-forming integral pr					3.35
	133656	BE149455	Hs.75415	Accession not listed in Genbank	2.65				
	133689	NM_001872	Hs.75572	carboxypeptidase B2 (plasma)		90.80			
80	133779	T58486	Hs.222566	ESTs				3.05	
	133978	AF035718	Hs.78061	transcription factor 21	2.92				
	133985	L34657	Hs.78146	platelet/endothelial cell adhesion molec					3.45
	134000	AW175787	Hs.334841	selenium binding protein 1					4.05
	134111	AI372588	Hs.8022	TU3A protein	4.49				
85	134185	AA285136	Hs.301914	Homo sapiens mRNA; cDNA DKFZp586K1220 (f				3.27	
	134204	AI873257	Hs.7994	ESTs; Weakly similar to CGI-69 protein [40.80			

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	134641	AI092634	Hs.156114	protein tyrosine phosphatase; non-recept				3.76
	134677	AA251363	Hs.177711	ESTs			32.20	
	134745	NM_000685	Hs.89472	angiotensin receptor 1B	15.00			
5	134749	T28499	Hs.89485	carbonic anhydrase IV		3.05		
	134786	T29618	Hs.89640	angiotensin 1 receptor; TEK tyrosine ki			57.80	
	134825	U33749	Hs.197764	thyroid transcription factor 1				3.73
	134978	AI829008	Hs.333383	ficollin (collagen/fibrinogen domain-cont		2.52		
	135010	N50465	Hs.92927	ESTs			31.60	
10	135053	AW796190	Hs.93678	ESTs				3.21
	135081	AF069517	Hs.173993	RNA binding motif protein 6	28.80			
	135091	AA493650	Hs.94367	ESTs				4.24
	135135	AA775910	Hs.95011	syntrophin; beta 1 (dystrophin-associate		8.00		
	135203	C15737	Hs.269386	ESTs				4.31
15	135236	AI636208	Hs.96901	ESTs	43.00			
	135266	R41179	Hs.97393	Human mRNA for KIAA0328 gene; partial cd				6.42
	135346	NM_000928	Hs.992	phospholipase A2; group IB (pancreas)		3.82		
	135378	AW961818	Hs.24379	potassium voltage-gated channel; shaker-		4.15		
	135387	NM_001972	Hs.99863	elastase 2; neutrophil	37.20			
20	135388	W27965	Hs.99865	EST	38.80			
	135402	L12398	Hs.99922	dopamine receptor D4				4.21

25 TABLE 2B shows the accession numbers for those primekeys lacking unigenelD's for Table 2A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

30 Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
35	108447	43452_7 AA079126
	108560	120073_1 AA084867 AA084996
	108655	127522_1 AA099960 AA113013
	102397	44371_1 U41898
40	126303	1525933_1 D78841 D78880
	125810	1554054_1 H00083 R81062
	103627	2615_2 Z48513 Z48512
	121366	280401_1 AI743515 AA405617 AW276706
	114609	116777_1 AA079505 AA079537
45	115272	172113_1 AW015947 AA211890 AA279425
	108338	112186_1 AA070773 AA070774
	108434	114012_1 AA078899 AA078782 AA075788
	123902	genbank_AA620448 AA620448
	102310	NOT_FOUND_entrez_U33839 U33839
	102636	entrez_U67092 U67092
50	104776	genbank_AA026349 AA026349
	120504	genbank_AA256837 AA256837
	113502	genbank_T89130T89130
	108499	genbank_AA083103 AA083103
	101308	entrez_L41390 L41390
55	108629	genbank_AA102425 AA102425
	103098	221_215 M86361 Z26593 X02850 D13070 AE000659 M17649 M87869 M87871 X61077 M16286 AF018169 X61079 S59351 X60142 AF043169
	103241	entrez_X76223 X76223
	103508	entrez_Y10141 Y10141
	103575	entrez_Z26256 Z26256
60	119514	NOT_FOUND_entrez_W37937 W37937
	121082	genbank_AA398722 AA398722
	128634	AA464918_at AA464918
	105817	genbank_AA397825 AA397825
	121518	genbank_AA412155 AA412155
65	114449	genbank_AA020736 AA020736
	114648	genbank_AA101056 AA101056
	121950	genbank_AA429515 AA429515
	107723	genbank_AA015967 AA015967

Table 3A shows 452 genes up-regulated in chronically diseased lung relative to normal lung. Chronically diseased lung samples represent chronic non-malignant lung diseases such as fibrosis, emphysema, and bronchitis. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: 80th percentile of AI for chronically diseased lung samples divided by the 90th percentile of AI for normal lung samples.
 R2: 80th percentile of AI for chronically diseased lung samples divided by the 90th percentile of normal lung samples, squamous cell carcinomas and adenocarcinomas
 R3: 70th percentile of AI for chronically diseased lung samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples divided by the 90th percentile of normal lung samples, squamous cell carcinomas and adenocarcinomas minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples

Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2	R3
135423	U50531	Hs.138751	Human BRCA2 region, mRNA sequence CG030	12.40		
135378	AW961818	Hs.24379	MUM2 protein			2.13
135346	NM_000928	Hs.992	phospholipase A2, group IB (pancreas)			
135235	AW298244	Hs.293507	ESTs	12.40		
135057	U90268	Hs.93810	cerebral cavernous malformations 1	11.67		
134951	BE305081	Hs.169358	hypothetical protein		8.00	
134799	M36821	Hs.89690	GRO3 oncogene		8.20	
134786	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous			
134772	NM_000829	Hs.163697	glutamate receptor, ionotropic, AMPA 4	29.80		
134752	BE246762	Hs.89499	arachidonate 5-lipoxygenase			1.93
134749	T28499	Hs.89485	carbonic anhydrase IV			2.07
134696	BE326276	Hs.8861	ESTs			
134636	NM_005582	Hs.87205	lymphocyte antigen 64 (mouse) homolog, r	13.60		
134627	AI018768	Hs.12482	glyceronephosphate O-acyltransferase			1.92
134622	AW975159	Hs.293097	ESTs, Weakly similar to A55380 faciogeni			1.92
134570	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	13.20		
134561	U76421	Hs.85302	adenosine deaminase, RNA-specific, B1 (h			1.78
134468	NM_001772	Hs.83731	CD33 antigen (gp67)		6.20	
134417	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic aci			
134343	D50683	Hs.82028	transforming growth factor, beta recepto			
134323	BE170651	Hs.8700	deleted in liver cancer 1			
134300	NM_001430	Hs.8136	endothelial PAS domain protein 1			
134299	AW580939	Hs.97199	complement component C1q receptor			
134253	X52075	Hs.80738	sialophorin (gpL115, leukosialin, CD43)	20.60		
134182	D52059	Hs.7972	KIAA0871 protein	12.20		
133985	L34657	Hs.78146	platelet/endothelial cell adhesion molec			
133978	AF035718	Hs.78061	transcription factor 21			
133835	AI677897	Hs.76640	RGC32 protein			
133651	AI301740	Hs.173381	dihydropyrimidinase-like 2			
133633	D21262	Hs.75337	nucleolar and coiled-body phosphoprotein	15.20		
133565	AW955776	Hs.313500	ESTs, Moderately similar to ALU7_HUMAN A			
133548	AW946384	Hs.178112	DNA segment, single copy probe LNS-CAI/L			1.77
133488	AA335295	Hs.74120	adipose specific 2			
133478	X83703	Hs.31432	cardiac ankyrin repeat protein			2.08
133337	AF085983	Hs.293676	ESTs		9.60	
133200	AB037715	Hs.183639	hypothetical protein FLJ10210			1.77
133153	AF070592	Hs.66170	HSKM-B protein	30.60		
133130	AI128606	Hs.6557	zinc finger protein 161	22.60		
133120	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein			
132928	AW168082	Hs.169449	protein kinase C, alpha	13.80		
132836	AB023177	Hs.29900	KIAA0960 protein			
132799	W73311	Hs.169407	SAC2 (suppressor of actin mutations 2,	41.60		
132742	AA025480	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	40.40		
132548	X12830	Hs.193400	interleukin 6 receptor		7.20	
132476	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi		4.76	
132439	AK001942	Hs.4863	hypothetical protein DKFZp566A1524			1.88
132240	AB018324	Hs.42676	KIAA0781 protein	21.20		
132210	NM_007203	Hs.42322	A kinase (PRKA) anchor protein 2			1.99
132199	AL041299	Hs.165084	ESTs	15.20		
131751	T96555	Hs.31562	ESTs			1.76
131745	AI828559	Hs.31447	ESTs, Moderately similar to A46010 X-II	27.80		
131694	NM_000246	Hs.3076	MHC class II transactivator		4.00	
131686	NM_012296	Hs.30687	GRB2-associated binding protein 2			
131676	AI126821	Hs.30514	ESTs		6.20	
131629	Z45794	Hs.238809	ESTs	21.40		
131589	C18825	Hs.29191	epithelial membrane protein 2			
131536	AA019201	Hs.269210	ESTs		9.40	
131517	AB037789	Hs.263395	sema domain, transmembrane domain (TM),		3.59	
131355	R52804	Hs.25956	DKFZP564D206 protein		4.48	
131253	R71802	Hs.24853	ESTs	15.00		
131207	AF104266	Hs.24212	latrophillin			1.75
131156	AI472209	Hs.323117	ESTs			1.84
131066	AW169287	Hs.22588	ESTs		3.54	
131061	N64328	Hs.268744	KIAA1796 protein			
131053	AA348541	Hs.296261	guanine nucleotide binding protein (G pr			1.93
130895	AA641767	Hs.21015	hypothetical protein DKFZp564L0864 simil	16.60		
130762	D84371	Hs.1898	paraoxonase 1	12.00		

	130657	AW337575	Hs.201591	ESTs		
	130655	AI831962	Hs.17409	cysteine-rich protein 1 (intestinal)		
	130589	AL110226	Hs.16441	DKFZP434H204 protein		2.08
5	130562	D50402	Hs.182611	solute carrier family 11 (proton-coupled		1.91
	130555	R69743	Hs.116774	integrin, alpha 1	9.60	
	130365	W56119	Hs.155103	eukaryotic translation initiation factor	11.60	
	130273	AW972422	Hs.153863	MAD (mothers against decapentaplegic, Dr	6.60	
	130259	NM_000328	Hs.153614	retinitis pigmentosa GTPase regulator		1.91
10	130090	H97878	Hs.132390	zinc finger protein 36 (KOX 18)	21.20	
	129958	R27496	Hs.1378	annexin A3	5.05	
	129898	AI672731	Hs.13256	ESTs		
	129875	AA181018	Hs.13056	hypothetical protein FLJ13920	18.60	
	129699	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligas		
15	129626	F13272	Hs.111334	ferritin, light polypeptide		
	129598	N30436	Hs.11556	Homo sapiens cDNA FLJ12566 fis, clone NT	22.63	
	129593	AI338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f		
	129565	X77777	Hs.198726	vasoactive intestinal peptide receptor 1		2.53
	129527	AA769221	Hs.270847	delta-tubulin	39.20	
20	129402	W72062	Hs.11112	ESTs		2.11
	129385	AA172106	Hs.110950	Rag C protein	15.20	
	129315	NM_014563	Hs.174038	spondyloepiphyseal dysplasia, late	12.40	
	129312	T97579	Hs.110334	ESTs, Weakly similar to I78885 serine/th	20.83	
	129240	AA361258	Hs.237868	interleukin 7 receptor		1.95
	129210	AL039940	Hs.202949	KIAA1102 protein		
25	129122	AW958473	Hs.301957	nudix (nucleoside diphosphate linked moi	4.20	
	129057	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)		
	128946	Y13153	Hs.107318	kynurenine 3-monooxygenase (kynurenine 3	5.20	
	128798	AF015525	Hs.302043	chemokine (C-C motif) receptor-like 2		
30	128789	AW368576	Hs.139851	caveolin 2		2.24
	128778	AA504776	Hs.186709	ESTs, Weakly similar to I38022 hypothet	12.20	
	128766	AW160432	Hs.296460	craniofacial development protein 1	26.40	
	128631	R44238	Hs.155546	KIAA1080 protein; Golgi-associated, gamm		1.78
	128624	BE154765	Hs.102647	ESTs, Weakly similar to TRHY_HUMAN TRICH		2.51
35	128609	NM_003616	Hs.102456	survival of motor neuron protein interac	16.00	
	128603	NM_004915	Hs.10237	ATP-binding cassette, sub-family G (WHIT	12.80	
	128598	AA305407	Hs.102308	potassium inwardly-rectifying channel, s	4.00	
	128458	H55864	Hs.56340	ESTs		
40	128061	AF150882	Hs.186877	sodium channel, voltage-gated, type XII,	17.20	
	127968	AA830201	Hs.124347	ESTs	21.30	
	127959	AI302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L		
	127944	AI557081	Hs.262476	S-adenosylmethionine decarboxylase 1	10.60	
	127925	AA805151	Hs.3628	mitogen-activated protein kinase kinase	13.40	
45	127896	AI669586	Hs.222194	ESTs	7.00	
	127859	AA761802	Hs.291559	ESTs	14.00	
	127817	AA836641	Hs.163085	ESTs	14.00	
	127742	AW293496	Hs.180138	ESTs	11.00	
	127628	AI240102	Hs.322430	NDRG family, member 4	11.10	
	127609	X80031	Hs.530	collagen, type IV, alpha 3 (Goodpasture		
50	127582	AA908954	Hs.130844	ESTs	19.60	
	127543	AK000787	Hs.157392	Homo sapiens cDNA FLJ20780 fis, clone CO	15.40	
	127535	AA568424	Hs.164450	ESTs	17.50	
	127404	AI379920	Hs.270224	ESTs	14.60	
	127396	L31968	Hs.187991	DKFZP564A122 protein	15.40	
55	127374	AA442797	Hs.312110	ESTs, Weakly similar to I38022 hypothet	14.60	
	127346	AA203616	Hs.44896	DnaJ (Hsp40) homolog, subfamily B, membe	21.00	
	127340	BE047653	Hs.119183	ESTs, Weakly similar to ZN91_HUMAN ZINC	15.80	
	127307	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5		
	127242	AW390395	Hs.181301	cathepsin S	22.60	
60	127167	AA625690	Hs.190272	ESTs	21.40	
	127046	AA321948	Hs.293968	ESTs	41.20	
	126928	AA480902	Hs.137401	ESTs	11.00	
	126900	AF137386	Hs.12701	plasmolipin		1.78
	126852	AA399961		gb:zu68c01.r1 Soares_testis_NHT Homo sap	5.60	
65	126816	AA248234		gb:csg2228.seq.F Human fetal heart, Lamb	12.20	
	126812	AB037860	Hs.173933	nuclear factor I/A	17.19	
	126666	AA648886	Hs.151999	ESTs	13.57	
	126645	AA316181	Hs.61635	six transmembrane epithelial antigen of	15.40	
	126592	AI611153	Hs.6093	Homo sapiens cDNA: FLJ22783 fis, clone K	4.67	
70	126556	AF255303	Hs.112227	membrane-associated nucleic acid binding	18.00	
	126433	AA325606		gb:EST28707 Cerebellum II Homo sapiens c	16.77	
	126299	AW979155	Hs.298275	amino acid transporter 2	14.60	
	126218	AL049801	Hs.13649	Novel human gene mapping to chromosome 13	3.50	
	126182	AA721331	Hs.293771	ESTs	13.40	
75	126177	AW752782	Hs.129750	hypothetical protein FLJ10546	18.20	
	126142	H86261	Hs.40568	ESTs	14.00	
	126077	M78772	Hs.210836	ESTs	16.59	
	125994	AI990529	Hs.270799	ESTs	17.40	
	125934	AA193325	Hs.32646	hypothetical protein FLJ21901	13.00	
80	125847	AW161885	Hs.249034	ESTs	49.57	
	125831	H04043		gb:yj45c03.r1 Soares placenta Nb2HP Homo		
	125731	R61771	Hs.26912	ESTs	13.20	
	125676	BE612918	Hs.151973	hypothetical protein FLJ23511	11.20	
	125561	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S		
	125552	H09701	Hs.278366	ESTs, Weakly similar to I38022 hypotheti	12.60	
85	125489	H49193	Hs.124984	ESTs, Moderately similar to ALU7_HUMAN A	33.40	

	125422	AA903229	Hs.153717	ESTs		1.80
	125331	AI422996	Hs.161378	ESTs	38.00	
	125309	T12411	Hs.183745	hypothetical protein FLJ13456	18.20	
5	125167	AL137540	Hs.102541	netrin 4		1.95
	125139	AW194933	Hs.9788	hypothetical protein MGC10924 similar to		1.84
	125042	T78906	Hs.269432	ESTs, Moderately similar to ALU1_HUMAN	21.80	
	124711	NM_004657	Hs.26530	serum deprivation response (phosphatidyl	10.60	
	124631	NM_014053	Hs.270594	FLVCR protein	23.20	
10	124578	N68321	Hs.231500	EST	21.43	
	124574	AL036596	Hs.42322	A kinase (PRKA) anchor protein 2		1.77
	124472	N52517	Hs.102670	EST	37.20	
	124438	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A		
	124357	N22401		gb:yw37g07.s1 Morton Fetal Cochlea Homo	14.64	
15	124306	AW973078	Hs.293039	ESTs		4.00
	124214	H58608	Hs.151323	ESTs		
	124097	AW298235	Hs.101689	ESTs	27.20	
	123978	T89832	Hs.170278	ESTs		2.03
	123972	T46848	Hs.70337	immunoglobulin superfamily, member 4	6.00	
20	123961	AL050184	Hs.21610	DKFZP434B203 protein		1.79
	123936	NM_004673	Hs.241519	angiopoietin-like 1	15.80	
	123802	AA620448		gb:ae58c09.s1 Stratagene lung carcinoma	4.23	
	123734	AA609861	Hs.312447	ESTs	4.20	
	123619	AA602964		gb:no97c02.s1 NCI_CGAP_Pr2 Homo sapiens	33.60	
25	123596	AA421130	Hs.112640	EST	10.93	
	123476	AA384564	Hs.108829	ESTs		2.18
	123340	AA504264	Hs.182937	peptidylprolyl isomerase A (cyclophilin	11.20	
	123190	AA489212	Hs.105228	EST	14.20	
	123136	AW451999	Hs.194024	ESTs		7.00
30	123073	AA485061	Hs.105652	ESTs	31.20	
	123055	AA482005	Hs.105102	ESTs, Weakly similar to reverse transcri		4.80
	122699	AA456130	Hs.301721	KIAA1255 protein		5.00
	122679	AA811286	Hs.192837	ESTs, Weakly similar to ALU5_HUMAN ALU S	14.40	
	122633	NM_001546	Hs.34853	inhibitor of DNA binding 4, dominant neg		
35	122553	AA451884	Hs.190121	ESTs	40.00	
	122544	AW973253	Hs.292689	ESTs	15.40	
	122485	AA524547	Hs.160318	FXD domain-containing ion transport reg		1.81
	122211	AA300900	Hs.98849	ESTs, Moderately similar to AF161511 i H	12.10	
	122127	AW207175	Hs.106771	ESTs		1.95
40	122011	AA431082		gb:zw78a10.s1 Soares_testis_NHT Homo sap		1.89
	121992	AI860775	Hs.98506	ESTs		3.60
	121989	W56487	Hs.193784	Homo sapiens mRNA; cDNA DKFZp586K1922 (f		2.01
	121835	AB033030	Hs.300670	KIAA1204 protein		1.85
	121726	AF241254	Hs.178098	angiotensin I converting enzyme (peptidy	12.43	
45	121690	AV660305	Hs.110286	ESTs		1.82
	121643	AA640987	Hs.193767	ESTs		
	121633	AA417011	Hs.98175	EST	14.00	
	121622	AA416931	Hs.126065	ESTs		16.40
	121497	AA412031	Hs.97901	EST	11.20	
50	121351	AW206227	Hs.287727	hypothetical protein FLJ23132	12.20	
	121314	W07343	Hs.182538	phospholipid scramblase 4		1.83
	121242	AA400857	Hs.97509	ESTs	22.40	
	121059	AA393283		gb:z174e03.r1 Soares_testis_NHT Homo sap	14.80	
55	120934	AA226198		gb:nc26a07.s1 NCI_CGAP_Pr1 Homo sapiens	21.20	
	120755	AA312934	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone		1.79
	120637	AA811804		gb:ob39a05.s1 NCI_CGAP_GCB1 Homo sapiens	20.00	
	120484	AA253170	Hs.96473	EST	40.20	
	120336	N85785	Hs.181165	eukaryotic translation elongation factor		6.60
	120266	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	16.80	
60	120132	W57554	Hs.125019	ESTs		4.73
	120041	AA830882	Hs.59368	ESTs		1.75
	119996	W88996	Hs.59134	EST		7.20
	119970	AA767718	Hs.93581	hypothetical protein FLJ10512	11.20	
	119861	W78816	Hs.49943	ESTs, Weakly similar to S65657 alpha-1C-		3.78
65	119824	W74536	Hs.184	advanced glycosylation end product-speci		
	119740	AW021407	Hs.21068	hypothetical protein	20.20	
	119271	AI061118	Hs.65328	Fanconi anemia, complementation group F	15.20	
	119221	C14322	Hs.250700	tryptase beta 1		
	119126	R45175	Hs.117183	ESTs	12.60	
70	119073	BE245360	Hs.279477	ESTs		
	118928	AA312799	Hs.283689	activator of CREM in testis		10.00
	118901	AW292577	Hs.94445	ESTs		3.96
	118661	AL137554	Hs.49927	protein kinase NYD-SP15		9.60
	118607	AI377444	Hs.54245	ESTs, Weakly similar to S65824 reverse t	10.40	
75	118449	AI813865	Hs.164478	hypothetical protein FLJ21939 similar to		1.90
	118416	N66028	Hs.49105	FKBP-associated protein	16.20	
	118379	N64491	Hs.48990	ESTs		4.00
	118329	N63520		gb:yy62f01.s1 Soares_multiple_sclerosis_		6.60
	118320	N63451	Hs.141600	ESTs, Weakly similar to alternatively s		3.80
80	118253	AA497044	Hs.20887	hypothetical protein FLJ10392	17.60	
	118124	N56968	Hs.46707	chromosome 21 open reading frame 37	14.00	
	118056	AB037746	Hs.42768	hypothetical protein DKFZp761O0113		1.86
	118032	N52802	Hs.47544	EST		5.00
	117840	T26379	Hs.48802	Homo sapiens clone 23632 mRNA sequence		4.00
85	117404	N39725	Hs.15220	zinc finger protein 106		1.90
	117314	N32498	Hs.42829	ESTs	14.20	

	117209	W03011	Hs.306881	MSTP043 protein			
	117023	AW070211	Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (f		2.31	
	116814	H50834		gb:yp86a10.s1 Soares fetal liver spleen	20.20		
5	116784	AB007979	Hs.301281	Homo sapiens mRNA, chromosome 1 specific		3.51	
	116766	AI608657	Hs.95097	ESTs	16.20		
	116712	AW901618	Hs.61935	Homo sapiens mRNA; cDNA DKFZp7611071 (fr		6.80	
	116707	H10344	Hs.49050	ESTs, Weakly similar to A Chain A, Human	18.60		
	116351	AL133623	Hs.82501	similar to mouse Xm1 / Dhms2 protein	19.40		
10	116279	AW971248	Hs.291289	ESTs, Weakly similar to ALU1_HUMAN ALU S			
	116166	AL039940	Hs.202949	KIAA1102 protein		2.13	
	116152	AL040521	Hs.15220	zinc finger protein 106		1.75	
	116117	BE613410	Hs.31575	SEC63, endoplasmic reticulum translocon	13.20		
	116107	AL133916	Hs.172572	hypothetical protein FLJ20093	30.11		
15	115965	AA001732	Hs.173233	hypothetical protein FLJ10970		2.36	
	115955	AF263613	Hs.44198	intracellular membrane-associated calciu	18.20		
	115844	AI373062	Hs.332938	hypothetical protein MGC5370	18.57		
	115683	AF255910	Hs.54650	junctional adhesion molecule 2		23.00	
	115673	AA406341	Hs.269908	Homo sapiens cDNA FLJ11991 fis, clone HE	11.82		
20	115672	AI889110	Hs.73251	ESTs	10.60		
	115566	AI142336	Hs.43977	Human DNA sequence from clone RP11-196N1		1.76	
	115313	AA808001	Hs.184411	albumin	25.20		
	115279	AW964897	Hs.290825	ESTs		8.00	
	115230	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L		1.80	
25	115110	AK001671	Hs.11387	KIAA1453 protein	14.20		
	114999	BE246481	Hs.87856	ESTs	19.20		
	114930	AA237022	Hs.188717	ESTs		5.60	
	114922	AA235672	Hs.87491	ESTs		3.60	
	114837	BE244930	Hs.166895	ESTs	43.70		
30	114769	AA149060	Hs.296100	ESTs	11.00		
	114761	AA143781	Hs.126280	hypothetical protein FLJ23393	14.00		
	114736	AI610347	Hs.103812	ESTs, Moderately similar to ALU1_HUMAN A		4.20	
	114596	AA310162	Hs.169248	cytochrome c	10.71		
	114518	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	20.40		
35	114455	H37908	Hs.271616	ESTs, Weakly similar to ALU8_HUMAN ALU S	20.40		
	114452	AI369275	Hs.243010	Homo sapiens cDNA FLJ14445 fis, clone HE		17.20	
	114359	NM_016929	Hs.283021	chloride intracellular channel 5		2.09	
	114357	R41677	Hs.6107	Homo sapiens cDNA FLJ14839 fis, clone OV	12.40		
40	114251	H15261	Hs.21948	ESTs		2.00	
	114138	AW384793	Hs.15740	Homo sapiens mRNA; cDNA DKFZp434E033 (fr		11.40	
	114124	W57554	Hs.125019	ESTs		6.04	
	113946	AW083883	Hs.37896	Homo sapiens cDNA FLJ13510 fis, clone PL		1.82	
	113695	T96965	Hs.17948	ESTs, Weakly similar to ALUB_HUMAN !!!!			
	113606	NM_013343	Hs.278951	NAG-7 protein		2.15	
45	113590	R49642	Hs.142447	ESTs, Weakly similar to ALU1_HUMAN ALU S		3.60	
	113560	T91015	Hs.268626	ESTs	32.00		
	113552	AI654223	Hs.16026	hypothetical protein FLJ23191			
	113540	AW152618	Hs.16757	ESTs			
50	113502	T89130		gb:ye12d01.s1 Stratagene lung (937210) H		8.35	
	113288	AI076838	Hs.12967	ESTs	12.40		
	113252	NM_004469	Hs.11392	c-fos induced growth factor (vascular en		4.27	
	113238	R45467	Hs.189813	ESTs			
	113203	AA743563	Hs.10305	ESTs	21.20		
	113195	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom		1.92	
55	113089	T40707	Hs.270862	ESTs	14.33		
	113076	AF033199	Hs.8198	zinc finger protein 204		6.00	
	113009	T23699	Hs.7246	ESTs		9.40	
	112937	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti		12.20	
	112891	T03927	Hs.293147	ESTs, Moderately similar to A46010 X-li	10.57		
60	112794	R97018		gb:yq74b08.s1 Soares fetal liver spleen	26.60		
	112691	R88708	Hs.220647	ESTs	15.33		
	112602	AW004045	Hs.203365	ESTs	15.60		
	112366	AF035318	Hs.12533	Homo sapiens clone 23705 mRNA sequence	15.40		
	112210	R49645	Hs.7004	ESTs	14.00		
65	112064	AL049390	Hs.22689	Homo sapiens mRNA; cDNA DKFZp586O1318 (f	13.00		
	111998	R42379	Hs.138283	ESTs	11.00		
	111987	NM_015310	Hs.6763	KIAA0942 protein	22.40		
	111803	AA593731	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A		1.77	
	111737	H04607	Hs.9218	ESTs		1.86	
70	111605	T91061	Hs.194178	ESTs, Moderately similar to PC4259 ferri	23.00		
	111510	R07856	Hs.16355	ESTs	11.02		
	111341	AL157484	Hs.22483	Homo sapiens mRNA; cDNA DKFZp762M127 (fr		1.88	
	111280	AA373527	Hs.19385	CGI-58 protein	18.40		
	111247	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f			
75	111232	AI247763	Hs.16928	ESTs	27.60		
	110942	R63503	Hs.28419	ESTs	14.80		
	110924	AW058463	Hs.12940	zinc-fingers and homeoboxes 1	24.71		
	110837	H03109	Hs.108920	HTO18 protein		2.18	
	110824	AI767183	Hs.26942	ESTs	12.20		
80	110776	AB032417	Hs.19545	frizzled (Drosophila) homolog 4		1.75	
	110576	H60869	Hs.37889	ESTs	13.00		
	110359	AK000768	Hs.107872	hypothetical protein FLJ20761		5.60	
	110099	R44557	Hs.23748	ESTs		2.31	
	109984	AI796320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PL			
85	109958	AA001266	Hs.133521	ESTs	11.25		
	109893	AA884208	Hs.30484	ESTs		2.68	

5	109842	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	23.83		
	109837	H00656	Hs.29792	ESTs, Weakly similar to I38022 hypotheti		17.20	3.91
	109796	AI800515	Hs.12024	ESTs		9.60	
	109688	R41900	Hs.22245	ESTs			
	109648	H17800	Hs.7154	ESTs	22.80		
10	109613	H47315	Hs.27519	ESTs			
	109550	AW021488	Hs.26981	ESTs			
	109523	AW193342	Hs.24144	ESTs			1.89
	109472	AK001989	Hs.91165	hypothetical protein		6.00	
	109355	AA524525	Hs.48297	DKFZP586C1620 protein	15.00		
15	109260	AW978515	Hs.131915	KIAA0863 protein	25.60		
	108781	AA128654		gb:zn98g07.s1 Stratagene fetal retina 93	14.20		
	108663	BE219231	Hs.292653	ESTs, Weakly similar to T26845 hypotheti	11.00		
	108573	AA086005		gb:zl84c04.s1 Stratagene colon (937204)	26.00		
	108480	AL133092	Hs.68055	hypothetical protein DKFZp434I0428			
20	108382	NM_006770	Hs.67726	macrophage receptor with collagenous str			1.83
	108174	AA055632	Hs.303070	ESTs	15.20		
	108138	AL049990	Hs.51515	Homo sapiens mRNA; cDNA DKFZp564G112 (fr		3.60	
	108087	AA045708	Hs.40545	ESTs	15.44		
	108048	AI797341	Hs.165195	Homo sapiens cDNA FLJ14237 fis, clone NT		11.40	
25	108041	AW204712	Hs.61957	ESTs			
	107997	AL049176	Hs.82223	chordin-like		4.76	
	107994	AA036811	Hs.48469	LIM domains containing 1			
	107922	BE153855	Hs.61460	Ig superfamily receptor LNIR	14.20		
	107681	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	51.80		
30	107666	AA010611	Hs.60418	EST	29.20		
	107332	T87750	Hs.183297	DKFZP566F2124 protein	10.73		
	107292	BE166479	Hs.4789	Homo sapiens serologically defined breas	32.00		
	107230	AI034467	Hs.34650	ESTs	17.40		
	107168	W57578	Hs.237955	RAB7, member RAS oncogene family	10.43		
35	107160	AA314490	Hs.27669	KIAA1563 protein	11.40		
	107054	AI076459	Hs.15978	KIAA1272 protein			
	107029	AF264750	Hs.288971	myeloid/lymphoid or mixed-lineage leukem	21.40		
	106999	H93281	Hs.10710	hypothetical protein FLJ20417	35.80		
	106954	AF128847	Hs.204038	indolethylamine N-methyltransferase			1.76
40	106870	AI983730	Hs.26530	serum deprivation response (phosphatidyl			
	106865	AW192535	Hs.19479	ESTs	13.40		
	106844	AA485055	Hs.158213	sperm associated antigen 6		7.13	
	106820	NM_016831	Hs.12592	period (Drosophila) homolog 3		7.00	
	106818	AK002135	Hs.3542	hypothetical protein FLJ11273	13.00		
45	106797	AI768801	Hs.169943	Homo sapiens cDNA FLJ13569 fis, clone PL			2.05
	106773	AA478109	Hs.188833	ESTs			
	106747	NM_007118	Hs.171957	triple functional domain (PTPRF interact	12.60		
	106743	BE613328	Hs.21938	hypothetical protein FLJ12492	10.60		
	106667	AW360847	Hs.16578	ESTs			
50	106605	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr			2.40
	106567	AW450408	Hs.86412	chromosome 9 open reading frame 5			1.78
	106562	AL031846	Hs.152151	plakophilin 4			1.76
	106536	AA329648	Hs.23804	ESTs, Weakly similar to PN0099 son3 prot			2.19
	106533	AL134708	Hs.145998	ESTs	23.20		
55	106507	AA259068	Hs.267819	protein phosphatase 1, regulatory (inhib	15.20		
	106490	AA404265	Hs.115537	putative dipeptidase			
	106474	BE383668	Hs.42484	hypothetical protein FLJ10618	10.44		
	106211	AA428240	Hs.126083	ESTs		29.80	
	105986	AB037722	Hs.8707	KIAA1301 protein		3.70	
60	105894	AI904740	Hs.25691	receptor (calcitonin) activity modifying			1.94
	105847	AW964490	Hs.32241	ESTs, Weakly similar to S65657 alpha-1C-			1.75
	105803	AW747996	Hs.160999	ESTs, Moderately similar to A56194 throm			2.47
	105731	AA834664	Hs.29131	nuclear receptor coactivator 2	10.71		
	105729	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds			
65	105688	AI299139	Hs.17517	ESTs	23.40		
	105510	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	37.20		
	105101	H63202	Hs.38163	ESTs		8.30	
	104989	R65998	Hs.285243	hypothetical protein FLJ22029		8.09	
	104986	AW088826	Hs.117176	poly(A)-binding protein, nuclear 1			1.92
70	104969	AI670947	Hs.78406	phosphatidylinositol-4-phosphate 5-kinas		5.40	
	104903	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,		7.60	
	104896	AW015318	Hs.23165	ESTs	13.80		
	104865	T79340	Hs.22575	Homo sapiens cDNA: FLJ21042 fis, clone C			
	104825	AA035613	Hs.141883	ESTs			1.87
75	104781	AA099904	Hs.21610	DKFZP434B203 protein			1.93
	104776	AA026349		gb:zj99f01.s1 Soares_pregnant_uterus_NbH		10.20	
	104691	U29590	Hs.37744	Homo sapiens beta-1 adrenergic receptor		5.69	
	104667	AI239923	Hs.30098	ESTs		3.82	
	104404	H58762		gb:EST00057 HE6W Homo sapiens cDNA clone		4.20	
80	104392	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	27.20		
	104212	AB002298	Hs.173035	KIAA0300 protein			1.91
	104074	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	11.20		
	103749	AL135301	Hs.8768	hypothetical protein FLJ10849	10.86		
	103645	AW246253	Hs.7043	succinate-CoA ligase, GDP-forming, alpha	12.00		
85	103554	AI878826	Hs.323469	caveolin 1, caveolae protein, 22kD			1.80
	103541	AI815601	Hs.79197	CD83 antigen (activated B lymphocytes, i			
	103496	Y09267	Hs.132821	flavin containing monooxygenase 2			
	103428	BE383507	Hs.78921	A kinase (PRKA) anchor protein 1	11.20		
	103353	X89399	Hs.119274	RAS p21 protein activator (GTPase activa	19.80		

	103295	X81479	Hs.2375	egf-like module containing, mucin-like,	3.60	
	103280	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula		
	103100	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)		1.76
5	103025	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t		2.15
	102698	M18667	Hs.1867	progastricsin (pepsinogen C)		
	102659	BE245169	Hs.211610	CUG triplet repeat, RNA-binding protein	11.00	
	102580	U60808	Hs.152981	CDP-diacylglycerol synthase (phosphatida	25.40	
	102417	AA034127	Hs.153487	signal transducing adaptor molecule (SH3	14.00	
10	102363	NM_003734	Hs.198241	amine oxidase, copper containing 3 (vasc		
	102302	AA306342	Hs.69171	protein kinase C-like 2	10.86	
	102283	AW161552	Hs.83381	guanine nucleotide binding protein 11		
	102188	U20350	Hs.78913	chemokine (C-X3-C) receptor 1		7.40
	102151	T27013	Hs.3132	steroidogenic acute regulatory protein	16.40	
15	101957	L28824	Hs.74101	spleen tyrosine kinase	15.40	
	101842	M93221	Hs.75182	mannose receptor, C type 1		
	101771	NM_002432	Hs.153837	myeloid cell nuclear differentiation ant		
	101764	AI198550	Hs.81256	S100 calcium-binding protein A4 (calcium		1.78
	101716	AF050658	Hs.2563	tachykinin, precursor 1 (substance K, su	18.80	
20	101678	M62505	Hs.2161	complement component 5 receptor 1 (C5a I		2.22
	101447	M21305		gb:Human alpha satellite and satellite 3	504.80	
	101383	NM_000132	Hs.79345	coagulation factor VIII, procoagulant co		31.00
	101346	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N		1.75
	101345	NM_005795	Hs.152175	calcitonin receptor-like		
25	101336	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene h		2.24
	101330	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do		
	101277	BE297626	Hs.296049	microfibrillar-associated protein 4		
	101262	L35854		gb:Human dystrophin (dp140) mRNA, 5' end	19.00	
	101168	NM_005308	Hs.211569	G protein-coupled receptor kinase 5		2.01
30	101102	NM_003243	Hs.79059	transforming growth factor, beta recepto		
	101088	X70697	Hs.553	solute carrier family 6 (neurotransmitte		7.52
	101066	AW970254	Hs.889	Charot-Leyden crystal protein	19.38	
	100971	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte		1.91
	100893	BE245294	Hs.180789	S164 protein	15.40	
35	100770	W25797.comp	Hs.177486	amyloid beta (A4) precursor protein (pro	11.20	
	100716	X89887	Hs.172350	HIR (histone cell cycle regulation defec	14.80	
	100555	M69181		gb:Human nonmuscle myosin heavy chain-B	33.00	
	100425	NM_014747	Hs.78748	KIAA0237 gene product	16.20	
40	100408	D86640	Hs.56045	src homology three (SH3) and cysteine ri		4.00
	100382	D83407	Hs.156007	Down syndrome critical region gene 1-lik		4.24
	100351	D64158				6.20
	100299	D49493	Hs.2171	growth differentiation factor 10		21.20
	100134	AA305746	Hs.49	macrophage scavenger receptor 1		
	100108	U09577	Hs.76873	hyaluronoglucosaminidase 2		1.79
45	100095	Z97171	Hs.78454	myocilin, trabecular meshwork inducible		5.40
	100066				11.29	

TABLE 3B shows the accession numbers for those primekeys lacking unigenelD's for Table 3A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

	Pkey	CAT number	Accessions
60	123619	371681_1	AA602964 AA609200
	126433	127143_1	AA325606 AA099517 N89423
	125831	1522905_1	H04043 D60988 D60337
65	126816	122973_1	AA248234 AA090985
	126852	136135_1	AA399961 AA128347
	121059	273450_1	AA393283 AA398628
	120637	200885_1	AA811804 AA809404 AA286907 AW977624
	122011	7617_-2	AA431082
70	120934	177521_1	AA226198 AA226513 AA383773
	123802	genbank_AA620448	AA620448
	116814	genbank_H50834	H50834
	118329	genbank_N63520	N63520
	104404	H58762_at	H58762
75	104776	genbank_AA026349	AA026349
	113502	genbank_T89130T89130	
	101262	entrez_L35854 L35854	
	108573	genbank_AA086005	AA086005
	101447	entrez_M21305 M21305	
80	124357	genbank_N22401	N22401
	108781	genbank_AA128654	AA128654
	112794	genbank_R97018	R97018
	100351	entrez_D64158	D64158
85	100555	tigr_HT2245	M69181 M81105 U51039

Table 4A shows 202 genes up-regulated in samples from patients treated with chemotherapy or radiotherapy. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: average of AI for samples from patients treated with chemotherapy or radiotherapy divided by the average of AI for normal lung samples.

Pkey	ExAccn	UnigenelD	Unigene Title	R1
100113	NM_001269	Hs.84746	chromosome condensation 1	27.20
100187	D17793	Hs.78183	aldo-keto reductase family 1, member C3	20.60
100210	D26361	Hs.3104	KIAA0042 gene product	20.40
100225	D28539	Hs.167185	glutamate receptor, metabotropic 5	20.60
100269	NM_001949	Hs.1189	E2F transcription factor 3	29.40
100438	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	23.50
100877	X80821	Hs.27973	KIAA0874 protein	35.56
100893	BE245294	Hs.180789	S164 protein	43.40
101273	Z11933	Hs.182505	POU domain, class 3, transcription facto	21.80
101447	M21305		gb:Human alpha satellite and satellite 3	193.60
101649	AW959908	Hs.1690	heparin-binding growth factor binding pr	38.40
101724	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	198.80
101748	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	78.60
101809	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	162.20
101879	AA176374	Hs.243886	nuclear autoantigenic sperm protein (hls	50.00
101915	AF207881	Hs.155185	cytosolic ovarian carcinoma antigen 1	26.00
101973	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	37.20
102025	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	
102031	U04898	Hs.2156	RAR-related orphan receptor A	32.00
102052	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	51.20
102391	AA296874	Hs.77494	deoxyguanosine kinase	13.90
102420	U44060	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	28.80
102610	U65011	Hs.30743	preferentially expressed antigen in mela	110.60
102829	NM_006183	Hs.80962	neurotensin	116.80
103000	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	2.30
103036	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	181.40
103507	AJ000512	Hs.296323	serum/glucocorticoid regulated kinase	49.20
103587	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	86.60
104660	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (fr	42.60
104896	AW015318	Hs.23165	ESTs	29.40
105038	AW503733	Hs.9414	KIAA1488 protein	21.50
105298	BE387790	Hs.26369	hypothetical protein FLJ20287	32.80
105510	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	20.20
105667	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	28.40
106073	AL157441	Hs.17834	downstream neighbor of SON	25.40
106205	AW965058	Hs.111583	ESTs, Weakly similar to I38022 hypotheti	32.00
106516	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (40.60
106533	AL134708	Hs.145998	ESTs	59.80
106575	AW970602	Hs.105421	ESTs	43.40
106654	AW075485	Hs.286049	phosphoserine aminotransferase	50.80
106851	AI458623		gb:tk04g09.x1 NCL_CGAP_Lu24 Homo sapiens	53.40
106995	AB023139	Hs.37892	KIAA0922 protein	20.88
107332	T87750	Hs.183297	DKFZP566F2124 protein	23.60
107532	AA443473	Hs.173684	Homo sapiens mRNA; cDNA DKFZp762G207 (fr	57.20
107922	BE153855	Hs.61460	Ig superfamily receptor LNIR	49.00
108609	BE409857	Hs.69499	hypothetical protein	19.67
108780	AU076442	Hs.117938	collagen, type XVII, alpha 1	48.17
109166	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rakbines	59.20
109260	AW978515	Hs.131915	KIAA0863 protein	28.60
109280	AK001355	Hs.279610	hypothetical protein FLJ10493	22.80
109292	AW975746	Hs.188662	KIAA1702 protein	
109384	AA219172	Hs.86849	ESTs	21.00
109415	U80736	Hs.110826	trinucleotide repeat containing 9	31.60
109445	AA232103	Hs.189915	ESTs	24.20
109502	AW967069	Hs.211556	hypothetical protein MGC5487	21.40
109633	AW003785	Hs.170267	ESTs	20.40
109786	AI989482	Hs.146286	kinesin family member 13A	19.60
109958	AA001266	Hs.133521	ESTs	24.00
110920	N47224	Hs.20521	HMT1 (hnRNP methyltransferase, S. cerevi	28.40
110924	AW058463	Hs.12940	zinc-fingers and homeoboxes 1	36.00
111084	H44186	Hs.15456	PDZ domain containing 1	61.20
111132	AB037807	Hs.83293	hypothetical protein	24.60
111229	AW389845	Hs.110855	ESTs	27.20
111337	AA837396	Hs.263925	LIS1-interacting protein NUDE1, rat homo	48.00
111987	NM_015310	Hs.6763	KIAA0942 protein	37.80
112046	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	26.80
112268	W39609	Hs.22003	solute carrier family 6 (neurotransmitte	63.80
112685	R87650	Hs.33439	ESTs, Weakly similar to ALU1_HUMAN ALU	26.40
112871	AL110216	Hs.12285	ESTs, Weakly similar to I55214 salivary	47.64
112897	AW206453	Hs.3782	ESTs	22.00
112973	AB033023	Hs.318127	hypothetical protein FLJ10201	65.00
112992	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	42.00
113073	N39342	Hs.103042	microtubule-associated protein 1B	55.40

	113494	T91451	Hs.86538	ESTs	22.80
	113560	T91015	Hs.268626	ESTs	22.80
	113849	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	51.80
5	113950	AI267652	Hs.30504	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	28.20
	114339	AA782845	Hs.22790	ESTs	20.20
	114365	H42169	Hs.18653	hypothetical protein FLJ14627	21.00
	114455	H37908	Hs.271616	ESTs, Weakly similar to ALU8_HUMAN ALU S	25.80
	114518	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	23.60
10	114824	AA960961	Hs.305953	zinc finger protein 83 (HPF1)	27.20
	114837	BE244930	Hs.166895	ESTs	30.20
	114974	AW966931	Hs.179662	nucleosome assembly protein 1-like 1	20.80
	115075	AA814043	Hs.88045	ESTs	30.60
	115084	BE383668	Hs.42484	hypothetical protein FLJ10618	28.86
15	115291	BE545072	Hs.122579	hypothetical protein FLJ10461	38.00
	115313	AA808001	Hs.184411	albumin	22.60
	115697	D31382	Hs.63325	transmembrane protease, serine 4	173.60
	115909	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	27.77
	116090	AI591147	Hs.61232	ESTs	20.80
20	116107	AL133916	Hs.172572	hypothetical protein FLJ20093	164.20
	116399	AA889120	Hs.110637	homeo box A10	38.00
	117099	H93699		gb:yy16a11.s1 Soares fetal liver spleen	21.60
	117881	AF161470	Hs.260622	butyrate-induced transcript 1	49.40
	118091	AW005054	Hs.47883	ESTs, Weakly similar to KCC1_HUMAN CALCI	22.40
25	118138	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	22.00
	118720	N73515		gb:za49d07.s1 Soares fetal liver spleen	20.00
	118873	AI824009	Hs.44577	ESTs	19.40
	119126	R45175	Hs.117183	ESTs	111.20
	119717	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	33.00
30	119940	AI050097	Hs.272531	DKFZP586B0319 protein	31.00
	120266	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	20.20
	120515	AA258356		gb:zr59c10.s1 Soares_NhHMPu_S1 Homo sapi	25.00
	120859	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol	95.40
	120983	AA398209	Hs.97587	EST	105.20
35	121054	AW976570	Hs.97387	ESTs	38.80
	121369	AW450737	Hs.128791	CGI-09 protein	41.60
	122335	AA443258	Hs.241551	chloride channel, calcium activated, fam	30.80
	122612	AA974832	Hs.128708	ESTs	19.60
40	123130	AA487200		gb:ab19f02.s1 Stratagene lung (937210) H	33.20
	123440	AI733692	Hs.112488	ESTs	23.17
	123596	AA421130	Hs.112640	EST	23.00
	123619	AA602964		gb:no97c02.s1 NCL_CGAP_Pr2 Homo sapiens	28.80
	124006	AI147155	Hs.270016	ESTs	77.60
	124169	BE079334	Hs.271630	ESTs	22.20
45	124281	AI333756	Hs.111801	arsenate resistance protein ARS2	42.20
	124472	N52517	Hs.102670	EST	32.60
	124617	AW628168	Hs.152684	ESTs	21.80
	124631	NM_014053	Hs.270594	FLVCR protein	30.40
	124839	R55784	Hs.140942	ESTs	21.20
50	125186	AA610620	Hs.181244	major histocompatibility complex, class	42.80
	125321	T86652	Hs.178294	ESTs	27.00
	125535	NM_013243	Hs.22215	secretogranin III	23.80
	125646	AA628962	Hs.75209	protein kinase (cAMP-dependent, catalyti	23.20
	125684	AW589427	Hs.158849	Homo sapiens cDNA: FLJ21663 fis, clone C	21.20
55	125724	AL360190	Hs.295978	Homo sapiens mRNA full length insert cDN	48.80
	125847	AW161885	Hs.249034	ESTs	31.00
	125934	AA193325	Hs.32646	hypothetical protein FLJ21901	21.20
	126077	M78772	Hs.210836	ESTs	49.80
	126299	AW979155	Hs.298275	amino acid transporter 2	21.80
60	126395	AI468004	Hs.278956	hypothetical protein FLJ12929	71.00
	126433	AA325606		gb:EST28707 Cerebellum II Homo sapiens c	23.20
	126509	R47400	Hs.23850	ESTs	23.80
	126538	AB030656	Hs.17377	coronin, actin-binding protein, 1C	23.10
	126666	AA648886	Hs.151999	ESTs	36.00
65	126812	AB037860	Hs.173933	nuclear factor I/A	20.80
	126872	AW450979		gb:U1-H-BI3-ala-a-12-0-U1.s1 NCL_CGAP_Su	46.29
	127046	AA321948	Hs.293968	ESTs	22.80
	127431	AW771958	Hs.175437	ESTs, Moderately similar to PC4259 ferri	30.00
	127489	AA650250	Hs.272076	ESTs	20.80
70	127521	AW297206	Hs.164018	ESTs	25.20
	127742	AW293496	Hs.180138	ESTs	28.00
	127925	AA805151	Hs.3628	mitogen-activated protein kinase kinase	21.20
	127930	AA809672	Hs.123304	ESTs	20.54
	127968	AA830201	Hs.124347	ESTs	28.20
75	127987	AI022103	Hs.124511	ESTs	19.60
	128116	H07103	Hs.286014	Homo sapiens, clone IMAGE:3867243, mRNA	20.40
	128609	NM_003616	Hs.102456	survival of motor neuron protein interac	34.40
	128777	AI878918	Hs.10526	cysteine and glycine-rich protein 2	53.80
	128949	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	23.00
80	129168	AI132988	Hs.109052	chromosome 14 open reading frame 2	37.60
	129404	AI267700	Hs.317584	ESTs	28.60
	129527	AA769221	Hs.270847	delta-tubulin	40.80
	129574	AA026815	Hs.11463	UMP-CMP kinase	31.20
	129598	N30436	Hs.11556	Homo sapiens cDNA FLJ12566 fis, clone NT	29.60
85	129785	H19006	Hs.184780	ESTs	72.20
	129970	AV655806	Hs.296198	chromosome 12 open reading frame 4	22.20

	130149	AW067805	Hs.172665	methyleneletrahydrofolate dehydrogenase	29.60
	130199	Z48579	Hs.172028	a disintegrin and metalloproteinase doma	27.60
	130441	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	28.36
5	130466	W19744	Hs.180059	Homo sapiens cDNA FLJ20653 fis, clone KA	20.20
	130482	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	22.40
	130617	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	19.60
	130703	R77776	Hs.18103	ESTs	19.40
	130732	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)	21.40
10	130867	NM_001072	Hs.284239	UDP glycosyltransferase 1 family, polype	110.00
	131028	AI879165	Hs.2227	CCAAT/enhancer binding protein (C/EBP),	25.20
	131086	AL035461	Hs.2281	chromogranin B (secretogranin 1)	40.60
	131284	NM_001429	Hs.25272	E1A binding protein p300	24.60
	131775	AB014548	Hs.31921	KIAA0648 protein	21.00
15	131860	BE383676	Hs.334	Rho guanine nucleotide exchange factor (33.40
	131945	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	60.80
	132040	NM_001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fis, clone H	20.40
	132084	NM_002267	Hs.3886	karyopherin alpha 3 (importin alpha 4)	29.40
	132389	AA310393	Hs.190044	ESTs	32.40
20	132437	AA152106	Hs.4869	cyclin L ania-6a	27.40
	132550	AW969253	Hs.170195	bone morphogenetic protein 7 (osteogenic	75.60
	132617	AF037335	Hs.5338	carbonic anhydrase XII	31.36
	132632	AU076916	Hs.5398	guanine monophosphate synthetase	32.40
	132672	W27721	Hs.54697	Cdc42 guanine exchange factor (GEF) 9	23.40
25	132742	AA025480	Hs.292812	ESTs, Weakly similar to T33468 hypothi	61.20
	132771	Y10275	Hs.56407	phosphoserine phosphatase	22.33
	133070	U92649	Hs.64311	a disintegrin and metalloproteinase doma	23.50
	133153	AF070592	Hs.66170	HSKM-B protein	30.00
	133181	X91662	Hs.66744	twist (<i>Drosophila</i>) homolog (<i>acrocephalos</i>	23.80
30	133282	AA449015	Hs.286145	SRB7 (suppressor of RNA polymerase B, ye	51.60
	133350	AI499220	Hs.71573	hypothetical protein FLJ10074	33.00
	133592	AV652066	Hs.75113	general transcription factor IIIA	82.00
	133658	AA319146	Hs.75426	secretogranin II (chromogranin C)	
	133865	AB011155	Hs.170290	discs, large (<i>Drosophila</i>) homolog 5	69.33
35	134032	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	33.20
	134125	NM_014781	Hs.50421	KIAA0203 gene product	31.60
	134158	U15174	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	30.60
	134321	BE538082	Hs.8172	ESTs, Moderately similar to A46010 X-lin	23.40
	134367	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	49.20
40	134570	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	20.20
	134753	NM_006482	Hs.173135	dual-specificity tyrosine-(Y)-phosphoryl	20.80
	135002	AA448542	Hs.251677	G antigen 7B	37.60
	135029	H58818	Hs.187579	hydroxysteroid (17-beta) dehydrogenase	53.40
	135047	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	31.60
45	135345	X53655	Hs.99171	neurotrophin 3	28.80

TABLE 4B shows the accession numbers for those primekeys lacking unigenelD's for Table 4A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT number	Accessions
123619	371681_1	AA602964 AA609200
126433	127143_1	AA325606 AA099517 N89423
126872	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359
		BE011367 BE011368 BE011362 BE011215 BE011365 BE011363
106851	322947_1	AI458623 AA639708 AA485409 R22065 AA485570
118720	genbank_N73515	N73515
120515	genbank_AA258356	AA258356
117099	321871_1	H93699 H97976 H80036
101447	entrez_M21305	M21305
123130	genbank_AA487200	AA487200

Table 5A shows 680 genes up-regulated in squamous cell carcinoma or adenocarcinoma lung tumors relative to normal lung and chronically diseased lung. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

5	Pkey:	Unique Eos probeset identifier number							
	ExAccn:	Exemplar Accession number, Genbank accession number							
	UnigeneID:	Unigene number							
	Unigene Title:	Unigene gene title							
10	R1:	70th percentile of AI for squamous cell carcinoma and adenocarcinoma lung tumor samples divided by the 90th percentile of AI for normal and chronically diseased lung samples.							
	R2:	80th percentile of AI adenocarcinoma lung tumor samples divided by the 90th percentile of AI for normal and chronically diseased lung samples.							
	R3:	80th percentile of AI squamous cell carcinoma lung tumor samples divided by the 90th percentile of AI for normal and chronically diseased lung samples.							
	R4:	80th percentile of AI adenocarcinoma lung tumor samples divided by the 80th percentile of AI for squamous cell carcinoma lung tumor samples.							
15	R5:	70th percentile of AI for squamous cell carcinoma and adenocarcinoma lung tumor samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples divided by 90th percentile of AI for normal and chronically diseased lung samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples							
	Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2	R3	R4	R5
20	100035			AFFX control: GAPDH					6.76
	100036			AFFX control: GAPDH					5.77
	100037			AFFX control: GAPDH					5.75
25	100071	A28102		Human GABAA receptor alpha-3 subunit		8.00			
	100114	X02308	Hs.82962	thymidylate synthetase					5.71
	100154	H60720	Hs.81892	KIAA0101 gene product	3.84				
	100187	D17793	Hs.78183	aldo-keto reductase family 1, member C3	3.33				
	100188	AW247090	Hs.57101	minichromosome maintenance deficient (S.					4.52
	100202	BE294407	Hs.99910	phosphofructokinase, platelet					5.49
30	100216	AA489908	Hs.1390	proteasome (prosome, macropain) subunit,					5.67
	100269	NM_001949	Hs.1189	E2F transcription factor 3	2.55				
	100287	AU076657	Hs.1600	chaperonin containing TCP1, subunit 5 (e					5.66
	100297	AU077258	Hs.182429	protein disulfide isomerase-related prot					3.81
	100330	AW410976	Hs.77152	minichromosome maintenance deficient (S.					4.50
35	100335	AW247529	Hs.6793	platelet-activating factor acetylhydrola	5.07				
	100360	W70171	Hs.75939	uridine monophosphate kinase					4.82
	100372	NM_014791	Hs.184339	KIAA0175 gene product					3.79
	100474	NM_000699	Hs.300280	amylase, alpha 2A; pancreatic				15.65	
40	100486	T19006	Hs.10842	RAN, member RAS oncogene family					5.49
	100491	D56165	Hs.275163	non-metastatic cells 2, protein (NM23B)					4.17
	100516	D90278	Hs.11	carcinoembryonic antigen-related cell ad		7.20			
	100522	X51501	Hs.99949	prolactin-induced protein				14.20	
	100559	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	3.10				
	100576	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid				9.30	
45	100629	AA015693	Hs.12191	mitogen-activated protein kinase kinase				20.60	
	100661	BE623001	Hs.132748	Homo sapiens ribosomal protein L39 mRNA,	3.85				
	100677	AA353686	Hs.57813	zinc ribbon domain containing, 1		8.60			
	100696	D14887	Hs.121686	general transcription factor IIA, 1 (37k				10.00	
	100709	N26539	Hs.100469	myeloid/lymphoid or mixed-lineage leukem			24.80		
50	100761	BE208491	Hs.295112	KIAA0618 gene product		7.60			
	100830	AC004770	Hs.4756	flap structure-specific endonuclease 1					7.99
	100867	U14622		gb:Human transketolase-like protein gene		10.20			
	100902	M16029	Hs.287270	ret proto-oncogene (multiple endocrine n		8.00			
55	100906	AU076916	Hs.5398	guanine monophosphate synthetase					5.16
	100960	J00124	Hs.117729	keratin 14 (epidermolysis bullosa simple	2.57				
	101045	J05614		gb:Human proliferating cell nuclear anti					4.69
	101061	NM_000175	Hs.180532	glucose phosphate isomerase					4.19
	101071	L02840	Hs.84244	potassium voltage-gated channel, Shab-re		12.91			
60	101124	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	3.12				
	101175	U82671	Hs.36980	melanoma antigen, family A, 2	3.50				
	101181	BE262621	Hs.73798	macrophage migration inhibitory factor (5.69
	101204	L24203	Hs.82237	ataxia-telangiectasia group D-associated	4.08				
	101210	L29301	Hs.2353	opioid receptor, mu 1			6.40		
65	101216	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	2.53				
	101228	AA333387	Hs.82916	chaperonin containing TCP1, subunit 6A (7.90
	101233	AL135173	Hs.878	sorbitol dehydrogenase					4.45
	101273	Z11933	Hs.182505	POU domain, class 3, transcription facto	8.50				
	101342	U52112	Hs.182018	interleukin-1 receptor-associated kinase					4.17
70	101346	A1738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N				21.89	
	101369	NM_000892	Hs.1901	kallikrein B, plasma (Fletcher factor) 1				12.80	
	101396	BE267931	Hs.78996	proliferating cell nuclear antigen	3.24				
	101431	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)					7.90
	101448	NM_000424	Hs.195850	keratin 5 (epidermolysis bullosa simplex	8.31				
75	101462	AL035668	Hs.73853	bone morphogenetic protein 2				38.80	
	101466	BE262660	Hs.170197	glutamic-oxaloacetic transaminase 2, mit					4.01
	101484	AA053486	Hs.20315	interferon-induced protein with tetratri				12.00	
	101502	M26958		gb:Human parathyroid hormone-related pro	10.50				
	101505	AA307680	Hs.75692	asparagine synthetase					4.46
	101526	NM_002197	Hs.154721	aconitase 1, soluble	4.02				
80	101535	X57152	Hs.99853	fibrillarin					4.65
	101577	M34353	Hs.1041	v-ros avian UR2 sarcoma virus oncogene h				9.09	
	101649	AW959908	Hs.1690	heparin-binding growth factor binding pr	54.00				
	101663	NM_003528	Hs.2178	H2B histone family, member Q	5.59				
	101664	AA436989	Hs.121017	H2A histone family, member A	7.00				
85	101669	L24498	Hs.80409	growth arrest and DNA-damage-inducible,		7.60			

	101695	M69136	Hs.135626	chymase 1, mast cell	4.79			
	101724	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	15.21			
	101748	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen)	55.50			
5	101759	M80244	Hs.184601	solute carrier family 7 (cationic amino)			4.10	
	101771	NM_002432	Hs.153837	myeloid cell nuclear differentiation ant		18.57		
	101804	M85699	Hs.169840	TTK protein kinase	4.50			
	101809	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	140.00			
	101833	AU076442	Hs.117938	collagen, type XVII, alpha 1	2.56			
10	101842	M93221	Hs.75182	mannose receptor, C type 1		12.80		
	101851	BE260964	Hs.82045	midkine (neurite growth-promoting factor			5.88	
	102002	NM_002484	Hs.81469	nucleotide binding protein 1 (E.coli Min	7.80			
	102039	AL134223	Hs.306098	aldo-keto reductase family 1, member C1			4.35	
	102072	U09410	Hs.78743	zinc finger protein 131 (clone pHZ-10)		7.40		
15	102083	T35901	Hs.75117	interleukin enhancer binding factor 2, 4			5.12	
	102111	L36196	Hs.81884	sulfotransferase family, cytosolic, 2A,		12.00		
	102123	NM_001809	Hs.1594	centromere protein A (17kD)	6.20			
	102154	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	2.62			
	102193	AL036335	Hs.313	secreted phosphoprotein 1 (osteopontin,	5.85			
20	102217	AA829978	Hs.301613	JTV1 gene			6.18	
	102224	NM_002810	Hs.148495	proteasome (prosome, macropain) 26S subu			4.49	
	102234	AW163390	Hs.278554	heterochromatin-like protein 1			5.80	
	102251	NM_004398	Hs.41706	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	4.50			
	102305	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)			5.15	
25	102330	BE298063	Hs.77254	chromobox homolog 1 (Drosophila HP1 beta			4.17	
	102340	U37055	Hs.278657	macrophage stimulating 1 (hepatocyte gro		9.33		
	102348	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	8.87			
	102368	U39817	Hs.36820	Bloom syndrome	15.91			
	102394	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma		19.20		
30	102404	NM_005429	Hs.79141	vascular endothelial growth factor C			14.00	
	102537	U57094	Hs.50477	RAB27A, member RAS oncogene family		12.00		
	102581	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2			4.57	
	102605	AI435128	Hs.181369	ubiquitin fusion degradation 1-like			3.98	
	102610	U65011	Hs.30743	preferentially expressed antigen in mela	77.50			
35	102623	AW249285	Hs.37110	melanoma antigen, family A, 9	12.50			
	102642	AA205847	Hs.23016	G protein-coupled receptor		22.00		
	102654	AV649989	Hs.24385	Human hbc647 mRNA sequence		12.00		
	102659	BE245169	Hs.211610	CUG triplet repeat, RNA-binding protein			12.80	
	102669	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	6.50			
40	102672	U72066	Hs.29287	retinoblastoma-binding protein 8	8.50			
	102687	NM_007019	Hs.93002	ubiquitin carrier protein E2-C			9.24	
	102696	BE540274	Hs.239	forkhead box M1			5.54	
	102768	U82321		gb:Homo sapiens clone 14.9B mRNA sequenc	6.60			
45	102781	BE258778	Hs.108809	chaperonin containing TCP1, subunit 7 (e			3.78	
	102784	U85658	Hs.61796	transcription factor AP-2 gamma (activat		14.40		
	102824	U90916	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H			4.26	
	102829	NM_006183	Hs.80962	neurotensin	8.00			
	102888	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1			5.50	
	102892	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin		6.70		
50	102913	NM_002275	Hs.80342	keratin 15	4.64			
	102935	BE561850	Hs.80506	small nuclear ribonucleoprotein polypept	2.93			
	102951	X15218	Hs.2969	v-ski avian sarcoma viral oncogene homol		11.40		
	102983	BE387202	Hs.118638	non-metastatic cells 1, protein (NM23A)			7.26	
	103023	AW500470	Hs.117950	multifunctional polypeptide similar to S	3.01			
55	103036	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	27.90			
	103038	AA926960	Hs.334883	CDC28 protein kinase 1			8.79	
	103060	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin			4.27	
	103099	AI693251	Hs.8248	NADH dehydrogenase (ubiquinone) Fe-S pro	9.80			
	103119	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	4.05			
60	103168	X53463	Hs.2704	glutathione peroxidase 2 (gastrointestin	3.07			
	103185	NM_006825	Hs.74368	transmembrane protein (63kD), endoplasm			5.62	
	103192	M22440	Hs.170009	transforming growth factor, alpha		7.40		
	103223	BE275607	Hs.1708	chaperonin containing TCP1, subunit 3 (g			4.70	
	103242	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o		100.00		
65	103316	X83301	Hs.324728	SMA5		9.80		
	103375	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	9.71			
	103376	AL036166	Hs.323378	coated vesicle membrane protein	14.00			
	103385	NM_007069	Hs.37189	similar to rat HREV107		11.00		
	103391	X94453	Hs.114366	pyrroline-5-carboxylate synthetase (glut	2.93			
70	103404	BE394784	Hs.78596	proteasome (prosome, macropain) subunit,			5.15	
	103430	BE564090	Hs.20716	translocase of inner mitochondrial membr			3.98	
	103446	X98834	Hs.79971	sal (Drosophila)-like 2		21.40		
	103476	Y07701	Hs.293007	aminopeptidase puromycin sensitive		13.00		
	103477	AJ011812	Hs.119018	transcription factor NRF		6.40		
75	103478	BE514982	Hs.38991	S100 calcium-binding protein A2	5.02			
	103515	Y10275	Hs.56407	phosphoserine phosphatase	10.50			
	103558	BE616547	Hs.2785	keratin 17	6.41			
	103580	AA328046	Hs.46405	polymerase (RNA) II (DNA directed) polyp			3.84	
	103587	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	78.50			
	103594	AI368680	Hs.816	SRY (sex determining region Y)-box 2	6.51			
80	103636	NM_006235	Hs.2407	POU domain, class 2, associating factor	3.50			
	103768	AF086009		gb:Homo sapiens full length insert cDNA			4.48	
	103841	AA314821	Hs.38178	hypothetical protein FLJ23468	8.00			
	103847	AF219946	Hs.102237	tubby super-family protein	10.40			
	103913	AW967500	Hs.133543	ESTs		15.60		
85	104094	AA418187	Hs.330515	ESTs		6.60		

	104150	AL122044	Hs.331633	hypothetical protein DKFZp566N034		26.00	
	104257	BE560621	Hs.9222	estrogen receptor binding site associate	6.80		
	104261	AW248364	Hs.5409	RNA polymerase I subunit		3.98	
5	104331	AB040450	Hs.279862	cdk inhibitor p21 binding protein	6.80		
	104415	BE410992	Hs.258730	heme-regulated initiation factor 2-alpha	10.29		
	104558	R56678	Hs.88959	hypothetical protein MGC4816	4.21		
	104590	AW373062	Hs.83623	nuclear receptor subfamily 1, group I, m		15.79	
	104658	AA360954	Hs.27268	Homo sapiens cDNA: FLJ21933 fis, clone H		17.40	
10	104660	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (fr	6.40		
	104689	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr		6.55	
	104754	AI206234	Hs.155924	cAMP responsive element modulator		10.00	
	104758	BE560269	Hs.7010	NPD002 protein		4.47	
	104971	BE311926	Hs.15830	hypothetical protein FLJ12691	2.87		
15	105011	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	3.83		
	105012	AF098158	Hs.9329	chromosome 20 open reading frame 1	2.86		
	105026	AA809485	Hs.124219	hypothetical protein FLJ12934	11.00		
	105076	AI598252	Hs.37810	hypothetical protein MGC14833		5.01	
	105132	AA148164	Hs.247280	HBV associated factor		3.99	
20	105143	AI368836	Hs.24808	ESTs, Weakly similar to I38022 hypothe	11.00		
	105158	AW976357	Hs.234545	hypothetical protein NUF2R	16.00		
	105175	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	4.32		
	105200	AA328102	Hs.24641	cytoskeleton associated protein 2	3.00		
	105264	AA227934		gb:zr57e08.s1 Soares_NhHMPu_S1 Homo sapi		10.00	
25	105298	BE387790	Hs.26369	hypothetical protein FLJ20287	3.69		
	105409	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8		9.20	
	105460	AW296078	Hs.271721	Homo sapiens, clone IMAGE:4179986, mRNA,		7.80	
	105667	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	4.12		
	105743	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	3.82		
30	105782	H09748	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro		27.00	
	105848	AW954064	Hs.24951	ESTs		7.60	
	105891	U55984	Hs.289088	heat shock 90kD protein 1, alpha		4.14	
	106019	AF221993	Hs.46743	McKusick-Kaufman syndrome		16.80	
	106069	BE566623	Hs.29899	ESTs, Weakly similar to G02075 transcrip		23.40	
35	106073	AL157441	Hs.17834	downstream neighbor of SON	9.50		
	106126	AA576953	Hs.22972	hypothetical protein FLJ13352	6.00		
	106159	AK001301	Hs.3487	hypothetical protein FLJ10439		3.95	
	106220	D61329	Hs.32196	mitochondrial ribosomal protein L36		6.04	
	106260	AI097144	Hs.5250	ESTs, Weakly similar to ALU1_HUMAN ALU S		13.20	
40	106300	Y10043	Hs.19114	high-mobility group (nonhistone chromoso		5.02	
	106307	AA436174	Hs.37751	ESTs, Weakly similar to putative p150 {	6.60		
	106318	AA025610	Hs.9605	cleavage and polyadenylation specific fa		5.04	
	106341	AF191020	Hs.5243	hypothetical protein, estradiol-induced		7.25	
	106440	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub		13.80	
45	106481	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	4.75		
	106586	AA243837	Hs.57787	ESTs		10.84	
	106605	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr		45.60	
	106654	AW075485	Hs.286049	phosphoserine aminotransferase	28.00		
	106785	Y15227	Hs.20149	deleted in lymphocytic leukemia, 1	3.00		
50	106813	C05766	Hs.181022	CGI-07 protein		11.40	
	106895	AK001826	Hs.25245	hypothetical protein FLJ11269		6.00	
	106913	AI219346	Hs.86178	M-phase phosphoprotein 9	6.56		
	106919	AW043637	Hs.21766	ESTs, Weakly similar to ALU5_HUMAN ALU S		4.27	
	107054	AI076459	Hs.15978	KIAA1272 protein		34.80	
55	107059	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	4.71		
	107098	AI823593	Hs.27688	ESTs		24.80	
	107104	AU076640	Hs.15243	nucleolar protein 1 (120kD)		7.05	
	107129	AC004770	Hs.4756	flap structure-specific endonuclease 1	2.60		
	107198	AV657225	Hs.9846	KIAA1040 protein	19.20		
60	107203	D20426	Hs.41639	programmed cell death 2	7.60		
	107217	AL080235	Hs.35861	DKFZP586E1621 protein	9.50		
	107284	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte	2.71		
	107318	T74445	Hs.5957	Homo sapiens clone 24416 mRNA sequence		8.71	
	107516	X57152	Hs.99853	fibrillarin		4.33	
65	107529	BE515065	Hs.296585	nucleolar protein (KKE/D repeat)		4.00	
	107728	AA019551	Hs.294151	Homo sapiens, clone IMAGE:3603836, mRNA,	10.80		
	107851	AA022953	Hs.61172	EST		8.00	
	107901	L42612	Hs.335952	keratin 6B	3.40		
	107922	BE153855	Hs.61460	Ig superfamily receptor LNIR	2.88		
70	107932	AW392555	Hs.18878	hypothetical protein FLJ21620	7.50		
	108015	AW298357	Hs.49927	protein kinase NYD-SP15		23.40	
	108056	AA043675	Hs.62633	ESTs		12.80	
	108075	AI867370	Hs.139709	hypothetical protein FLJ12572		12.80	
	108187	BE245374	Hs.27842	hypothetical protein FLJ11210	7.00		
75	108296	N31256	Hs.161623	ESTs	6.60		
	108305	AA071391		gb:zm61e06.r1 Stratagene fibroblast (937		11.80	
	108393	AA075211		gb:zm86a08.r1 Stratagene ovarian cancer		11.80	
	108480	AL133092	Hs.68055	hypothetical protein DKFZp434I0428		20.80	
	108554	AA084948		gb:zn13b09.s1 Stratagene hNT neuron (937	6.40		
80	108573	AA086005		gb:z184c04.s1 Stratagene colon (937204)		25.40	
	108584	AA088326	Hs.120905	Homo sapiens cDNA FLJ11448 fis, clone HE	9.60		
	108597	AK000292	Hs.278732	hypothetical protein FLJ20285		14.60	
	108695	AB029000	Hs.70823	KIAA1077 protein	3.00		
	108699	AA121514	Hs.70832	ESTs		10.00	
85	108700	AA121518	Hs.193540	ESTs, Moderately similar to 2109260A B c		11.00	
	108780	AU076442	Hs.117938	collagen, type XVII, alpha 1	11.21		

	108810	AW295647	Hs.71331	hypothetical protein MGC5350	8.50			
	108816	AA130884	Hs.270501	ESTs, Moderately similar to ALU2_HUMAN		7.40		
	108857	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	4.00			
5	108860	AA133334	Hs.129911	ESTs	6.09			
	108937	AL050107	Hs.24341	transcriptional co-activator with PDZ-bi	3.00			
	109010	NM_007240	Hs.44229	dual specificity phosphatase 12	2.69			
	109121	BE389387	Hs.49767	NADH dehydrogenase (ubiquinone) Fe-S pro			4.53	
	109166	AA219691	Hs.73625	RAB6 interacting, kinesin-like (raklines	10.58			
10	109227	AA766998	Hs.85874	Human DNA sequence from clone RP11-16L21		9.00		
	109415	U80736	Hs.110826	trinucleotide repeat containing 9		51.40		
	109418	AI866946	Hs.161707	ESTs			11.00	
	109454	AA232255	Hs.295232	ESTs, Moderately similar to A46010 X-II		17.60		
	109502	AW967069	Hs.211556	hypothetical protein MGC5487		9.49		
15	109543	AA564994	Hs.222851	ESTs	12.67			
	109648	H17800	Hs.7154	ESTs			10.40	
	109680	AB037734	Hs.4993	KIAA1313 protein		33.20		
	109700	F09609		gb:HSC33H092 normalized infant brain cDN			16.00	
	109704	AI743880	Hs.12876	ESTs		11.00		
20	109792	R49625		gb:yg61f03.s1 Soares infant brain 1NIB H			12.60	
	109981	BE546208	Hs.26090	hypothetical protein FLJ20272	4.00			
	109998	AL042201	Hs.21273	transcription factor NYD-sp10		7.80		
	110039	H11938	Hs.21907	histone acetyltransferase		7.00		
	110156	AA581322	Hs.4213	hypothetical protein MGC16207			4.24	
25	110500	AA907723	Hs.36962	ESTs	4.50			
	110551	AW450381	Hs.14529	ESTs		8.60		
	110561	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	3.06			
	110854	BE612992	Hs.27931	hypothetical protein FLJ10607 similar to		6.80		
	110886	AW274992	Hs.72249	three-PDZ containing protein similar to		8.80		
30	110916	BE178102	Hs.24349	ESTs		6.80		
	111003	N52980	Hs.83765	dihydrofolate reductase			16.80	
	111337	AA837396	Hs.263925	LIS1-interacting protein NUDE1, rat homo	2.54			
	111434	R01608	Hs.142736	ESTs			9.80	
	111439	AI476429	Hs.19238	ESTs			10.40	
35	111540	U82670	Hs.9786	zinc finger protein 275		15.40		
	111597	R11499	Hs.189716	ESTs			9.20	
	111895	T80581	Hs.12723	Homo sapiens clone 25153 mRNA sequence		6.80		
	111929	AF027208	Hs.112360	prominin (mouse)-like 1			14.67	
40	112054	R43590		gb:yc85g02.s1 Soares infant brain 1NIB H		10.80		
	112210	R49645	Hs.7004	ESTs			10.20	
	112244	AB029000	Hs.70823	KIAA1077 protein	2.99			
	112382	R59904		gb:yh07g12.s1 Soares infant brain 1NIB H		6.60		
	112392	R60763	Hs.193274	ESTs, Moderately similar to I57588 HSrel		7.10		
	112442	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	3.00			
45	112539	R70318	Hs.339730	ESTs			37.20	
	112772	AI992283	Hs.35437	ESTs, Moderately similar to I38026 MLN 6			14.60	
	112869	BE261750	Hs.4747	dyskeratosis congenita 1, dyskerin				4.83
	112935	R71449	Hs.268760	ESTs	2.73			
	112970	AA694010	Hs.6932	Homo sapiens clone 23809 mRNA sequence			12.00	
50	112973	AB033023	Hs.318127	hypothetical protein FLJ10201	11.50			
	112992	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f		10.89		
	113063	W15573	Hs.5027	ESTs, Weakly similar to A47582 B-cell gr	15.00			
	113073	N39342	Hs.103042	microtubule-associated protein 1B		15.31		
	113078	T40444	Hs.118354	CAT56 protein		7.00		
55	113238	R45467	Hs.189813	ESTs			41.20	
	113591	T91881	Hs.200597	KIAA0563 gene product			9.40	
	113702	T97307		gb:ye53h05.s1 Soares fetal liver spleen	25.00			
	113844	AI369275	Hs.243010	Homo sapiens cDNA FLJ14445 fis, clone HE			13.91	
60	113984	R96696	Hs.35598	ESTs		7.80		
	114073	R44953	Hs.22908	Homo sapiens mRNA; cDNA DKFZp434J1027 (f		7.20		
	114162	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	3.42			
	114208	AL049466	Hs.7859	ESTs		6.74		
	114251	H15261	Hs.21948	ESTs			33.20	
	114285	R44338	Hs.22974	ESTs			13.20	
65	114313	H18456	Hs.27946	ESTs			10.00	
	114339	AA782845	Hs.22790	ESTs		7.80		
	114407	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f				4.14
	114560	AI452469	Hs.165221	ESTs			9.80	
70	114699	AA127386		gb:zn90d09.r1 Stratagene lung carcinoma		7.60		
	114767	AI859865	Hs.154443	minichromosome maintenance deficient (S	3.21			
	114793	AA158245		gb:zo76c03.s1 Stratagene pancreas (93720		6.00		
	114833	AI417215	Hs.87159	hypothetical protein FLJ12577			11.40	
	115047	BE270930	Hs.82916	chaperonin containing TCP1, subunit 6A (4.31
	115060	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3				4.03
75	115097	AA256213	Hs.72010	ESTs			35.40	
	115113	AA256460		gb:zr81a04.s1 Soares_NhHMPu_S1 Homo sapi			15.20	
	115123	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m				4.19
	115134	AW968073	Hs.194331	ESTs, Highly similar to A55713 inositol			12.40	
	115291	BE545072	Hs.122579	hypothetical protein FLJ10461	25.00			
80	115347	AA356792	Hs.334824	hypothetical protein FLJ14825		7.00		
	115414	AA662240	Hs.283099	AF15q14 protein	3.25			
	115522	BE614387	Hs.333893	c-Myc target JPO1	3.68			
	115536	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	10.50			
	115566	AI142336	Hs.43977	Human DNA sequence from clone RP11-196N1			24.40	
85	115645	AI207410	Hs.69280	Homo sapiens, clone IMAGE:3636299, mRNA,	4.17			
	115648	AW016811	Hs.234478	Homo sapiens cDNA: FLJ22648 fis, clone H		6.00		

	115652	BE093589	Hs.38178	hypothetical protein FLJ23468	3.81				
	115697	D31382	Hs.63325	transmembrane protease, serine 4	62.14				
	115793	AA424883	Hs.70333	hypothetical protein MGC10753				11.80	
5	115816	BE042915	Hs.287588	Homo sapiens cDNA FLJ13675 fis, clone PL				9.71	
	115892	AA291377	Hs.50831	ESTs			27.40		
	115906	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	2.53				
	115909	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	11.82				
	115965	AA001732	Hs.173233	hypothetical protein FLJ10970				34.29	
10	115978	AL035864	Hs.69517	cDNA for differentially expressed CO16 g					8.23
	115985	AA447709	Hs.268115	ESTs, Weakly similar to T08599 probable	3.00				
	116090	AI591147	Hs.61232	ESTs	5.17				
	116096	AA682382	Hs.59982	ESTs			8.20		
	116127	AF126743	Hs.279884	DNAJ domain-containing		10.60			
15	116157	BE439838	Hs.44298	mitochondrial ribosomal protein S17					5.82
	116190	AI949095	Hs.67776	ESTs, Weakly similar to T22341 hypotheti					4.08
	116278	NM_003686	Hs.47504	exonuclease 1	9.50				
	116335	AK001100	Hs.41690	desmocollin 3	3.67				
	116496	AW450694	Hs.21433	hypothetical protein DKFZp547J036		7.00			
20	116503	AI925316	Hs.212617	ESTs				12.60	
	116674	AI768015	Hs.92127	ESTs			32.00		
	116929	AA586922	Hs.80475	polymerase (RNA) II (DNA directed) polyp		7.60			
	116973	AI702054	Hs.166982	phosphatidylinositol glycan, class F		9.80			
	116993	AI417023	Hs.40478	ESTs					10.20
25	117079	H92325		gb:ys85f05.s1 Soares retina N2b4HR Homo					15.20
	117317	AI263517	Hs.43322	ESTs					13.40
	117326	N23629	Hs.241420	Homo sapiens mRNA for KIAA1756 protein,					20.60
	117396	W20128	Hs.296039	ESTs					10.60
	117412	N32536	Hs.42645	ESTs					16.00
	117519	N32528	Hs.146286	kinesin family member 13A					9.11
30	117693	AW179019	Hs.112110	mitochondrial ribosomal protein L42					4.01
	117721	N46100	Hs.93939	EST				19.80	
	117881	AF161470	Hs.260622	butyrate-induced transcript 1	2.71				
	117903	AA768283	Hs.47111	ESTs				17.80	
35	117992	AI015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586I2022 (f				10.60	4.17
	118013	AI674126	Hs.94031	ESTs			8.82		
	118017	AI813444	Hs.42197	ESTs					
	118186	N22886	Hs.42380	ESTs		7.00			
	118325	AI868065	Hs.166184	intersectin 2				13.80	
40	118367	N64269	Hs.48946	EST			6.14		
	118368	N64339	Hs.48956	gap junction protein, beta 6 (connexin 3	3.14				
	118472	AL157545	Hs.42179	bromodomain and PHD finger containing, 3			12.40		
	118709	AA232970	Hs.293774	ESTs				12.20	
	119025	BE003760	Hs.55209	Homo sapiens mRNA; cDNA DKFZp434K0514 (f	4.50				
45	119027	AF086161	Hs.114611	hypothetical protein FLJ11808	3.22				
	119052	R10889		gb:yf38d02.s1 Soares fetal liver spleen		9.60			
	119164	AF221993	Hs.46743	McKusick-Kaufman syndrome			6.60		
	119186	AI979147	Hs.101265	hypothetical protein FLJ22593				10.80	
	119243	T12603		gb:CHR90123 Chromosome 9 exon II Homo sa				9.44	
50	119490	AA195276	Hs.263858	ESTs, Moderately similar to B34087 hypot				11.80	
	119499	AI918906	Hs.55080	ESTs			14.80		
	119599	W45552		gb:zc26d03.s1 Soares_senescent_fibroblas		12.60			
	119780	NM_016625	Hs.191381	hypothetical protein	17.00				
	119845	W79123	Hs.58561	G protein-coupled receptor 87	13.50				
55	119941	AA699485	Hs.58896	ESTs		8.00			
	119994	AA642402	Hs.59142	ESTs	7.73				
	120102	W67353	Hs.170218	KIAA0251 protein			39.60		
	120104	AK000123	Hs.180479	hypothetical protein FLJ20116	2.91				
	120294	AK000059	Hs.153881	Homo sapiens NY-REN-62 antigen mRNA, par			8.20		
60	120486	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	8.73				
	120599	AA804448	Hs.104463	ESTs		7.00			
	120699	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos				10.00	
	120715	AA292700		gb:zs59a06.s1 NCL_CGAP_GCB1 Homo sapiens		9.40			
	120821	Y19062	Hs.96870	staufer (Drosophila, RNA-binding protein				13.80	
65	120859	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol		9.00			
	120880	AA360240	Hs.97019	EST		15.60			
	120983	AA398209	Hs.97587	EST			27.66		
	121034	AL389951	Hs.271623	nucleoporin 50kD			20.80		
	121121	AA399371	Hs.189095	similar to SALL1 (sal (Drosophila)-like		22.80			
70	121313	AA402713	Hs.97872	ESTs				10.00	
	121369	AW450737	Hs.128791	CGI-09 protein	25.71				
	121376	AA448103	Hs.187958	solute carrier family 6 (neurotransmitte					5.42
	121476	AA412311	Hs.97903	ESTs		8.30			
	121509	AA868939	Hs.97888	ESTs		8.59			
75	121553	AA412488	Hs.48820	TATA box binding protein (TBP)-associat	18.50				
	121753	AK000552	Hs.323518	WD repeat domain 5	7.00				
	121838	AA425680	Hs.98441	ESTs				10.40	
	121857	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	6.00				
	121991	AA430058	Hs.98649	EST				12.20	
80	122089	AW016543	Hs.98682	hypothetical protein FKSG32			8.60		
	122105	AW241685	Hs.98699	ESTs			6.14		
	122163	AA435702	Hs.98829	EST					10.40
	122318	AA429743		gb:zv60b05.r1 Soares_testis_NHT Homo sap				18.20	
	122335	AA443258	Hs.241551	chloride channel, calcium activated, fam	13.50				
85	122338	AA443311	Hs.98998	ESTs	4.80				
	122414	AI313473	Hs.99087	ESTs, Weakly similar to S47073 finger pr		8.00			

	122512	AF053305	Hs.98658	budding uninhibited by benzimidazoles 1	8.80		
	122516	AA449352	Hs.99217	ESTs		9.40	
	122702	AI220089	Hs.99439	ESTs	9.20		
5	122852	AI580056	Hs.98992	ESTs		10.40	
	122925	AW268962	Hs.111335	ESTs	6.80		
	123005	AW369771	Hs.52620	integrin, beta 8		12.60	
	123044	AK001035	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro			5.35
	123160	AA488687	Hs.284235	ESTs, Weakly similar to I38022 hypothe		6.06	
10	123315	AA496369		gb:zv37d10.s1 Soares ovary tumor NbHOT H		12.40	
	123329	Z47542	Hs.179312	small nuclear RNA activating complex, po		11.80	
	123497	AA765256	Hs.135191	ESTs, Weakly similar to unnamed protein	12.00		
	123518	AL035414	Hs.21068	hypothetical protein		13.00	
	123519	AW015887	Hs.112574	ESTs	12.20		
15	123614	AK000492	Hs.98806	hypothetical protein		7.80	
	123616	AA680003	Hs.109363	Homo sapiens cDNA: FLJ23603 fis, clone L		10.60	
	123673	BE550112	Hs.158549	ESTs, Weakly similar to T2D3_HUMAN TRANS	23.00		
	123727	AI083986	Hs.282977	hypothetical protein FLJ13490	7.00		
	123731	AA609839		gb:ae62f01.s1 Stratagene lung carcinoma		9.80	
20	123752	AA227714	Hs.179703	KIAA0129 gene product	3.50		
	123900	AA621223	Hs.112953	EST		12.80	
	124006	AI147155	Hs.270016	ESTs	97.00		
	124059	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothe	3.02		
	124069	AF134160	Hs.7327	claudin 1		27.80	
25	124191	T96509	Hs.248549	ESTs, Moderately similar to S65657 alpha		35.80	
	124273	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	7.20		
	124297	AL080215	Hs.102301	Homo sapiens mRNA; cDNA DKFZp586J0323 (f		11.00	
	124305	AW963221		gb:EST375294 MAGE resequences, MAGH Homo		16.00	
	124676	AI360119.comp	Hs.181013	phosphoglycerate mutase 1 (brain)		6.08	
30	124874	BE550182	Hs.127826	RalGEF-like protein 3, mouse homolog		21.00	
	124904	AK000483	Hs.93872	KIAA1682 protein	9.40		
	124969	AI650360	Hs.100256	ESTs		10.80	
	125000	T58615	Hs.110640	ESTs		9.80	
	125201	AA693960	Hs.103158	ESTs, Weakly similar to T33296 hypothe	7.60		
35	125266	W90022	Hs.186809	ESTs, Highly similar to LCT2_HUMAN LEUKO	6.59		
	125299	T32982	Hs.102720	ESTs		9.57	
	125356	AI057052	Hs.133554	ESTs, Weakly similar to Z195_HUMAN ZINC		14.00	
	125370	AA256743	Hs.134158	Homo sapiens, Similar to KIAA0092 gene p	8.20		
	125418	AA777690	Hs.188501	ESTs		13.20	
40	125433	AL162066	Hs.54320	hypothetical protein DKFZp762D096	21.40		
	125437	AI609449	Hs.140197	ESTs	6.96		
	125446	BE219987	Hs.166982	phosphatidylinositol glycan, class F	8.80		
	125711	AA305800	Hs.5672	hypothetical protein AF140225		11.20	
	125756	BE174587	Hs.289721	growth arrest specific transcript 5		4.31	
45	125757	AI274906	Hs.166835	ESTs, Highly similar to 1814460A p53-ass		15.60	
	125769	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	3.20		
	125839	AW836261	Hs.337717	ESTs	8.20		
	125850	W85858	Hs.99804	ESTs	2.65		
	125875	H14480		gb:ym18b09.r1 Soares infant brain 1NIB H	7.40		
50	125924	BE272506	Hs.82109	syndecan 1		4.23	
	125972	AI927475	Hs.35406	ESTs, Highly similar to unnamed protein		3.98	
	126034	H60340		gb:yr39b04.r1 Soares fetal liver spleen		10.60	
	126327	AA432266	Hs.44648	ESTs	11.60		
	126345	N49713		gb:yv23f06.s1 Soares fetal liver spleen	6.67		
55	126435	AW614529	Hs.285847	CGI-19 protein		10.60	
	126487	AA283809	Hs.184601	solute carrier family 7 (cationic amino		4.38	
	126521	AI475110	Hs.203933	ESTs	6.60		
	126522	W31912		gb:zc76d03.s1 Pancreatic Islet Homo sapi		14.80	
	126543	AL035864	Hs.69517	cDNA for differentially expressed CO16 g		4.01	
60	126567	AA058394	Hs.57887	ESTs, Weakly similar to KIAA0758 protein	7.80		
	126605	AA676910		gb:zj65h07.s1 Soares_fetal_liver_spleen_		11.60	
	126627	AA497044	Hs.20887	hypothetical protein FLJ10392		14.60	
	126628	N49776	Hs.170994	hypothetical protein MGC10946	8.00		
	126737	AW976516	Hs.283707	Homo sapiens cDNA: FLJ21354 fis, clone C	2.92		
65	126795	AW975076	Hs.172589	nuclear phosphoprotein similar to S. cer	7.50		
	126802	AW805510	Hs.97056	hypothetical protein FLJ21634	11.60		
	126892	AF121856	Hs.284291	sorting nexin 6	3.50		
	126928	AA480902	Hs.137401	ESTs		22.83	
	126979	AA210954		gb:zq89h10.r1 Stratagene hNT neuron (937		11.80	
70	126986	AI279892	Hs.46801	sorting nexin 14		11.60	
	126992	AI809521		gb:wf30e03.x1 Soares_NFL_T_GBC_S1 Homo s		20.80	
	127066	R25066		gb:yq42c07.r1 Soares infant brain 1NIB H		27.60	
	127099	AA347668		gb:EST54026 Fetal heart II Homo sapiens		21.60	
	127139	AA830233	Hs.293585	ESTs		11.20	
75	127209	AA305023	Hs.81964	SEC24 (S. cerevisiae) related gene famil	3.10		
	127221	BE062109	Hs.241551	chloride channel, calcium activated, fam	2.76		
	127225	AA315933	Hs.120879	ESTs		16.80	
	127313	AK002014	Hs.47546	Homo sapiens cDNA FLJ11458 fis, clone HE	14.00		
	127444	AW978474	Hs.7560	Homo sapiens mRNA for KIAA1729 protein,		13.60	
80	127500	AW971353	Hs.162115	ESTs	11.20		
	127524	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin		7.80	
	127540	N45572	Hs.105362	Homo sapiens, clone MGC:18257, mRNA, com	3.53		
	127599	AA613204	Hs.150399	ESTs		13.80	
	127609	X80031	Hs.530	collagen, type IV, alpha 3 (Goodpasture		28.00	
85	127662	W80755	Hs.8294	KIAA0196 gene product		19.80	
	127668	AI343257	Hs.139993	ESTs		11.20	

	127746	AI239495	Hs.120189	ESTs			14.18
	127812	AA741368	Hs.291434	ESTs	4.50		
	127817	AA836641	Hs.163085	ESTs			24.60
5	127959	AI302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L			9.20
	127960	AI613226	Hs.41569	phosphatidic acid phosphatase type 2A			16.83
	127969	F06498	Hs.93748	Homo sapiens cDNA FLJ14676 fis, clone NT	13.60		
	128015	Z21169	Hs.334659	hypothetical protein MGC14139	7.00		
	128027	AI433721	Hs.164153	ESTs			37.40
10	128077	AI310330	Hs.128720	ESTs			9.60
	128166	NM_006147	Hs.11801	interferon regulatory factor 6			9.24
	128226	AI284940	Hs.289082	GM2 ganglioside activator protein	19.00		
	128305	AI954968	Hs.279009	matrix Gla protein			10.40
	128341	AA191420	Hs.185030	ESTs	9.00		
15	128527	AA504583	Hs.101047	transcription factor 3 (E2A immunoglobul			4.30
	128539	R46163	Hs.258618	ESTs	12.60		
	128568	H12912	Hs.274691	adenylate kinase 3			4.56
	128572	AA933022	Hs.256583	interleukin enhancer binding factor 3, 9			10.00
	128777	AI878918	Hs.10526	cysteine and glycine-rich protein 2	16.80		
20	128781	N71826	Hs.105465	small nuclear ribonucleoprotein polypept			4.48
	128796	AJ000152	Hs.105924	defensin, beta 2	8.12		
	128920	AA622037	Hs.166468	programmed cell death 5			4.62
	128924	BE279383	Hs.26557	plakophilin 3			4.04
	128971	H05132	Hs.107510	ESTs	12.60		
25	129008	AL079648	Hs.301088	ESTs	8.80		
	129041	BE382756	Hs.169902	solute carrier family 2 (facilitated glu			6.05
	129075	BE250162	Hs.83765	dihydrofolate reductase	2.59		
	129105	AI769160	Hs.108681	Homo sapiens brain tumor associated prot		6.67	
	129189	AB023179	Hs.9059	KIAA0962 protein	8.00		
30	129229	AF013758	Hs.109643	polyadenylate binding protein-interactin	4.00		
	129241	AI878857	Hs.109706	hematological and neurological expressed			4.06
	129300	W94197	Hs.110165	ribosomal protein L26 homolog	2.55		
	129404	AI267700	Hs.317584	ESTs	18.00		
	129457	X61959	Hs.207776	aspartylglucosaminidase	6.50		
35	129466	L42583	Hs.334309	keratin 6A	12.94		
	129494	AI148976	Hs.112052	ESTs			11.00
	129605	AF061812	Hs.115947	keratin 16 (focal non-epidermolytic palm			4.46
	129641	AI911527	Hs.11805	ESTs			12.00
40	129665	AW163331	Hs.118778	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic			4.70
	129703	BE388665	Hs.179999	Homo sapiens, clone IMAGE:3457003, mRNA			4.02
	129720	AA156214	Hs.12152	APMCF1 protein			5.71
	129748	M16707	Hs.123053	H4 histone, family 2	3.50		
	129890	AI868872	Hs.282804	hypothetical protein FLJ22704			4.21
	129896	BE295568	Hs.13225	UDP-Gal:betaGlcNAc beta 1,4- galactosylt	2.56		
45	129945	BE514376	Hs.165998	PAL-1 mRNA-binding protein			4.03
	130010	AA301116	Hs.142838	nucleolar phosphoprotein Nopp34		7.00	
	130026	T40480	Hs.332112	EST	6.40		
	130080	X14850	Hs.147097	H2A histone family, member X			4.65
50	130149	AW067805	Hs.172665	methylentetrahydrofolate dehydrogenase	2.74		
	130285	AA063546	Hs.75981	ubiquitin specific protease 14 (tRNA-gua		7.40	
	130441	U63630	Hs.155637	protein kinase, DNA-activated, catalytic			3.91
	130482	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	4.87		
	130500	AB007913	Hs.158291	KIAA0444 protein			9.60
	130524	U89995	Hs.159234	forkhead box E1 (thyroid transcription f		13.40	
55	130541	X05608	Hs.211584	neurofilament, light polypeptide (68kD)		8.20	
	130553	AF062649	Hs.252587	pituitary tumor-transforming 1			6.06
	130567	AA383092	Hs.1608	replication protein A3 (14kD)		7.00	
	130577	M69241	Hs.162	insulin-like growth factor binding prote	3.04		
	130627	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	3.87		
60	130648	AI458165	Hs.17296	hypothetical protein MGC2376			16.20
	130697	L29472	Hs.1802	major histocompatibility complex, class			17.80
	130744	H59696	Hs.18747	POP7 (processing of precursor, S. cerevi			5.28
	130800	AI187292	Hs.19574	hypothetical protein MGC5469			4.43
	130867	NM_001072	Hs.284239	UDP glycosyltransferase 1 family, polype	16.84		
65	130869	J03626	Hs.2057	uridine monophosphate synthetase (orotal			4.92
	130925	AF093419	Hs.169378	multiple PDZ domain protein			9.60
	130994	W17044	Hs.327337	ESTs	12.40		
	131028	AI879165	Hs.2227	CCAAT/enhancer binding protein (C/EBP),	10.21		
70	131031	NM_001650	Hs.288650	aquaporin 4			9.80
	131041	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,			9.60
	131058	W28545	Hs.101514	hypothetical protein FLJ10342			17.00
	131090	AI143139	Hs.2288	visinin-like 1	2.74		
	131112	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f		8.80	
75	131148	AW953575	Hs.303125	p53-induced protein PIGPC1	3.12		
	131185	BE280074	Hs.23960	cyclin B1	3.07		
	131200	BE540516	Hs.293732	hypothetical protein MGC3195	3.07		
	131219	W25005	Hs.24395	small inducible cytokine subfamily B (Cy	2.87		
	131257	AW339037	Hs.24908	ESTs			14.67
	131375	AW293165	Hs.143134	ESTs		19.20	
80	131460	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	3.50		
	131476	AI521663	Hs.334644	hypothetical protein FLJ14668	15.00		
	131510	BE245374	Hs.27842	hypothetical protein FLJ11210		7.80	
	131646	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom		7.00	
	131786	BE000971	Hs.306083	Novel human gene mapping to chromosome 22	2.65		
85	131839	AB014533	Hs.33010	KIAA0633 protein			35.20
	131843	AA192315	Hs.184062	putative Rab5-interacting protein			4.11

	131877	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	19.00			
	131885	BE502341	Hs.3402	ESTs	6.48			
	131921	AA456093	Hs.34720	ESTs		8.40		
5	131945	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	56.00			
	131958	NM_014062	Hs.3566	ART-4 protein			3.82	
	131965	W79283	Hs.35962	ESTs	3.03			
	132000	AW247017	Hs.36978	melanoma antigen, family A, 3		9.80		
	132040	NM_001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fis, clone H	3.30			
10	132109	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	21.00			
	132114	NM_006152	Hs.40202	lymphoid-restricted membrane protein		8.40		
	132162	AA315805	Hs.94560	desmoglein 2			12.25	
	132164	AI752235	Hs.41270	procollagen-lysine, 2-oxoglutarate 5-dio	2.70			
	132180	NM_004460	Hs.418	fibroblast activation protein, alpha	2.71			
15	132181	AW961231	Hs.16773	Homo sapiens clone TCCCA00427 mRNA sequ	3.83			
	132182	NM_014210	Hs.70499	ecotropic viral integration site 2A			13.20	
	132231	AA662910	Hs.42635	hypothetical protein DKFZp434K2435	9.50			
	132277	AK001745	Hs.184628	hypothetical protein FLJ10883	4.50			
	132328	NM_014787	Hs.44896	DnaJ (Hsp40) homolog, subfamily B, membe			9.20	
20	132394	AK001680	Hs.30488	DKFZP434F091 protein			19.80	
	132424	AA417878	Hs.48401	ESTs, Moderately similar to ALU8_HUMAN A		8.60		
	132528	T78736	Hs.50758	SMC4 (structural maintenance of chromoso		27.40		
	132543	BE568452	Hs.5101	protein regulator of cytokinesis 1	4.38			
	132544	L19778	Hs.51011	H2A histone family, member P		7.00		
25	132550	AW969253	Hs.170195	bone morphogenetic protein 7 (osteogenic	2.64			
	132552	BE621985	Hs.296922	thiopurine S-methyltransferase			15.83	
	132581	AK000631	Hs.52256	hypothetical protein FLJ20624		6.60		
	132617	AF037335	Hs.5338	carbonic anhydrase XII	4.95			
	132638	AI796870	Hs.54277	DNA segment on chromosome X (unique) 992		8.20		
30	132653	Z15008	Hs.54451	laminin, gamma 2 (niclin (100kD), kalini	4.38			
	132669	W38586	Hs.293981	guanine nucleotide binding protein (G pr			4.36	
	132710	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	4.60			
	132771	Y10275	Hs.56407	phosphoserine phosphatase	3.71			
	132799	W73311	Hs.169407	SAC2 (suppressor of actin mutations 2,			9.48	
35	132833	U78525	Hs.57783	eukaryotic translation initiation factor			5.83	
	132892	AW834050	Hs.9973	tensin			12.00	
	132906	BE613337	Hs.234896	geminin	3.09			
	132959	AW014195	Hs.61472	ESTs, Weakly similar to YAE6_YEAST HYPOT			3.87	
40	132962	AA576635	Hs.6153	CGI-48 protein	3.50			
	132990	X77343	Hs.334334	transcription factor AP-2 alpha (activat	6.18			
	132994	AA112748	Hs.279905	clone HQ0310 PRO0310p1	3.19			
	133000	AL042444	Hs.62402	p21/Cdc42/Rac1-activated kinase 1 (yeast	2.96			
	133050	X73424	Hs.63788	propionyl Coenzyme A carboxylase, beta p	2.55			
45	133083	BE244588	Hs.6456	chaperonin containing TCP1, subunit 2 (b			4.00	
	133086	L17131	Hs.139800	high-mobility group (nonhistone chromoso			8.96	
	133134	AF198620	Hs.65648	RNA binding motif protein 8A			4.28	
	133155	M58583	Hs.662	cerebellin 1 precursor			10.80	
	133181	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	3.00			
	133204	BE267696	Hs.254105	enolase 1, (alpha)			4.63	
50	133412	U41493	Hs.73112	guanine nucleotide binding protein (G pr		12.50		
	133421	AF134160	Hs.7327	claudin 1	2.85			
	133451	AW970026	Hs.73818	ubiquinol-cytochrome c reductase hinge p			4.66	
	133453	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept		6.80		
	133504	NM_004415	Hs.74316	desmoplakin (DPI, DPII)	6.14			
55	133506	BE562958	Hs.74346	hypothetical protein MGC14353			4.55	
	133615	M62843	Hs.75236	ELAV (embryonic lethal, abnormal vision,			17.80	
	133627	NM_002047	Hs.75280	glycyl-tRNA synthetase			4.85	
	133649	U25849	Hs.75393	acid phosphatase 1, soluble			6.34	
	133669	NM_006925	Hs.166975	splicing factor, arginine/serine-rich 5			14.00	
60	133749	L20852	Hs.10018	solute carrier family 20 (phosphate tran		6.11		
	133776	BE268649	Hs.177766	ADP-ribosyltransferase (NAD+; poly (ADP-			4.91	
	133865	AB011155	Hs.170290	discs, large (Drosophila) homolog 5	3.07			
	133946	AJ001258	Hs.173878	NIPSNAP, C. elegans, homolog 1			4.60	
	133973	N55540	Hs.78026	ESTs, Weakly similar to similar to ankyr			13.00	
65	134047	BE262529	Hs.78771	phosphoglycerate kinase 1			3.85	
	134098	BE513171	Hs.79086	mitochondrial ribosomal protein L3	2.56			
	134107	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte		8.20		
	134112	AW449809	Hs.79150	chaperonin containing TCP1, subunit 4 (d			4.08	
	134158	U15174	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	31.00			
70	134160	T98152	Hs.79432	fibillin 2 (congenital contractural ara		24.60		
	134168	AA398908	Hs.181634	Homo sapiens cDNA: FLJ23602 fis, clone L			6.71	
	134185	AA285136	Hs.301914	neuronal specific transcription factor D			14.74	
	134201	L35035	Hs.79886	ribose 5-phosphate isomerase A (ribose 5		8.40		
	134272	X76040	Hs.278614	protease, serine, 15	4.50			
75	134276	BE083936	Hs.80976	antigen identified by monoclonal antibod		9.00		
	134353	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m			16.40	
	134367	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	2.80			
	134380	AU077143	Hs.179565	minichromosome maintenance deficient (S.	4.68			
	134423	H53497	Hs.83006	CGI-139 protein			3.84	
	134469	AA279661	Hs.83753	small nuclear ribonucleoprotein polypept			5.81	
80	134470	X54942	Hs.83758	CDC28 protein kinase 2			4.21	
	134498	AW246273	Hs.84131	threonyl-tRNA synthetase			7.30	
	134502	BE148534	Hs.84168	UV-B repressed sequence, HUR 7		13.60		
	134510	NM_002757	Hs.250870	mitogen-activated protein kinase kinase			9.70	
	134548	N95406	Hs.333495	Deleted in split-hand/split-foot 1 regio			4.63	
85	134654	AK001741	Hs.8739	hypothetical protein FLJ10879	6.00			

5	134724	AF045239	Hs.321576	ring finger protein 22		12.00
	134743	AA044163	Hs.89463	potassium large conductance calcium-acti	4.00	
	134781	AA374372	Hs.89626	parathyroid hormone-like hormone		25.20
	134806	AD001528	Hs.89718	spermine synthase		4.58
	134853	BE268326	Hs.90280	5-aminoimidazole-4-carboxamide ribonucle		4.79
	134859	D26488	Hs.90315	KIAA0007 protein		6.20
	134891	R51083	Hs.90787	ESTs		7.40
	134960	BE246400	Hs.285176	acetyl-Coenzyme A transporter	4.00	
10	134993	BE409809	Hs.301005	purine-rich element binding protein B		4.48
	135047	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	9.50	
	135080	AI761180	Hs.94211	rd1 (required for cell differentiation,	5.00	
	135103	NM_003428	Hs.9450	zinc finger protein 84 (HPF2)		11.00
	135145	AW014729	Hs.95262	nuclear factor related to kappa B bindin		4.01
15	135184	U13222	Hs.96028	forkhead box D1		7.00
	135242	AI583187	Hs.9700	cyclin E1	13.50	
	135286	AW023482	Hs.97849	ESTs	6.46	
	135289	AW372569	Hs.9788	hypothetical protein MGC10924 similar to		8.80
	135355	AK001652	Hs.99423	ATP-dependent RNA helicase	10.00	
20	135371	NM_006025	Hs.997	protease, serine, 22	8.00	
	135393	L11244	Hs.99886	complement component 4-binding protein,		14.60

TABLE 5B shows the accession numbers for those primekeys lacking unigenelD's for Table 5A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
35	117079	1621717_1 H92325 T97125
	124305	242183_1 AW963221 AA344870 AA344871 H93331
	101502	18202_-6 M26958
	109792	754958_1 R49625 F10674
	126034	1598157_1 H60340 N91637
40	102768	44641_1 U82321 H68077
	126345	1653833_1 N49713 N49819 W03810
	127066	1703458_1 R25066 R20144 R20145 Z43845
	127099	244301_1 AA347668 AW956810 Z44271 F07065 F07064 R13506
	119243	1774795_1 T12603 T12604
45	125875	1566433_1 H14480 N98295
	112054	1538292_1 R43590 F10439
	126979	171411_1 AA210954 AA211007
	126992	880655_1 AI809521 H12174 Z42556
	122318	292419_1 AA429743 AA442754
	114699	135322_1 AA127386 R15644 AA127404
50	114793	150742_1 AA158245 AA158235
	108305	111550_1 AA071391 AA069892 AA069891
	108393	113411_1 AA075211 AA075245 AA075126 AA075496
	100867	tigr_HT4586 U14622
55	123731	genbank_AA609839 AA609839
	109700	genbank_F09609 F09609
	120715	genbank_AA292700 AA292700
	113702	genbank_T97307 T97307
	115113	genbank_AA256460 AA256460
60	101045	entrez_J05614 J05614
	108554	genbank_AA084948 AA084948
	108573	genbank_AA086005 AA086005
	119052	149538_1 R10889 R10888
	126522	416020_1 W31912 AI167491
65	126605	439280_1 AA676910 AA778853 AA778865 W86800
	103768	46922_1 W42667 AI580740 AI690440 AI661350 AW467906 AW151450 AI825927 AL041716 AI885600 AI742213 AW248624 AI955498 AA033947
		AA845593 AI623711 N68583 C00064 AA193567 AW053868 AW163216 AA191595 AA522778 AI628008 AI915518 AA843508 AI926195
		AA176265 AW167963 AA992115 W93647 AW103572 AI862994 AI342059 AA911719 AA176155 AA024712 AA069988 AA205591 AI591107
		AI199673 AI811766 AI275832 AI422233 AI191852 AI096682 AI580124 AI683612 AA582453 AA927559 AA486415 T32414 AI084978 H44849
70		H44848 H20477 T91695 W47039 AA070055 AA024795 AA328855 AA379248 AA379330 AA385580 W25920 W03688 AA448359 AA093881
		AW362477 AA089997 AI350265 W93479 N99688 AA932257 AW351469 H68590 AA663402 AA069771 AW087986 AI858420 AA600214
		AI970774 AI857712 AI683081 AI885584 AW131150 AI567981 AW002714 AW189973 AW075495 AW168303 AA953714 AW516881 AI357375
		AI566663 AW512676 AI570580 AI023690 AA448216 AI079853 AI422707 AA779516 AW026972 AW130082 AW162307 AW438646 AA709332
		AW192394 AI167350 AI217879 AI129152 AA719509 AI350480 AA663418 AI003634 AW118546 AA180261 AA442833 AI268625 AA888881
75		AI038759 AA846723 AI248770 AA993694 AI280335 AI885107 AW518649 AA641563 AA995835 AA582521 AI276744 AA436478 AI017360
		AI620763 AI859887 N73926 AI076327 AI741615 AI160617 AW172819 AI492005 AA677429 AA996334 AI693771 AI950039 AI245629 AI288515
		AI866186 T93293 AI173262 AA599779 AI680092 AW439316 AI084555 AI272672 AI583507 AW473219 AA738132 AW473283 AI367492
		AA995410 AI689624 AA206353 AI033095 AI040382 AA873630 AI221074 AI934840 AI418680 AA844306 R94503 AA773520 AA843169
		AA219425 AA629658 AI811719 AW411275 AI590981 W37907 AI591178 AI684051 AA983238 AA669347 AA976239 AA704570 AI628339
80		AI884391 AI241580 AI003539 AW176687 AA009650 N34566 AI333493 AI186070 AA070827 AA411683 AI280884 AA872023 AA207255
		AA021576 N71953 AI885888 AW076039 T15777 AI537673 AW248048 H09554 W93480 W47001 AW079114 AA063160 AA757453 R60788
		AI859431 H20478 AA218882 AA757465 AA100995 AI864135 AI934209 AA070503 H47008 AA219646 W61039 W93907 AW385050 W37967
		W78028 AA189007 AA479136 R93650 AA442312 T30287 AA847628 AA180262 AA009649 C03892 AW149464 AA310963 AA219693
		AA069747 R29207 AA094784 AA293615 AA447848 AI984167 N90393 C05097 N56499 AW292351 AW149681 AW473258 AA629322 AI004409
85		AW105577 AI954937 AI811070 AA902422 AW514437 AA535460 AA916877 AW517122 AA974657 AA975649 AW517130 AW517129 F31737
		W07688 AA193645 AA378994 AA489273 F32267 W39303 AA021181 N68810 AA406524 AA062553 AA436801 H08985 H15979 N40310

AA436789 AA232172 AW360778 W25862 R60282 AA436530 AA378894 AA187461 AI940535 AA604210 AA089514 AA360421 N88243 N84281
 AA209340 N56174 N88374 AA191088 AW247691 AA249013 AA093111 AA972536 AW298594 AA375893 T12139 W28186 AW243849
 AI288629 AA843996 W15260 AI188286 AW248079 R15836

5 119599 genbank_W45552 W45552
 112382 genbank_R59904 R59904
 105264 genbank_AA227934 AA227934
 100071 entrez_A28102 A28102
 123315 714071_1 AA496369 AA496646

10

Table 6A shows 99 genes up-regulated nonsmokers with lung cancer relative to smokers with lung cancer. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

15

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title

20

R1: average of AI for samples from non-smokers with adenocarcinoma divided by the 90th percentile of AI for samples from smokers with adenocarcinoma
 R2: average of AI for samples from non-smokers with squamous cell carcinoma divided by the 90th percentile of AI for samples from smokers with squamous cell carcinoma

	Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
25	100971	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte		3.64
	101174	L17330	Hs.280	pre-T/NK cell associated protein	15.00	
	101296	Y12490	Hs.85092	thyroid hormone receptor interactor 11		2.46
	101304	AA001021	Hs.6685	thyroid hormone receptor interactor 8		12.00
30	101806	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias		2.68
	101972	S82472		gb:beta-pol=DNA polymerase beta (exon a		2.11
	102274	U30930	Hs.158540	UDP glycosyltransferase 8 (UDP-galactose	7.50	
	102394	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.50	
	102832	U92015		gb:Human clone 143789 defective mariner	13.50	
	103010	X52509	Hs.161640	tyrosine aminotransferase	9.50	
35	103439	X98266		gb:H.sapiens mRNA for ligase like protei		2.50
	103563	L02911	Hs.150402	activin A receptor, type I	9.00	
	103857	AI076795	Hs.45033	lacrimal proline rich protein		3.94
	104239	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	13.50	
40	104590	AW373062	Hs.83623	nuclear receptor subfamily 1, group I, m		12.66
	104907	AA055829	Hs.196701	ESTs, Weakly similar to ALU1_HUMAN ALU	16.50	
	106131	BE514788	Hs.296244	SNARE protein		2.17
	106672	H47233	Hs.30643	ESTs	7.00	
	106872	T56887	Hs.18282	KIAA1134 protein	11.50	
45	106960	AA156238	Hs.32501	ESTs		2.38
	106971	Z43846	Hs.194478	Homo sapiens mRNA; cDNA DKFZp434O1572 (f	9.50	
	107982	AA035375	Hs.57887	ESTs, Weakly similar to KIAA0758 protei		2.95
	108562	AA100796		gb:zm26c06.s1 Stratagene pancreas (93720	16.50	
	108599	AB018549	Hs.69328	MD-2 protein	13.00	
50	108663	BE219231	Hs.292653	ESTs, Weakly similar to T26845 hypotheti		2.40
	109247	AA314907	Hs.85950	ESTs	7.00	
	109630	R44607	Hs.22672	ESTs		5.00
	110193	AI004874	Hs.310764	Homo sapiens mRNA; cDNA DKFZp434M082 (fr	12.50	
	110234	H24458	Hs.32085	EST	16.50	
55	110644	R94207	Hs.268989	ESTs, Highly similar to type II CALM/AF1	8.00	
	110886	AW274992	Hs.72249	three-PDZ containing protein similar to	17.00	
	111057	T79639	Hs.14629	ESTs	16.50	
	111950	AF071594	Hs.110457	Wolf-Hirschhorn syndrome candidate 1	11.00	
	112291	R53972	Hs.26026	ESTs		3.00
60	112956	Z43784	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)		2.79
	113009	T23699	Hs.7246	ESTs		4.50
	113060	BE564162	Hs.250820	hypothetical protein FLJ14827	9.79	
	113073	N39342	Hs.103042	microtubule-associated protein 1B	32.50	
	113074	AK001335	Hs.31137	protein tyrosine phosphatase, receptor t		3.82
65	113121	T48011	Hs.8764	EST		2.21
	113125	AA968672	Hs.8929	hypothetical protein FLJ11362	19.50	
	113757	AA703095	Hs.18631	ESTs		2.65
	113848	W52854	Hs.27099	hypothetical protein FLJ23293 similar to	6.00	
	113884	AI333076	Hs.28529	chromosome 12 open reading frame 2		6.00
70	113936	W17056	Hs.83623	nuclear receptor subfamily 1, group I, m		4.63
	114875	AA235609	Hs.236443	Homo sapiens mRNA; cDNA DKFZp564N1063 (7.00
	114987	AA251016	Hs.87808	EST		6.00
	115460	AW958439	Hs.38613	ESTs		2.27
	115722	W91892	Hs.59609	ESTs		9.00
75	116261	AA481788	Hs.190150	ESTs	9.50	
	116830	H61037	Hs.70404	ESTs, Weakly similar to ALU2_HUMAN ALU	8.50	
	116970	AB023179	Hs.9059	KIAA0962 protein	7.50	
	117178	H98675	Hs.269034	ESTs		2.68
	117757	AF088019	Hs.46732	EST	7.50	
	118283	AA287747	Hs.173012	ESTs, Weakly similar to A46010 X-linked	16.50	
80	118384	AF217525	Hs.49002	Down syndrome cell adhesion molecule		2.50
	118657	AI822106	Hs.49902	ESTs		2.39
	120328	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi		3.50
	120404	AB023230	Hs.96427	KIAA1013 protein	7.00	
	120524	AA261852	Hs.192905	ESTs	6.00	
85	120688	AW207555	Hs.97093	Homo sapiens cDNA: FLJ23004 fis, clone L	17.92	

	121558	AA412497	gb:zt95g12.s1 Soares_testis_NHT Homo sap		2.95
	121676	H56037	Hs.108146 ESTs	10.00	
	121936	AI024600	Hs.98612 ESTs	15.00	
5	121938	AA428659	Hs.98610 ESTs	14.00	
	122177	AA435789	Hs.98833 EST	8.93	
	123442	AA299652	Hs.111496 Homo sapiens cDNA FLJ11643 fis, clone HE	13.04	
	123551	AA608837	gb:af03h12.s1 Soares_testis_NHT Homo sap	11.50	
	123756	AA609971	Hs.112795 EST	11.00	
10	123861	AA620840	gb:af89g01.s1 Soares_testis_NHT Homo sap		2.50
	124371	N24924	Hs.188601 ESTs	6.50	
	127477	BE328720	Hs.280651 ESTs		4.33
	127591	AI190540	Hs.131092 ESTs		3.02
	128252	AA455924	Hs.192228 ESTs	7.00	
15	128426	AI265784	Hs.145197 ESTs		2.08
	128925	R67419	Hs.21851 Homo sapiens cDNA FLJ12900 fis, clone NT		2.11
	128945	AI990506	Hs.8077 Homo sapiens mRNA; cDNA DKFZp547E184 (fr	10.00	
	129105	AI769160	Hs.108681 Homo sapiens brain tumor associated prot	15.50	
	129235	AW977238	Hs.126084 KIAA1055 protein		4.25
20	129506	AB020684	Hs.11217 KIAA0877 protein	6.50	
	129595	U09550	Hs.1154 oviductal glycoprotein 1, 120kD (mucin 9		10.00
	130160	AA305688	Hs.267695 UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	20.00	
	130340	D82326	Hs.239106 solute carrier family 3 (cystine, dibasi	11.50	
	131220	AB023194	Hs.300855 KIAA0977 protein	17.50	
25	131430	AI879148	Hs.26770 fatty acid binding protein 7, brain	6.10	
	132114	NM_006152	Hs.40202 lymphoid-restricted membrane protein		6.15
	132458	AA935315	Hs.48965 Homo sapiens cDNA: FLJ21693 fis, clone C		5.58
	132647	NM_006927	Hs.54432 sialyltransferase 4B (beta-galactosidase	7.50	
	132655	D49372	Hs.54460 small inducible cytokine subfamily A (Cy		2.53
30	132682	AI077500	Hs.54900 serologically defined colon cancer antig		2.50
	132747	AA345241	Hs.55950 ESTs, Weakly similar to KIAA1330 protein		2.83
	132812	R50333	Hs.92186 Leman coiled-coil protein		3.82
	133337	AF085983	Hs.293676 ESTs		5.00
35	133876	AL134906	Hs.771 phosphorylase, glycogen; liver (Hers dis		3.00
	134119	AW157837	Hs.79226 fasciculation and elongation protein zet		2.06
	134464	AA302983	Hs.239720 CCR4-NOT transcription complex, subunit		2.27
	134542	M14156	Hs.85112 insulin-like growth factor 1 (somatomedi		11.50
	135002	AA448542	Hs.251677 G antigen 7B	87.00	
40	135305	AA203555	Hs.98288 Homo sapiens cDNA FLJ14903 fis, clone PL		6.50

TABLE 6B show the accession numbers for those primekeys lacking unigenelD's for Table 6A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
108562	36375_1	AA100796 AF020589 AA074629 AA075946 AA100849 AA085347 AA126309 AA079311 AA079323 AA085274
103439	35330_1	X98266 N41124
123551	genbank_AA608837	AA608837
123861	genbank_AA620840	AA620840
102832	entrez_U92015	U92015
101972	entrez_S82472	S82472
121558	genbank_AA412497	AA412497

Table 7A shows 98 genes down-regulated in non-smokers with lung cancer relative to smokers with lung cancer. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

5	Pkey:	Unique Eos probeset identifier number				
	ExAccn:	Exemplar Accession number, Genbank accession number				
	UnigeneID:	Unigene number				
	Unigene Title:	Unigene gene title				
10	R1:	90th percentile of AI for samples from smokers with adenocarcinoma divided by the average of AI for samples from non-smokers with adenocarcinoma.				
	R2:	90th percentile of AI for samples from smokers with squamous cell carcinoma divided by the average of AI for samples from non-smokers with squamous cell carcinoma.				
	Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
15	100187	D17793	Hs.78183	aldo-keto reductase family 1, member C3		164.10
	100380	D82343	Hs.18551	neuroblastoma (nerve tissue) protein		77.40
	100576	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid	102.40	
	100971	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	463.80	
20	101046	K01160		(NONE)	672.00	
	101066	AW970254	Hs.889	Charol-Leyden crystal protein	66.00	
	101175	U82671	Hs.36980	melanoma antigen, family A, 2		77.20
	101497	W05150	Hs.37034	homeo box A5	62.80	
	101663	NM_003528	Hs.2178	H2B histone family, member Q	78.00	
	101677	NM_000715	Hs.1012	complement component 4-binding protein,	186.20	
25	101745	M88700	Hs.150403	dopa decarboxylase (aromatic L-amino aci	80.08	
	101941	S77583		gb:HERVK10/HUMMTV reverse transcriptase	99.20	
	102125	NM_006456	Hs.288215	sialyltransferase		103.10
	102242	U27185	Hs.82547	retinoic acid receptor responder (tazaro	67.00	
30	102340	U37055	Hs.278657	macrophage stimulating 1 (hepatocyte gro	71.60	
	102369	U39840	Hs.299867	hepatocyte nuclear factor 3, alpha		69.70
	102457	NM_001394	Hs.2359	dual specificity phosphatase 4	153.00	
	102669	U71207	Hs.29279	eyes absent (Drosophila) homolog 2		65.70
	102796	AL079646	Hs.107019	sympleskin; Huntingtin interacting protei		58.80
35	102829	NM_006183	Hs.80962	neurotensin		268.80
	103207	X72790		gb:Human endogenous retrovirus mRNA for	70.00	
	103242	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o		212.10
	103260	X78416	Hs.3155	casein, alpha		130.70
	103351	X89211		gb:H.sapiens DNA for endogenous retrovir	64.60	
40	104212	AB002298	Hs.173035	KIAA0300 protein	66.80	
	104252	AF002246	Hs.210863	cell adhesion molecule with homology to	63.80	
	104258	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	94.40	
	105024	AA126311	Hs.9879	ESTs	68.20	
	106260	AI097144	Hs.5250	ESTs, Weakly similar to ALU1_HUMAN ALU S		74.60
45	106440	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub		71.10
	106566	BE298210		gb:601118016F1 NIH_MGC_17 Homo sapiens c	73.20	
	106605	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr	83.80	
	106614	AA648459	Hs.335951	hypothetical protein AF301222		62.30
	106654	AW075485	Hs.286049	phosphoserine aminotransferase		202.40
50	106999	H93281	Hs.10710	hypothetical protein FLJ20417		89.60
	108700	AA121518	Hs.193540	ESTs, Moderately similar to 2109260A B c		66.40
	108810	AW295647	Hs.71331	hypothetical protein MGC5350		95.50
	108857	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act		63.40
	109597	AA989362	Hs.293780	ESTs	85.00	
55	109691	T65568	Hs.12860	ESTs		58.70
	109704	AI743880	Hs.12876	ESTs		60.60
	110942	R63503	Hs.28419	ESTs	76.40	
	111722	R23924	Hs.23596	EST	74.60	
	112891	T03927	Hs.293147	ESTs, Moderately similar to A46010 X-li	64.80	
60	112992	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f		76.70
	113073	N39342	Hs.103042	microtubule-associated protein 1B		120.20
	114251	H15261	Hs.21948	ESTs	127.20	
	115230	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	174.00	
	115291	BE545072	Hs.122579	hypothetical protein FLJ10461		91.00
65	115815	AW905328	Hs.180842	ribosomal protein L13	66.40	
	115909	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH		226.60
	115965	AA001732	Hs.173233	hypothetical protein FLJ10970	82.80	
	116107	AL133916	Hs.172572	hypothetical protein FLJ20093		361.60
	116552	D20508	Hs.164649	hypothetical protein DKFZp434H247	69.00	
70	116571	D45652		gb:HUMGS02848 Human adult lung 3' direct	64.20	
	118466	N66741		gb:yz33g08.s1 Morion Fetal Cochlea Homo		63.50
	120484	AA253170	Hs.96473	EST	81.60	
	120983	AA398209	Hs.97587	EST		81.10
	121034	AL389951	Hs.271623	nucleoporin 50kD		66.20
75	121423	AW973352	Hs.290585	ESTs	64.40	
	122553	AA451884	Hs.190121	ESTs		60.40
	122946	AI718702	Hs.308026	major histocompatibility complex, class	188.60	
	123130	AA487200		gb:ab19f02.s1 Stratagene lung (937210) H		80.20
	124472	N52517	Hs.102670	EST	71.00	
80	124526	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci		104.90
	125489	H49193	Hs.124984	ESTs, Moderately similar to ALU7_HUMAN A		72.00
	125731	R61771	Hs.26912	ESTs		69.90
	125747	NM_002884	Hs.865	RAP1A, member of RAS oncogene family	69.00	
	126020	H79863	Hs.114243	ESTs		62.40
	126547	U47732	Hs.84072	transmembrane 4 superfamily member 3		62.80
85	126966	R38438	Hs.182575	solute carrier family 15 (H+/peptide tra		60.10

	127472	AA761378	Hs.192013	ESTs	70.20	
	127610	AA960867	Hs.150271	ESTs, Highly similar to unnamed protein	64.00	
	127742	AW293496	Hs.180138	ESTs	85.20	
	127987	AI022103	Hs.124511	ESTs	96.60	
5	128233	AW889132	Hs.11916	ribokinase		78.90
	128420	AA650274	Hs.41296	fibronectin leucine rich transmembrane p		106.90
	128766	AW160432	Hs.296460	craniofacial development protein 1	66.80	
	129014	AW935187	Hs.170162	KIAA1357 protein		58.53
10	129215	AB040930	Hs.126085	KIAA1497 protein	64.20	
	130090	H97878	Hs.132390	zinc finger protein 36 (KOX 18)	63.80	
	130385	AW067800	Hs.155223	stanniocalcin 2		139.60
	130732	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)		64.60
	131025	AB040900	Hs.6189	KIAA1467 protein	64.40	
15	131241	BE501914	Hs.24654	Homo sapiens cDNA FLJ11640 fis, clone HE	76.20	
	131775	AB014548	Hs.31921	KIAA0648 protein	97.80	
	132240	AB018324	Hs.42676	KIAA0781 protein		71.00
	132856	NM_001448	Hs.58367	glypican 4		88.40
	132977	AA093322	Hs.301404	RNA binding motif protein 3	133.20	
20	133749	L20852	Hs.10018	solute carrier family 20 (phosphate tran		59.30
	133818	AI110684	Hs.7645	fibrinogen, B beta polypeptide	341.00	
	134264	AF149297	Hs.8087	NAG-5 prtein		64.30
	134265	M83772	Hs.80876	flavin containing monooxygenase 3		232.53
	134346	X84002	Hs.82037	TATA box binding protein (TBP)-associate	66.00	
25	134395	AA456539	Hs.8262	lysosomal-associated membrane protein 2		75.80
	135047	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su		108.30
	135056	N75765	Hs.93765	lipoma HMGIC fusion partner	71.40	
	135309	AI564123	Hs.42500	ADP-ribosylation factor-like 5	70.40	

30 TABLE 7B shows the accession numbers for those primekeys lacking unigenelD's for Table 7A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

35 Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
103207	30635_4	X72790
106566	120358_1	BE298210 AI672315 AW086489 BE298417 AA455921 AA902537 BE327124 R14963 AA085210 AW274273 AI333584 AI369742 AI039658 AI885095 AI476470 AI287650 AI885299 AI985381 AW592624 AW340136 AI266556 AA456390 AI310815 AA484951
116571	genbank_D45652	D45652
118466	genbank_N66741	N66741
101046	entrez_K01160	K01160
101941	entrez_S77583	S77583
103351	entrez_X89211	X89211
123130	genbank_AA487200	AA487200

Table 8A shows 1720 genes either up or down-regulated in lung tumors or chronically diseased lung relative to a broad collection of over 40 distinct normal body tissues. Chronically diseased lung samples represent chronic non-malignant lung diseases such as fibrosis, emphysema, and bronchitis. These genes were selected from 39494 probesets on the Eos/Affymetrix Hu02 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: 70th percentile of AI for lung tumors divided by 90th percentile of AI for normal lung
 R2: 70th percentile of AI for chronically diseased lung divided by 90th percentile of AI for normal lung

Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
300097	AI916973	Hs.213603	ESTs	5.46	4.69
300117	AW189787	Hs.147474	ESTs	0.58	0.56
300197	AI686661	Hs.218286	ESTs	4.26	5.44
300201	AI308300		gb:ta90c06.x1 NCI_CGAP_Bm20 Homo sapien	0.62	0.83
300225	AI989963	Hs.197505	ESTs	1.68	1.75
300247	AW274682	Hs.161394	ESTs	1.08	2.28
300256	AI469095	Hs.298241	Transmembrane protease, serine 3	0.86	1.00
300337	AI707881	Hs.202090	ESTs	5.80	9.09
300362	Z42308		gb:HSC0FB121 normalized infant brain cDN	4.18	12.78
300374	AI859947	Hs.314158	ESTs	2.99	4.38
300387	AW270150	Hs.254516	ESTs	1.50	2.53
300440	AI421541	Hs.146164	ESTs	3.98	5.25
300441	R10367	Hs.307921	EST, Weakly similar to Z232_HUMAN ZINC F	3.18	6.80
300449	AI362967	Hs.132221	hypothetical protein FLJ12401	0.43	0.62
300469	AW135830	Hs.233955	hypothetical protein FLJ20401	0.16	0.83
300552	X85711	Hs.21838	hypothetical protein FLJ11191	4.10	9.75
300627	W27363		gb:ab37d01.r1 Stratagene HeLa cell s3 93	4.60	12.60
300630	AW118822	Hs.128757	ESTs	2.91	5.86
300716	AI216113	Hs.126280	hypothetical protein FLJ23393	1.00	0.92
300738	AI623332	Hs.130541	KIAA1542 protein	1.82	1.71
300777	AA235361	Hs.96840	KIAA1527 protein	4.48	8.22
300790	AI492471	Hs.188270	ESTs	1.29	1.18
300832	AI688147	Hs.220615	ESTs, Weakly similar to T03829 transcrip	5.51	8.56
300836	Z44942	Hs.22958	calcium channel alpha2-delta3 subunit	4.90	6.34
300838	AI582897	Hs.192570	hypothetical protein FLJ22028	1.70	2.81
300878	AW449802	Hs.285901	Homo sapiens cDNA FLJ20428 fis, clone KA	4.56	7.91
300897	AI890356	Hs.127804	ESTs, Weakly similar to T17233 hypotheti	2.23	1.58
300926	AA504860		gb:ab03a10.s1 Stratagene fetal retina 93	2.13	3.50
300960	AI041019	Hs.152454	ESTs	2.74	4.46
300961	AW204069	Hs.312716	ESTs, Weakly similar to unnamed protein	1.00	1.00
300962	AA593373	Hs.293744	ESTs	1.46	1.51
300967	AA565209	Hs.269439	ESTs	0.39	1.30
300987	AW450840	Hs.148590	ESTs, Weakly similar to AF208846 1 BM-00	1.49	1.08
300988	AI927208	Hs.208952	ESTs	0.16	0.37
301050	AW136973	Hs.288516	ESTs, Weakly similar to S69890 mitogen i	3.23	1.94
301098	AA677570	Hs.185918	ESTs	6.76	14.28
301157	AA729905	Hs.231916	ESTs	3.16	8.85
301162	AI142118	Hs.129004	ESTs	1.68	7.18
301170	AA737594	Hs.247606	ESTs	4.40	6.42
301192	AI808751	Hs.121188	ESTs	6.38	11.59
301193	AA758115	Hs.128350	ESTs, Weakly similar to JC5423 2-hydroxy	4.35	7.78
301267	AW297762	Hs.255690	ESTs	1.56	1.61
301281	AA843986	Hs.190586	ESTs	2.19	1.78
301341	AI819198	Hs.208229	ESTs	0.76	0.76
301382	AA912839	Hs.163369	ESTs	1.00	1.81
301407	AW450466	Hs.126830	ESTs	1.48	1.51
301452	AA975688	Hs.159955	ESTs	0.51	1.46
301483	AW272467	Hs.254655	Untitled	2.40	5.02
301494	AI678034	Hs.131099	ESTs	2.79	3.41
301521	AI733621	Hs.133011	zinc finger protein 117 (HPF9)	0.67	0.67
301531	AI077462	Hs.134084	ESTs	2.52	3.76
301580	AI878959	Hs.73737	splicing factor, arginine/serine-rich 1	7.41	11.92
301676	Z43570	Hs.27453	ESTs, Moderately similar to G01251 Rar p	8.31	10.70
301690	F05865	Hs.108323	ubiquitin-conjugating enzyme E2E 2 (homo	2.70	4.22
301718	F07744	Hs.7987	DKFZP434F162 protein	4.20	8.78
301799	AA384252	Hs.286132	D15F37 (pseudogene)	5.93	7.04
301804	AA581004	Hs.62180	anillin (Drosophila Scraps homolog), act	1.70	0.76
301822	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	1.58	1.36
301846	R20002	Hs.6823	hypothetical protein FLJ10430	1.00	1.00
301868	T71508	Hs.13861	ESTs, Weakly similar to pH sensitive max	2.88	5.49
301882	T78054		gb:yc97g09.r1 Soares infant brain 1N1B H	2.28	3.80
301905	AI991127	Hs.117202	ESTs	1.00	1.00
301948	AA344647	Hs.116724	aldo-keto reductase family 1, member B11	5.28	2.28
301960	AW070252	Hs.27973	KIAA0874 protein	5.38	6.48
302011	T91418	Hs.125156	transcriptional adaptor 2 (ADA2, yeast,	3.03	3.42
302016	N40834	Hs.23495	hypothetical protein FLJ11252	1.00	1.25
302041	NM_001501	Hs.129715	gonadotropin-releasing hormone 2	0.71	0.99
302072	AJ238381	Hs.132576	paired box gene 9	1.60	1.71
302094	AI286176	Hs.6786	ESTs	0.52	1.20
302095	AW044300	Hs.137506	Homo sapiens BAC clone RP11-120J2 from 7	2.75	4.93
302148	AW269618	Hs.23244	ESTs	3.04	3.87

	302155	AI088485	Hs.144759	ESTs	0.45	1.15
	302201	AJ006276	Hs.159003	transient receptor potential channel 6	0.33	0.84
	302202	AF097159	Hs.159140	UDP-Gal:betaGlcNAc beta 1,4- galactosylt	0.52	0.94
5	302206	AI937193	Hs.41143	phosphoinositide-specific phospholipase	2.76	3.65
	302209	AF047445	Hs.159297	killer cell lectin-like receptor subfam1	1.00	1.00
	302235	AL049987	Hs.166361	Homo sapiens mRNA; cDNA DKFZp564F112 (fr	1.68	1.50
	302290	AL117607	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	1.00	2.11
	302328	AA354849	Hs.23240	Homo sapiens cDNA FLJ13496 fis, clone PL	9.38	13.08
10	302346	AL039101	Hs.194625	dynein, cytoplasmic, light intermediate	3.27	7.24
	302360	AJ010901	Hs.198267	mucin 4, tracheobronchial	2.54	1.88
	302384	Y08982	Hs.202676	synaptonemal complex protein 2	1.00	0.91
	302406	U86751	Hs.211956	CD3-epsilon-associated protein; antisens	2.63	2.67
	302409	AF155156	Hs.218028	adaptor-related protein complex 4, epsil	5.82	9.34
	302423	AB028977	Hs.225974	KIAA1054 protein	3.66	3.18
15	302432	AL080068	Hs.272534	Homo sapiens mRNA; cDNA DKFZp564J062 (fr	2.44	6.77
	302435	AF092047	Hs.227277	sine oculis homeobox (Drosophila) homolo	0.44	0.84
	302437	AB024730	Hs.227473	UDP-N-acetylglucosamine:alpha-1,3-D-mannosid	4.18	5.64
	302455	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	1.85	0.92
20	302472	AA317451	Hs.6335	SWI/SNF related, matrix associated, acti	2.04	2.13
	302476	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein LSm8	1.44	1.89
	302489	T80660	Hs.230424	Homo sapiens cDNA FLJ13540 fis, clone PL	0.51	1.10
	302490	AA885502	Hs.187032	ESTs	2.64	4.87
	302562	AJ005585	Hs.48956	gap junction protein, beta 6 (connexin 3	5.34	2.68
25	302566	AA085996	Hs.248572	hypothetical protein FLJ22965	1.00	1.21
	302630	AB029488	Hs.272100	SMS3 protein	0.52	1.24
	302634	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	1.00	1.00
	302638	AA463798	Hs.102696	MCT-1 protein	1.58	1.02
	302647	X57723	Hs.198273	NADH dehydrogenase (ubiquinone) 1 beta s	2.72	6.85
30	302655	AJ227892	Hs.146274	ESTs	1.00	4.32
	302656	AW293005	Hs.70704	Homo sapiens, clone IMAGE:2823731, mRNA,	2.97	0.93
	302668	AA580691	Hs.180789	S164 protein	0.80	0.95
	302679	H65022		gb:yu66g11.r1 Weizmann Olfactory Epithel	1.68	5.04
	302680	AW192334	Hs.38218	ESTs	2.70	7.98
35	302697	AJ001408		gb:Homo sapiens mRNA for immunoglobulin	4.25	8.13
	302705	U09060		gb:Human immunoglobulin heavy chain, V-r	3.91	8.68
	302711	L08442		gb:Human autonomously replicating sequen	2.20	2.73
	302719	W69724	Hs.288959	hypothetical protein FLJ20920	0.54	1.02
	302742	L12069		gb:Homo sapiens (clone WR4.10VH) anti-th	4.28	11.57
40	302755	AW384815	Hs.149208	KIAA1555 protein	1.57	2.38
	302771	H98476	Hs.42522	ESTs	2.94	4.68
	302789	AJ245067		gb:Homo sapiens mRNA for immunoglobulin	3.49	6.31
	302795	AJ245313	Hs.272838	hypothetical protein FLJ10494	0.80	2.74
	302802	Y08250		gb:H.sapiens mRNA for variable region of	1.13	0.77
45	302803	AA442824	Hs.293961	ESTs, Moderately similar to putative DNA	3.14	10.68
	302812	N31301	Hs.152664	hypothetical protein FLJ20051	3.04	8.24
	302847	X98940		gb:H.sapiens rearranged Ig heavy chain (1.80	1.92
	302885	AL137763	Hs.132127	hypothetical protein LOC57822	1.00	1.00
	302943	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	0.53	0.67
50	302977	AW263124	Hs.315111	hypothetical protein FLJ12894	2.45	2.62
	303006	AF078950	Hs.24139	Homo sapiens cDNA: FLJ23137 fis, clone L	4.88	8.61
	303011	AF090405		gb:Homo sapiens clone 2A1 scFV anttbody	1.41	1.86
	303013	F07898	Hs.288968	RAB22A, member RAS oncogene family	1.51	1.19
	303061	AF151882	Hs.27693	peptidylprolyl isomerase (cyclophilin)-l	0.72	0.76
55	303077	AF163305		gb:H.sapiens T-cell receptor mRNA	1.17	3.90
	303090	AA443259	Hs.146286	kinesin family member 13A	4.08	6.46
	303091	AF192913	Hs.130683	zinc finger protein 180 (HHZ168)	2.50	4.37
	303094	AF195513	Hs.278953	Pur-gamma	5.38	8.38
	303095	AF202051	Hs.134079	NM23-H8	3.26	4.08
60	303131	AW081061	Hs.103180	DC2 protein	2.02	1.83
	303195	AA082211	Hs.233936	myosin, light polypeptide, regulatory, n	1.32	3.95
	303196	AA082298	Hs.59710	ESTs	0.77	0.53
	303216	AA581439	Hs.152328	ESTs	0.24	0.63
	303222	AA333538	Hs.204501	hypothetical protein FLJ10534	3.56	6.22
65	303234	AA132255	Hs.143951	ESTs	2.28	3.17
	303251	AW340037	Hs.115897	protocadherin 12	0.38	1.02
	303295	AA205625	Hs.208067	ESTs	2.30	1.00
	303297	T80072	Hs.13423	Homo sapiens clone 24468 mRNA sequence	1.86	4.48
	303316	AF033122	Hs.14125	p53 regulated PA26 nuclear protein	0.10	0.80
70	303467	AA398801	Hs.323397	ESTs	4.54	9.65
	303506	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	0.09	0.04
	303552	AA359799	Hs.224662	ESTs, Weakly similar to unnamed protein	1.00	1.72
	303598	AA382814		gb:EST96097 Testis I Homo sapiens cDNA 5	4.96	9.14
75	303637	AF056083	Hs.24879	phosphatidic acid phosphatase type 2C	2.06	2.02
	303655	AA504702	Hs.258802	ATPase, (Na+)/K+ transporting, beta 4 po	1.00	1.24
	303756	AI738488	Hs.115838	ESTs	1.08	1.43
	303856	AA968589	Hs.180532	glucose phosphate isomerase	1.76	1.31
	303893	N88597	Hs.113503	karyopherin (importin) beta 3	2.30	2.57
	303907	AW467774	Hs.171880	polymerase (RNA) II (DNA directed) polyp	3.10	5.79
80	303946	AW474196	Hs.306637	Homo sapiens cDNA FLJ12363 fis, clone MA	5.06	11.86
	303978	AW513315		gb:xo43c12.x1 NCL_CGAP_U11 Homo sapiens	5.14	7.31
	303981	AW513804	Hs.278834	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.83	4.06
	303990	AW515465		gb:xu71a11.x1 NCL_CGAP_Kid8 Homo sapiens	1.15	2.35
	303998	AW516449		gb:xt68f05.x1 NCL_CGAP_U12 Homo sapiens	2.20	9.35
85	303999	AW516611		gb:xp70b11.x1 NCL_CGAP_Ov39 Homo sapiens	4.85	6.28
	304006	AW517947		gb:xt66h02.x1 NCL_CGAP_U12 Homo sapiens	3.21	4.07

	304008	AW518198	Hs.3297	ribosomal protein S27a	6.50	11.08
	304009	AW518206	Hs.181165	eukaryotic translation elongation factor	1.88	3.27
	304024	T03036		gb:FB21B7 Fetal brain, Stratagene Homo s	2.15	3.55
5	304026	T03160		gb:FB26F2 Fetal brain, Stratagene Homo s	5.88	11.80
	304028	T03266		gb:FB7C1 Fetal brain, Stratagene Homo sa	5.59	13.46
	304036	T16855	Hs.244621	ribosomal protein S14	6.55	14.43
	304046	T54803		gb:yb42d06.s1 Stratagene fetal spleen (9	6.18	12.19
	304061	T61521		gb:yb73g01.s1 Stratagene ovary (937217)	2.64	8.23
10	304063	T62536		gb:yc04c12.s1 Stratagene lung (937210) H	0.53	1.61
	304097	R25376	Hs.177592	ribosomal protein, large, P1	6.49	11.67
	304114	R78946		gb:yi87g02.s1 Soares placenta Nb2HP Homo	2.90	4.18
	304122	H28966		gb:ym31a06.s1 Soares infant brain 1NIB H	1.00	2.76
	304155	H68696		gb:yr78b05.s1 Soares fetal liver spleen	0.79	1.18
15	304203	N56929		gb:yy82d08.s1 Soares_multiple_sclerosis_	4.28	11.34
	304234	W81608		gb:zd88h06.s1 Soares_fetal_heart_NbHH19W	6.47	11.03
	304267	AA064862	Hs.73742	ribosomal protein, large, P0	1.34	1.16
	304270	AA069711	Hs.297753	vimentin	3.40	5.40
	304287	AA079286	Hs.78466	proteasome (prosome, macropain) 26S sub	2.93	4.42
20	304348	AA179868		gb:zp38g12.s1 Stratagene muscle 937209 H	3.98	10.96
	304415	AA290747	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	3.32	5.99
	304430	AA347682		gb:EST54044 Fetal heart II Homo sapiens	1.00	1.00
	304456	AA411240		gb:zv26g05.s1 Soares_NhHMPu_S1 Homo sapi	1.42	3.33
	304521	AA464716		gb:zx82c11.s1 Soares ovary tumor NbHOT H	2.18	1.15
25	304526	AA476427		gb:zx02c05.s1 Soares_total_fetus_Nb2HF8_	5.38	14.11
	304542	AA482602	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	4.16	8.23
	304546	AA486074	Hs.297681	serine (or cysteine) proteinase inhibitor	0.55	1.20
	304607	AA513322		gb:nh85e08.s1 NCL_CGAP_Br1.1 Homo sapien	1.95	2.10
	304640	AA524440	Hs.111334	ferritin, light polypeptide	2.10	2.83
30	304650	AA527489	Hs.3463	ribosomal protein S23	3.33	12.62
	304735	AA576453		gb:nm75h11.s1 NCL_CGAP_Co9 Homo sapiens	1.33	0.88
	304760	AA580401		gb:nm13g09.s1 NCL_CGAP_Co12 Homo sapiens	3.68	8.14
	304849	AA588157	Hs.13801	KIAA1685 protein	2.77	3.70
	304917	AA602685	Hs.284136	PRO2047 protein	7.16	11.01
35	304921	AA603092	Hs.297753	vimentin	2.47	4.24
	304966	AA613893	Hs.282435	ESTs	6.78	11.66
	304987	AA618044	Hs.300697	immunoglobulin heavy constant gamma 3 (G	0.90	1.23
	305016	AA626876		gb:zu89h06.s1 Soares_testis_NHT Homo sapi	6.46	10.17
	305034	AA630128		gb:ab99c04.s1 Stratagene lung (937210) H	1.00	1.00
40	305072	AA641012		gb:nr72a12.s1 NCL_CGAP_Pr24 Homo sapiens	5.68	11.59
	305111	AA644187	Hs.303405	ESTs	1.48	1.37
	305148	AA654070		gb:nt01g08.s1 NCL_CGAP_Lym3 Homo sapiens	1.76	4.61
	305159	AA659166	Hs.275668	EST, Weakly similar to EF1D_HUMAN ELONG	1.00	2.15
	305190	AA665955		gb:ag57d12.s1 Gessler Wilms tumor Homo s	5.31	8.14
45	305232	AA670052	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	0.78	1.18
	305235	AA670480		gb:ag37e01.s1 Jia bone marrow stroma Hom	3.11	8.66
	305245	AA676695	Hs.81328	nuclear factor of kappa light polypeptid	4.38	7.53
	305312	AA700201		gb:zj44f07.s1 Soares_fetal_liver_spleen_	2.13	2.66
	305322	AA701597	Hs.163019	EST	1.20	1.40
50	305394	AA720942	Hs.300697	immunoglobulin heavy constant gamma 3 (G	1.16	0.68
	305413	AA724659		gb:al10f08.s1 Soares_parathyroid_tumor_N	5.86	9.87
	305447	AA737856		gb:nx10c08.s1 NCL_CGAP_GC3 Homo sapiens	2.21	2.86
	305476	AA745664	Hs.287445	hypothetical protein FLJ11726	3.36	6.54
	305483	AA748030	Hs.303512	EST	1.00	2.02
55	305528	AA769156		gb:nz12e05.s1 NCL_CGAP_GCB1 Homo sapiens	6.44	9.10
	305612	AA782347	Hs.272572	hemoglobin, alpha 2	0.19	0.79
	305614	AA782866		gb:aj09h02.s1 Soares_parathyroid_tumor_N	1.00	1.00
	305616	AA782884	Hs.275865	ribosomal protein S18	7.57	10.20
	305637	AA806124		gb:oe29a12.s1 NCL_CGAP_Pr25 Homo sapiens	4.78	12.42
60	305639	AA806138		gb:oe29c12.s1 NCL_CGAP_Pr25 Homo sapiens	0.89	0.70
	305650	AA807709		gb:nw31e04.s1 NCL_CGAP_GCB0 Homo sapiens	4.49	8.71
	305690	AA813477		gb:al67a05.s1 Soares_testis_NHT Homo sapi	4.91	9.40
	305726	AA828156	Hs.73742	ribosomal protein, large, P0	0.19	0.81
	305728	AA828209		gb:of34a02.s1 NCL_CGAP_Kid6 Homo sapiens	5.12	9.29
65	305759	AA835353		gb:ak72b06.s1 Barstead spleen HPLRB2 Hom	1.66	4.11
	305792	AA845256		gb:ak84a08.s1 Barstead spleen HPLRB2 Hom	2.34	4.25
	305864	AA864374	Hs.73742	ribosomal protein, large, P0	0.30	1.40
	305901	AA872968		gb:oh63h08.s1 NCL_CGAP_Kid5 Homo sapiens	2.10	5.21
	305910	AA875981		gb:nx21h02.s1 NCL_CGAP_GC3 Homo sapiens	0.32	1.01
70	306015	AA897116		gb:am08b07.s1 Soares_NFL_T_GBC_S1 Homo sapi	1.56	1.12
	306017	AA897221	Hs.109058	ribosomal protein S6 kinase, 90kD, polyp	5.21	7.90
	306020	AA897630	Hs.130027	EST	1.96	6.59
	306063	AA906316		gb:ok03g03.s1 Soares_NFL_T_GBC_S1 Homo s	7.38	20.69
75	306065	AA906725		gb:ok78g02.s1 NCL_CGAP_GC4 Homo sapiens	7.19	13.48
	306104	AA910956		gb:ok85h11.s1 NCL_CGAP_Kid3 Homo sapiens	6.50	9.13
	306109	AA911861		gb:og21a07.s1 NCL_CGAP_PNS1 Homo sapiens	4.21	5.25
	306148	AA917409	Hs.288036	tRNA isopentenylpyrophosphate transferas	2.20	2.70
	306242	AA932805		gb:oc60g04.s1 NCL_CGAP_Lu5 Homo sapiens	2.84	5.35
	306288	AA936900		gb:oi53h05.s1 NCL_CGAP_HN3 Homo sapiens	1.60	1.12
80	306325	AA953072	Hs.210546	interleukin 21 receptor	1.65	2.26
	306353	AA961382	Hs.275865	ribosomal protein S18	3.78	6.32
	306375	AA968650	Hs.276018	EST, Moderately similar to JC4662 ribos	4.30	5.74
	306396	AA970223		gb:op09d05.s1 NCL_CGAP_Kid6 Homo sapiens	0.95	2.45
	306428	AA975110	Hs.191228	hypothetical protein FLJ20284	3.19	4.10
85	306442	AA976899		gb:og35e09.s1 NCL_CGAP_GC4 Homo sapiens	4.67	7.44
	306446	AA977348		gb:og72e12.s1 NCL_CGAP_Kid6 Homo sapiens	3.92	6.27

5	306458	AA978186		gb:op33c06.s1 Soares_NFL_T_GBC_S1 Homo s	3.35	5.77
	306467	AA983508	Hs.163593	ribosomal protein L18a	3.72	5.37
	306510	AA988546		gb:or84d07.s1 NCI_CGAP_Lu5 Homo sapiens	1.00	1.00
	306555	AA994304	Hs.276083	EST, Weakly similar to RL23_HUMAN 60S R	6.61	10.91
	306557	AA994530		gb:ou57e08.s1 NCI_CGAP_Br2 Homo sapiens	16.20	31.83
10	306572	AA995686		gb:os25c12.s1 NCI_CGAP_Kid5 Homo sapiens	2.51	6.52
	306582	AA996248		gb:os18c10.s1 NCI_CGAP_Kid5 Homo sapiens	1.42	3.13
	306598	AI000320	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	4.91	8.68
	306605	AI000497	Hs.119500	ribosomal protein, large P2	1.96	8.60
	306656	AI004024		gb:ou11b07.x1 Soares_NFL_T_GBC_S1 Homo s	0.11	0.45
15	306676	AI005603	Hs.284136	PRO2047 protein	9.56	17.28
	306686	AI015615		gb:ov29f10.x1 Soares_testis_NHT Homo sap	1.86	3.60
	306702	AI022565	Hs.307670	EST	1.47	1.19
	306728	AI027359	Hs.272572	hemoglobin, alpha 2	1.28	2.83
	306751	AI032589		gb:ow70h12.s1 Soares_fetal_liver_spleen_	3.91	5.21
20	306767	AI038963	Hs.249118	ESTs	3.33	6.06
	306892	AI092465		gb:qa75h12.x1 Soares_fetal_heart_NbHH19W	3.77	7.46
	306897	AI093967		gb:qa33c06.s1 Soares_NhHMPu_S1 Homo sapi	2.12	2.85
	306956	AI125111		gb:am66f03.s1 Barstead spleen HPLRB2 Hom	6.10	10.52
	306958	AI125152		gb:am55e09.x1 Johnston frontal cortex Ho	1.72	1.56
25	307035	AI142774	Hs.119122	ribosomal protein L13a	2.00	4.70
	307041	AI144243		gb:qb85b12.x1 Soares_fetal_heart_NbHH19W	9.12	12.56
	307091	AI167439		gb:ox70h06.s1 Soares_NhHMPu_S1 Homo sapi	4.88	8.52
	307181	AI189251		gb:qc99g06.x1 Soares_pregnant_uterus_NbH	3.55	6.44
	307297	AI205798	Hs.111334	ferritin, light polypeptide	2.46	4.65
30	307317	AI208303	Hs.147333	EST	5.64	10.13
	307327	AI214142	Hs.246381	CD68 antigen	3.18	5.15
	307382	AI223158	Hs.147885	ESTs	2.02	3.73
	307410	AI241715	Hs.77039	ribosomal protein S3A	0.72	0.48
	307415	AI242118		gb:qh92b02.x1 Soares_NFL_T_GBC_S1 Homo s	2.38	3.51
35	307423	AI243206	Hs.179573	collagen, type I, alpha 2	2.60	5.44
	307426	AI243364		gb:qh30g11.x1 Soares_NFL_T_GBC_S1 Homo s	3.18	7.67
	307517	AI275055		gb:ql72d03.x1 Soares_NhHMPu_S1 Homo sapi	1.00	1.00
	307551	AI281556		gb:qu52f11.x1 NCI_CGAP_Lym6 Homo sapiens	3.40	11.20
	307561	AI282207		gb:qp65a12.x1 Soares_fetal_lung_NbHL19W	4.74	15.51
40	307608	AI290295		gb:qm01f02.x1 Soares_NhHMPu_S1 Homo sapi	3.50	7.19
	307657	AI306428	Hs.298262	ribosomal protein S19	1.76	2.44
	307691	AI318285		gb:tb17b01.x1 NCI_CGAP_Ov37 Homo sapiens	1.59	1.31
	307701	AI318583	Hs.276672	EST, Weakly similar to RL6_HUMAN 60S RI	1.90	2.13
	307718	AI333406	Hs.83753	small nuclear ribonucleoprotein polypept	0.45	0.99
45	307730	AI336092		gb:qt43b07.x1 Soares_fetal_lung_NbHL19W	1.51	0.99
	307760	AI342387		gb:qt27f07.x1 Soares_pregnant_uterus_NbH	1.00	1.00
	307764	AI342731		gb:qo26a07.x1 NCI_CGAP_Lu5 Homo sapiens	4.52	12.58
	307783	AI347274		gb:tc05d02.x1 NCI_CGAP_Co16 Homo sapiens	1.42	1.00
	307796	AI350556		gb:qt18f09.x1 NCI_CGAP_GC4 Homo sapiens	6.57	9.61
50	307807	AI351799		gb:qt09d02.x1 NCI_CGAP_GC4 Homo sapiens	3.38	7.68
	307808	AI351826		gb:qt09g03.x1 NCI_CGAP_GC4 Homo sapiens	0.33	0.86
	307820	AI355761		gb:qt94a11.x1 NCI_CGAP_Co14 Homo sapiens	7.94	21.57
	307830	AI358722	Hs.276737	EST, Weakly similar to R5HU22 ribosomal	2.05	3.32
	307852	AI365541		gb:qz08g05.x1 NCI_CGAP_CLL1 Homo sapiens	3.18	5.21
55	307902	AI380462		gb:tg02h05.x1 NCI_CGAP_CLL1 Homo sapiens	3.13	4.99
	307997	AI434512	Hs.181165	eukaryotic translation elongation factor	1.00	3.01
	308002	AI435240	Hs.283442	ESTs	5.86	12.64
	308011	AI439473		gb:ti60a08.x1 NCI_CGAP_Lym12 Homo sapien	3.79	5.83
	308023	AI452732	Hs.251577	hemoglobin, alpha 1	0.38	0.88
60	308041	AI458824	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	4.36	6.06
	308059	AI468938	Hs.276877	EST, Weakly similar to RL10_HUMAN 60S R	1.80	1.98
	308085	AI474135	Hs.181165	eukaryotic translation elongation factor	3.38	4.14
	308101	AI475950	Hs.181165	eukaryotic translation elongation factor	1.30	3.87
	308106	AI476803		gb:lj77e12.x1 Soares_NSF_F8_9W_OT_PA_P_S2.38	8.72	8.72
65	308122	AI480123	Hs.309411	EST	2.70	3.86
	308154	AI500600		gb:tn93d08.x1 NCI_CGAP_Ut2 Homo sapiens	0.66	1.33
	308171	AI523632	Hs.298766	ESTs, Weakly similar to schlafen4 [M.mu	2.48	4.86
	308211	AI557029	Hs.278572	anaplastic lymphoma kinase (Ki-1)	2.43	2.14
	308213	AI557041		gb:PT2.1_12_E04.r tumor2 Homo sapiens cD	3.34	3.79
70	308216	AI557135		gb:PT2.1_13_H06.r tumor2 Homo sapiens cD	4.61	4.78
	308219	AI557246		gb:PT2.1_15_D07.r tumor2 Homo sapiens cD	4.87	7.94
	308271	AI567844	Hs.252259	ribosomal protein S3	2.40	6.35
	308319	AI583983	Hs.181165	eukaryotic translation elongation factor	2.45	3.33
	308362	AI613519	Hs.105749	KIAA0553 protein	1.24	1.41
75	308413	AI636253	Hs.196511	ESTs	3.16	4.82
	308450	AI660860	Hs.96840	KIAA1527 protein	1.79	2.68
	308464	AI672425	Hs.277117	EST, Moderately similar to I38055 myosi	4.87	8.27
	308588	AI718299		gb:as51g12.x1 Barstead aorta HPLRB6 Homo	3.90	5.64
	308599	AI719893		gb:as47d07.x1 Barstead aorta HPLRB6 Homo	3.32	5.12
80	308615	AI738593	Hs.101774	hypothetical protein FLJ23045	3.11	2.36
	308643	AI745040		gb:tr19a12.x1 NCI_CGAP_Ov23 Homo sapiens	3.98	3.69
	308673	AI760864		gb:wi09c10.x1 NCI_CGAP_CLL1 Homo sapiens	0.82	0.99
	308697	AI767143		gb:wi97a07.x1 NCI_CGAP_Kid12 Homo sapien	2.76	5.59
	308762	AI807405	Hs.259408	ESTs	3.17	6.30
85	308778	AI811109		gb:tr04c11.x1 NCI_CGAP_Ov23 Homo sapiens	1.00	1.00
	308782	AI811767	Hs.2186	eukaryotic translation elongation factor	2.94	5.15
	308808	AI818289		gb:wk52c01.x1 NCI_CGAP_Pr22 Homo sapiens	4.41	8.34
	308823	AI824118	Hs.217493	annexin A2	1.85	1.92
	308875	AI832332		gb:at48g03.x1 Barstead colon HPLRB7 Homo	2.52	3.80

	308879	AI832763	Hs.75968	thymosin, beta 4, X chromosome	3.38	7.96
	308886	AI833240		gb:al76d10.x1 Barstead colon HPLRB7 Homo	3.06	2.65
	308898	AI858845		gb:wl32d10.x1 NCI_CGAP_Ut1 Homo sapiens	2.45	3.44
	308934	AI865023	Hs.177	phosphatidylinositol glycan, class H	4.14	6.76
5	308966	AI870704		gb:wl47h01.x1 NCI_CGAP_Ut1 Homo sapiens	1.00	1.00
	308979	AI873111		gb:wl52h05.x1 NCI_CGAP_Brn25 Homo sapien	7.15	11.10
	309045	AI910902		gb:tlq39f01.x1 NCI_CGAP_Ut1 Homo sapiens	0.61	0.59
	309051	AI911975		gb:wd78d01.x1 NCI_CGAP_Lu24 Homo sapiens	1.78	4.42
10	309069	AI917366	Hs.78202	SWI/SNF related, matrix associated, act	3.27	5.88
	309083	AI922426	Hs.119598	ribosomal protein L3	2.39	3.34
	309105	AI925503	Hs.265884	ESTs	5.54	17.78
	309122	AI928178		gb:wo95a11.x1 NCI_CGAP_Kid11 Homo sapien	1.00	2.92
	309128	AI928816	Hs.180842	ribosomal protein L13	1.38	5.55
15	309164	AI937761		gb:wp84b09.x1 NCI_CGAP_Brn25 Homo sapien	2.43	3.11
	309177	AI951118		gb:wx63g05.x1 NCI_CGAP_Br18 Homo sapiens	0.81	0.97
	309288	AI991525	Hs.299426	ESTs	4.86	7.46
	309299	AW003478		gb:wq66c06.x1 NCI_CGAP_GC6 Homo sapiens	4.36	9.43
	309303	AW004823		gb:ws93a08.x1 NCI_CGAP_Co3 Homo sapiens	2.88	7.54
20	309411	AW085201	Hs.244144	EST	4.30	7.14
	309437	AW090702	Hs.278242	tubulin, alpha, ubiquitous	2.49	3.11
	309459	AW117645	Hs.65114	keratin 18	2.88	4.55
	309476	AW129368		gb:xe14b05.x1 NCI_CGAP_Ut4 Homo sapiens	2.08	6.60
	309499	AW136325	Hs.279771	Homo sapiens clone PP1596 unknown mRNA	2.82	3.55
	309529	AW150807	Hs.181357	laminin receptor 1 (67kD, ribosomal pro	4.78	3.95
25	309532	AW151119		gb:xg33e10.x1 NCI_CGAP_Ut1 Homo sapiens	1.18	4.40
	309626	AW192004	Hs.297681	serine (or cysteine) proteinase inhibit	4.46	12.06
	309641	AW194230	Hs.253100	EST, Moderately similar to GHU Ig gamm	1.47	1.39
	309675	AW205681	Hs.253506	EST, Moderately similar to ATPN_HUMAN A	5.68	15.20
30	309693	AW237221	Hs.181357	laminin receptor 1 (67kD, ribosomal prot	1.00	1.00
	309695	AW238011	Hs.295605	mannosidase, alpha, class 2A, member 2	5.45	9.61
	309700	AW241170	Hs.179661	tubulin, beta polypeptide	1.41	1.25
	309747	AW264889		gb:xq36h02.x1 NCI_CGAP_Lu28 Homo sapiens	5.00	8.35
	309769	AW272346		gb:xs13c10.x1 NCI_CGAP_Kid11 Homo sapien	5.76	11.90
35	309782	AW275156	Hs.156110	immunoglobulin kappa constant	0.42	0.69
	309783	AW275401	Hs.254798	EST	1.00	4.11
	309799	AW276964		gb:xp58h01.x1 NCI_CGAP_Ov39 Homo sapiens	1.68	1.44
	309866	AW299916		gb:xs44c01.x1 NCI_CGAP_Kid11 Homo sapien	3.02	5.04
	309903	AW339071	Hs.300697	immunoglobulin heavy constant gamma 3 (G	1.05	1.18
40	309923	AW340684		gb:hd05g08.x1 Soares_NFL_T_GBC_S1 Homo s	2.30	3.67
	309928	AW341418		gb:hd08c03.x1 Soares_NFL_T_GBC_S1 Homo s	7.41	13.71
	309931	AW341683		gb:hd13d01.x1 Soares_NFL_T_GBC_S1 Homo s	1.20	12.70
	309933	AW341936		gb:hb73f10.x1 NCI_CGAP_Ut2 Homo sapiens	4.90	18.29
	309964	AW449111	Hs.257111	hypothetical protein MGC3265	1.99	3.07
45	310002	AI439096	Hs.323079	Homo sapiens mRNA; cDNA DKFZp564P116 (fr	0.20	0.47
	310096	AW136822	Hs.172824	ESTs, Weakly similar to B48013 proline-r	1.51	1.22
	310098	AI685841	Hs.161354	ESTs	0.31	0.76
	310109	AI203094	Hs.148633	ESTs	2.06	5.83
	310112	AW197233	Hs.147253	ESTs	2.92	3.55
50	310115	AI611317	Hs.223796	ESTs	1.25	0.84
	310121	AW195642	Hs.148901	ESTs	1.00	2.71
	310146	AI206614	Hs.197422	ESTs	9.50	15.31
	310193	AI627653	Hs.147562	ESTs	2.85	4.18
	310255	AW450439	Hs.153378	ESTs	4.26	10.63
55	310261	AI240483	Hs.201217	ESTs	3.28	4.40
	310264	AI915771	Hs.74170	metallothionein 1E (functional)	0.26	0.86
	310275	AI242102	Hs.213636	ESTs	5.43	8.19
	310282	AI243332	Hs.156055	ESTs	3.15	8.06
	310290	AW013815	Hs.149103	ESTs	2.19	3.12
60	310333	AI253200	Hs.145402	ESTs	1.17	1.91
	310346	AI261340	Hs.145517	ESTs	4.81	9.95
	310385	AI263392	Hs.156151	ESTs	5.96	7.79
	310443	AW119018	Hs.164231	ESTs	2.90	4.63
	310444	AW196632	Hs.252956	ESTs	0.85	1.01
65	310446	AI275715	Hs.145926	ESTs	2.18	3.85
	310468	AI984074	Hs.196398	ESTs	3.39	5.19
	310477	AI948801	Hs.171073	ESTs	1.00	1.00
	310512	AW275603	Hs.200712	ESTs	3.87	8.12
	310514	AI681145	Hs.160724	ESTs	3.30	7.33
70	310524	AW082270	Hs.12496	ESTs, Highly similar to AC004836 1 simil	0.72	1.44
	310547	AI302654	Hs.208024	ESTs	3.26	3.46
	310584	AI653007	Hs.156304	ESTs	2.39	4.08
	310608	AI962234	Hs.196102	ESTs	5.60	6.49
	310624	AI341594		gb:Human endogenous retrovirus H proteas	4.91	9.09
75	310636	AI814373	Hs.164175	ESTs	1.85	1.71
	310648	AI347863	Hs.156672	ESTs	0.17	0.69
	310694	AI654370	Hs.157752	Homo sapiens mRNA full length insert cDN	5.40	13.22
	310695	AI472124	Hs.157757	ESTs	4.82	6.27
	310714	AI418446	Hs.157882	ESTs	1.76	3.51
80	310722	AI989803	Hs.157289	ESTs	1.14	6.85
	310756	AI916560	Hs.158707	ESTs	8.46	13.01
	310764	AI376769	Hs.167172	ESTs	4.76	7.37
	310848	AI459554	Hs.161286	ESTs	2.84	1.96
	310851	AW291714	Hs.221703	ESTs	1.00	2.32
85	310854	AI421677	Hs.161332	ESTs	6.37	7.94
	310858	AI871000	Hs.161330	ESTs	6.07	9.84

	310864	AI924558	Hs.161399	ESTs	0.87	0.78
	310875	T47764	Hs.132917	ESTs	1.00	3.63
	310896	AW157731	Hs.270982	ESTs, Moderately similar to ALU7_HUMAN A	7.07	16.68
5	310922	AW195634	Hs.170401	ESTs	1.00	1.00
	310955	AI560210	Hs.263912	ESTs	10.08	17.66
	310957	AW190974	Hs.196918	ESTs	2.18	3.18
	311000	AI521830	Hs.171050	ESTs	3.06	6.64
	311012	AW298070	Hs.241097	ESTs	1.23	3.77
10	311034	AI564023	Hs.311389	ESTs, Moderately similar to PT0375 natur	2.44	2.09
	311074	AW290922	Hs.199848	ESTs	6.04	14.19
	311134	AI990849	Hs.196971	ESTs	3.54	6.96
	311174	AW450552	Hs.205457	periastin	0.65	0.95
	311187	AI638374	Hs.224189	ESTs	2.46	2.78
15	311220	AI656040	Hs.196532	ESTs	1.10	2.52
	311230	AI989808	Hs.197663	ESTs	1.41	1.75
	311236	AI653378	Hs.197674	ESTs	2.18	2.11
	311242	AW016812	Hs.200266	ESTs	0.63	5.11
	311258	AI671221	Hs.199887	ESTs	1.00	1.41
20	311277	AW072813	Hs.270868	ESTs, Moderately similar to ALU4_HUMAN A	2.56	1.94
	311294	AA826425	Hs.291829	ESTs	1.04	2.69
	311308	F12664	Hs.49000	ESTs	1.96	6.70
	311351	AI682303	Hs.201274	ESTs	4.77	9.38
	311390	AW392997	Hs.202280	ESTs	2.80	6.06
25	311405	AW290961	Hs.201815	ESTs	3.80	11.66
	311409	AI698839		gb:wd31f02.x1 Soares_NFL_T_GBC_S1 Homo s	3.84	6.94
	311420	AI936291	Hs.209867	ESTs	5.30	12.56
	311443	AI791521	Hs.192206	ESTs	4.39	6.09
	311467	AI934909	Hs.175377	ESTs	1.00	1.04
30	311479	AI933672	Hs.211399	ESTs	2.76	5.61
	311488	R57390	Hs.301064	arfaptin 1	2.50	5.73
	311495	AW300077	Hs.221358	ESTs	3.63	6.09
	311511	AW444568	Hs.210303	ESTs	2.00	2.87
	311534	AW130351	Hs.243549	ESTs	0.31	1.33
35	311537	AI805121	Hs.211828	ESTs	3.69	5.85
	311543	AI681360	Hs.201259	ESTs	1.73	1.34
	311551	AW449774	Hs.296380	POM (POM121 rat homolog) and ZP3 fusion	3.31	6.12
	311557	AI819230	Hs.211238	interleukin-1 homolog 1	1.00	1.00
	311558	Z44432	Hs.63128	KIAA1292 protein	2.25	3.41
40	311559	AW008271	Hs.265848	similar to rat myomegalin	2.68	5.90
	311563	AI922143	Hs.211334	ESTs	2.39	3.32
	311586	AI827834	Hs.211227	ESTs	2.47	3.85
	311616	AW450675	Hs.212709	ESTs	1.00	1.00
	311621	AI924307	Hs.213464	ESTs	4.16	6.74
45	311635	AI928456	Hs.213081	ESTs	2.17	3.76
	311668	AW193674	Hs.240044	ESTs	2.60	3.12
	311672	R11807	Hs.20914	hypothetical protein FLJ23056	2.79	5.18
	311683	AW183738	Hs.232644	ESTs	0.19	0.96
	311700	R49601	Hs.171495	retinoic acid receptor, beta	6.28	8.83
50	311714	AW131785	Hs.246831	ESTs, Weakly similar to CLKG_HUMAN VOLTA	5.00	8.17
	311735	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT	0.96	0.72
	311743	T99079	Hs.191194	ESTs	1.00	1.95
	311783	AI682478	Hs.13528	hypothetical protein FLJ14054	0.16	0.77
	311785	AI056769	Hs.133512	ESTs	1.34	3.97
55	311799	AA780791	Hs.14014	ESTs, Weakly similar to KIAA0973 protein	8.52	13.32
	311819	AW265275	Hs.254325	ESTs	3.58	3.91
	311823	AI089422	Hs.131297	ESTs	1.40	1.72
	311877	AA349893	Hs.85339	G protein-coupled receptor 39	0.95	0.91
	311886	AA522738	Hs.132554	ESTs	0.88	0.87
60	311896	AW206447		gb:U1-H-BI1-afg-g-02-0-U1.s1 NCI_CGAP_Su	1.66	1.13
	311910	N28365	Hs.22579	Homo sapiens clone CDABP0036 mRNA sequen	1.66	2.30
	311923	T60843	Hs.189679	ESTs	0.42	2.63
	311933	AI597963	Hs.118726	ESTs	1.88	3.02
	311959	T67262	Hs.124733	ESTs	2.02	2.33
65	311960	AW440133	Hs.189690	ESTs	3.87	6.62
	311967	AI382726	Hs.182434	ESTs	5.80	8.14
	311975	AA804374	Hs.272203	Homo sapiens cDNA FLJ20843 fis, clone AD	0.98	3.26
	312005	T78450	Hs.13941	ESTs	0.12	1.39
	312028	T78886	Hs.284450	ESTs	3.78	4.92
70	312046	AI580018	Hs.268591	ESTs	4.11	7.32
	312056	T83748	Hs.268594	ESTs	2.36	3.08
	312064	AA676713	Hs.191155	ESTs	3.34	5.28
	312088	AW303760	Hs.13685	ESTs	1.60	1.15
	312093	T91809	Hs.121296	ESTs	0.68	0.85
75	312094	Z78390		gb:HSZ78390 Human fetal brain S. Meier-E	3.05	4.48
	312097	AI352096	Hs.112180	zinc finger protein 148 (pHZ-52)	4.52	9.70
	312118	T85332	Hs.178294	ESTs	2.40	2.60
	312128	AI052609	Hs.17631	Homo sapiens cDNA FLJ20118 fis, clone CO	2.39	3.53
	312147	T89855	Hs.195648	ESTs	0.67	1.03
80	312175	AA953383	Hs.127554	ESTs	5.85	10.60
	312179	AI052572	Hs.269864	ESTs	2.41	3.32
	312201	AI928365	Hs.91139	solute carrier family 1 (neuronal/epithe	0.24	0.89
	312207	H90213	Hs.191330	ESTs	2.20	4.55
	312220	N74613		gb:za55a07.s1 Soares fetal liver spleen	4.28	11.13
85	312252	AI128388	Hs.143655	ESTs	1.64	1.57
	312304	AA491949	Hs.269392	ESTs	0.12	2.47

	312318	AW235092	Hs.143981	ESTs	3.46	5.69
	312319	AA216698	Hs.180780	TERA protein	5.78	4.46
	312321	R66210	Hs.186937	ESTs	0.44	1.74
5	312331	AA825512	Hs.289101	glucose regulated protein, 58kD	3.73	5.96
	312339	AA524394	Hs.165544	ESTs	3.07	0.95
	312363	AI675558	Hs.181867	ESTs	10.08	16.73
	312375	AI375096	Hs.172405	cell division cycle 27	2.78	3.71
	312376	R52089	Hs.172717	ESTs	1.00	1.00
10	312389	AI863140		gb:tz43h12.x1 NCL_CGAP_Brn52 Homo sapien	2.37	3.98
	312437	AA995028		gb:RC4-BT0629-120200-011-b10 BT0629 Homo	4.06	5.41
	312440	AI051133	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	1.00	1.00
	312451	R59989	Hs.176539	ESTs	4.96	10.04
	312458	AI167637	Hs.148924	ESTs	1.11	1.00
15	312507	AI168177	Hs.143653	ESTs	5.89	8.24
	312520	AI742591	Hs.205392	ESTs	3.30	8.92
	312548	AI566228	Hs.159426	hypothetical protein PRO2121	1.38	1.65
	312564	H21520	Hs.35088	ESTs	0.40	0.77
	312583	AI193122	Hs.124141	ESTs	0.13	0.94
20	312589	AI865073	Hs.125720	ESTs	3.75	5.29
	312602	AA046451	Hs.165200	ESTs	6.78	12.93
	312645	H52121	Hs.193007	ESTs	0.38	1.13
	312666	AI240582	Hs.214678	ESTs	0.98	2.03
	312689	AW450461	Hs.203965	ESTs	0.21	0.61
25	312817	H75459	Hs.233425	ESTs	1.51	0.85
	312846	AW152104	Hs.200879	ESTs	8.93	13.78
	312873	AI690071	Hs.283552	ESTs, Weakly similar to unnamed protein	4.20	6.23
	312893	AI016204	Hs.172922	ESTs	2.67	3.15
30	312902	AW292797	Hs.130316	ESTs, Weakly similar to T2D3_HUMAN TRANS	1.19	0.71
	312925	N90868	Hs.271695	ESTs	2.50	4.25
	312936	AI681581	Hs.121525	ESTs	1.00	1.17
	312975	AI640506	Hs.293119	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.30	4.80
	312978	N24887	Hs.292500	ESTs	0.80	1.05
	312980	AA497043	Hs.115685	ESTs	3.12	3.60
35	312984	N25871	Hs.177337	ESTs	2.03	2.13
	313000	AI147412	Hs.146657	ESTs	5.52	8.42
	313029	AA731520	Hs.170504	ESTs	0.96	1.39
	313039	AI419290	Hs.149990	ESTs, Weakly similar to unnamed protein	6.48	13.20
40	313049	AW293055	Hs.119357	ESTs	6.44	10.73
	313056	AI651930	Hs.135684	ESTs	1.51	2.04
	313058	D81015	Hs.125382	ESTs	0.25	1.50
	313070	AI422023	Hs.161338	ESTs	8.56	11.60
	313097	AI676164	Hs.204339	ESTs	3.72	4.56
	313130	AW449171	Hs.168677	ESTs	3.28	5.06
45	313136	N59284	Hs.288010	ESTs	0.49	1.36
	313153	AI240838	Hs.132750	ESTs	5.36	5.52
	313210	N74077	Hs.197043	ESTs	0.30	0.66
	313236	AW238169	Hs.83513	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.16	8.76
	313239	W19632	Hs.124170	ESTs	1.00	3.87
50	313265	N93466	Hs.121764	ESTs, Weakly similar to testicular tekti	0.74	2.06
	313267	AI770008	Hs.129583	ESTs	0.23	1.30
	313275	AI027604	Hs.159650	ESTs	6.68	9.57
	313290	AI753247	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	1.34	1.07
	313292	AI362991	Hs.202121	ESTs, Weakly similar to env protein [H.s	2.00	4.32
55	313325	AI420611	Hs.127832	ESTs	1.20	2.27
	313357	AW074848	Hs.201501	ESTs	4.02	5.33
	313393	AI674685	Hs.200141	ESTs	1.36	2.84
	313399	AW376889	Hs.194097	ESTs	2.58	5.26
	313414	AI241540	Hs.132933	ESTs	6.57	15.07
60	313417	AA741151	Hs.137323	ESTs	0.63	3.01
	313457	AA576052	Hs.193223	Homo sapiens cDNA FLJ11646 fis, clone HE	2.78	4.70
	313499	AI261390	Hs.146085	KIAA1345 protein	0.91	2.37
	313516	AA029058	Hs.135145	ESTs	3.41	7.08
	313556	AA628517	Hs.118502	ESTs	0.23	0.70
65	313569	AI273419	Hs.135146	hypothetical protein FLJ13984	1.88	1.00
	313570	AA041455	Hs.209312	ESTs	0.73	2.27
	313638	AI753075	Hs.104627	Homo sapiens cDNA FLJ10158 fis, clone HE	1.00	1.72
	313662	AA740151	Hs.130425	ESTs	0.20	1.42
	313671	W49823	Hs.104613	RP42 homolog	1.00	1.00
70	313672	AW468891	Hs.122948	ESTs	3.46	5.80
	313690	AI493591	Hs.78146	platelet/endothelial cell adhesion molec	0.51	0.97
	313711	AA398070	Hs.133471	ESTs	0.18	1.01
	313723	AA070412		gb:zm68c10.s1 Stratagene neuroepithelium	1.08	1.03
	313726	AI744687	Hs.257806	ESTs	2.13	2.99
75	313774	AW136836	Hs.144583	ESTs	1.38	1.19
	313784	AA910514	Hs.134905	ESTs	3.88	5.78
	313790	AW078569	Hs.177043	ESTs	0.22	2.06
	313832	AW271022	Hs.133294	ESTs	1.15	0.91
	313834	AW418779	Hs.114889	ESTs	0.68	3.14
80	313835	AI538438	Hs.159087	ESTs	5.74	8.88
	313852	H18633	Hs.123641	protein tyrosine phosphatase, receptor t	0.16	1.14
	313854	AW470806	Hs.275002	ESTs	2.09	4.06
	313865	AA731470	Hs.163839	ESTs	3.41	4.09
	313871	AW471088	Hs.145950	ESTs	5.28	6.83
85	313883	AI949384		gb:nu76d01.s1 NCL_CGAP_Alv1 Homo sapiens	2.90	10.91
	313915	AI969390	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	1.00	1.00

	313926	AW473830	Hs.171442	ESTs	3.40	4.11
	313948	AW452823	Hs.135268	ESTs	5.77	9.15
	313978	AI870175	Hs.13957	ESTs	0.46	0.75
5	313983	AI829133	Hs.226780	ESTs	4.10	6.40
	314035	AA164199	Hs.270152	ESTs	5.88	7.90
	314037	AW300048	Hs.275272	ESTs	1.00	3.79
	314040	AA166970	Hs.118748	ESTs	7.60	11.33
	314067	AW293538	Hs.51743	KIAA1340 protein	1.86	1.21
10	314103	AI028477	Hs.132775	ESTs	2.90	5.29
	314107	AA806113	Hs.189025	ESTs	2.00	1.66
	314113	AA218986	Hs.118854	ESTs	0.91	4.17
	314124	AW118745	Hs.9460	Homo sapiens mRNA; cDNA DKFZp547C244 (fr	2.53	3.32
	314126	AA226431		gb:nc18b12.s1 NCL_CGAP_Pr1 Homo sapiens	3.13	5.08
15	314128	AA935633	Hs.194628	ESTs	2.90	6.35
	314151	AA236163	Hs.202430	ESTs	4.15	6.45
	314184	AW081795	Hs.233465	ESTs	3.44	4.65
	314192	AW290975	Hs.118923	ESTs	1.00	1.23
	314244	AL036450	Hs.103238	ESTs	2.88	3.67
20	314253	AA278679	Hs.189510	ESTs	4.98	7.16
	314262	AW086215	Hs.246096	ESTs	0.38	1.94
	314320	AA811598	Hs.275809	ESTs	3.34	5.66
	314332	AL037551	Hs.95612	ESTs	2.85	2.09
	314335	AA287443	Hs.142570	Homo sapiens clone 24629 mRNA sequence	4.35	4.78
25	314340	AW304350	Hs.130879	ESTs, Moderately similar to putative p15	0.77	0.86
	314351	AA292275	Hs.193746	ESTs	3.07	3.77
	314376	AI628633	Hs.324679	ESTs	4.10	6.11
	314443	AA827125	Hs.192043	ESTs	6.20	13.67
	314458	AI217440	Hs.143873	ESTs	0.58	2.49
30	314466	AA767818	Hs.122707	ESTs	2.53	2.62
	314478	AI521173	Hs.125507	DEAD-box protein	3.94	5.65
	314482	AL043807	Hs.134182	ESTs	1.30	1.44
	314506	AA833655	Hs.206868	Homo sapiens cDNA FLJ14056 fis, clone HE	3.28	3.47
	314519	R42554	Hs.210862	T-box, brain, 1	3.12	6.16
35	314529	AL046412	Hs.202151	ESTs	3.43	6.87
	314546	AW007211	Hs.16131	hypothetical protein FLJ12876	1.38	1.00
	314562	AI564127	Hs.143493	ESTs	2.29	5.27
	314579	AW197442	Hs.116996	ESTs	3.87	5.75
	314580	AW451832	Hs.255938	ESTs, Moderately similar to KIAA1200 pro	0.10	0.71
40	314585	AA918474	Hs.216363	ESTs	1.08	1.40
	314589	AW384790	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	1.00	1.00
	314592	AA435761	Hs.192148	ESTs	0.90	2.60
	314603	AA418024	Hs.270670	ESTs	4.56	6.29
	314604	AA946582	Hs.8700	deleted in liver cancer 1	3.42	3.92
45	314606	AA418241	Hs.188767	ESTs	2.97	4.55
	314648	AA878419		gb:EST391378 MAGE resequences, MAGP Homo1.42	1.36	1.36
	314699	AI038719	Hs.132801	ESTs	3.66	4.97
	314701	AI754634	Hs.131987	ESTs	0.03	0.90
	314710	AI669131	Hs.290989	EST	3.40	7.52
50	314750	AI095005	Hs.135174	ESTs	2.80	6.54
	314767	AW135412	Hs.164002	ESTs	3.20	4.26
	314801	AA481027	Hs.109045	hypothetical protein FLJ10498	1.00	1.00
	314817	AI694139	Hs.192855	ESTs	0.91	0.99
	314835	AI281370	Hs.76064	ribosomal protein L27a	5.75	7.44
55	314852	AI903735		gb:MR-BT035-200199-031 BT035 Homo sapien	1.68	4.34
	314853	AA729232	Hs.153279	ESTs	0.60	1.85
	314940	AW452768	Hs.162045	ESTs	10.10	16.20
	314941	AA515902	Hs.130650	ESTs	0.31	1.02
	314943	AI476797	Hs.184572	cell division cycle 2, G1 to S and G2 to	2.18	0.37
60	314955	AA521382	Hs.192534	ESTs	2.59	3.90
	314973	AW273128	Hs.300268	ESTs	1.05	1.25
	315004	AA527941	Hs.325351	EST	5.64	13.63
	315006	AI538613	Hs.298241	Transmembrane protease, serine 3	0.52	1.78
	315033	AI493046	Hs.146133	ESTs	2.46	1.00
65	315035	AI569476	Hs.177135	ESTs	0.34	1.33
	315056	AI202703	Hs.152414	ESTs	2.10	2.64
	315069	AI821517	Hs.105866	ESTs	1.00	1.30
	315071	AA552690	Hs.152423	Homo sapiens cDNA: FLJ21274 fis, clone C	1.78	1.00
	315073	AW452948	Hs.257631	ESTs	1.17	1.52
70	315078	AA568548	Hs.190616	ESTs	3.00	3.79
	315080	AA744550	Hs.136345	ESTs	1.00	1.00
	315120	AA564991	Hs.269477	ESTs	0.64	1.44
	315175	AI025842	Hs.152530	ESTs	0.61	1.91
	315193	AI241331	Hs.131765	ESTs	1.06	0.97
75	315196	AA972756	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	0.48	1.96
	315200	AI808235	Hs.307686	EST	3.76	9.40
	315254	AI474433	Hs.179566	ESTs	5.37	9.36
	315353	AW452608	Hs.279610	hypothetical protein FLJ10493	1.00	1.30
	315397	AA218940	Hs.137516	figelatin-like 1	3.38	2.24
80	315403	AW362980	Hs.163924	ESTs	2.04	5.23
	315431	AA622104	Hs.184838	ESTs	2.36	8.04
	315454	AI239473		gb:qh36f02.x1 Soares_NFL_T_GBC_S1 Homo s	3.46	7.64
	315455	AW393391	Hs.156919	ESTs	3.78	5.76
	315473	AI681671	Hs.312671	ESTs, Moderately similar to OVCA1	0.89	2.15
85	315483	AW512763	Hs.222024	transcription factor BMAL2	2.32	1.96
	315526	AI193048	Hs.128685	ESTs	1.67	1.78

	315530	AI200852	Hs.127780	ESTs	1.05	1.01
	315541	AI168233	Hs.123159	sperm associated antigen 4	0.85	0.56
	315552	AW445034	Hs.256578	ESTs	1.00	2.22
5	315562	AA737415	Hs.152826	ESTs	2.66	2.48
	315577	AW513545	Hs.17283	hypothetical protein FLJ10890	2.20	2.25
	315587	AI268399	Hs.140489	ESTs	1.00	1.04
	315589	AW072387	Hs.158258	Homo sapiens mRNA; cDNA DKFZp434B1272 (f	0.14	1.05
	315623	AA364078	Hs.258189	ESTs	7.44	12.56
10	315634	AA837085	Hs.220585	ESTs	0.50	1.40
	315668	AA912347	Hs.136585	ESTs	0.43	1.22
	315677	AI932662	Hs.164073	ESTs	0.60	1.39
	315706	AW440742	Hs.155556	hypothetical protein FLJ20202	2.18	3.77
	315707	AI418055	Hs.161160	ESTs	2.88	2.63
15	315730	H25899	Hs.201591	ESTs	0.11	0.60
	315745	AI821759	Hs.191856	ESTs	3.50	7.25
	315791	AA678177		gb:z15a05.s1 Soares_fetal_liver_spleen_	1.78	2.63
	315801	AA827752	Hs.266134	ESTs	4.31	6.23
	315820	AI652022	Hs.258785	ESTs	2.35	3.01
20	315878	AA683336	Hs.189046	ESTs	2.12	2.64
	315905	AI821911	Hs.209452	ESTs	1.03	1.97
	315923	AI052789	Hs.133263	ESTs	2.63	5.06
	315954	AW276810	Hs.254859	ESTs, Moderately similar to ALU5_HUMAN A	1.21	0.85
	315978	AA830893	Hs.119769	ESTs	3.09	3.41
25	316001	AI248584	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone C	2.20	6.82
	316011	AW516953	Hs.201372	ESTs	0.35	1.63
	316012	AA764950	Hs.119898	ESTs	6.56	8.13
	316040	AI983409	Hs.189226	ESTs	5.69	10.69
	316048	AI720759	Hs.224971	ESTs	2.84	10.45
30	316076	AW297895	Hs.116424	ESTs	0.30	1.05
	316124	AI308862	Hs.167028	ESTs	1.00	1.43
	316151	AI806016	Hs.156520	ESTs	5.80	9.03
	316187	AW518299	Hs.192253	ESTs	1.20	3.96
	316204	AA731509	Hs.120257	ESTs	4.92	6.94
35	316232	AW297853	Hs.251203	ESTs	1.48	1.60
	316275	AI671041	Hs.292611	ESTs, Moderately similar to ALU1_HUMAN A	5.86	12.14
	316291	AW375974	Hs.156704	ESTs	2.73	2.69
	316303	AA740994	Hs.209609	ESTs	1.53	1.26
	316344	AA744518	Hs.120610	ESTs	3.66	8.34
40	316346	AI028478	Hs.157447	ESTs	3.51	6.69
	316365	AI627845	Hs.210776	ESTs	2.50	4.33
	316380	AI393378	Hs.164496	ESTs	1.16	2.16
	316470	AA809902	Hs.243813	ESTs	5.40	10.34
	316509	AA767310	Hs.291766	ESTs	2.46	2.89
45	316514	AA768037	Hs.291671	ESTs	4.70	6.04
	316519	AI929097		gb:od10c11.s1 NCL_CGAP_GCB1 Homo sapiens	4.41	9.70
	316609	AW292520	Hs.122082	ESTs	1.00	2.89
	316633	AI125586	Hs.127955	ESTs	2.61	3.72
	316700	AW172316	Hs.252961	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.46	4.64
50	316711	AI743721	Hs.285316	ESTs, Moderately similar to ALU7_HUMAN A	4.45	6.95
	316713	AI090671	Hs.134807	hypothetical protein FLJ12057	0.30	2.40
	316715	AI440266	Hs.170673	ESTs, Weakly similar to AF126780 1 retin	0.20	1.45
	316787	AW369770	Hs.130351	ESTs	4.05	5.53
	316809	AA825839	Hs.202238	ESTs	2.25	3.82
55	316811	AA922060	Hs.132471	ESTs	1.00	1.32
	316812	AW135045	Hs.232001	ESTs	3.28	4.70
	316818	AA827176	Hs.124316	ESTs	0.67	1.81
	316824	AA837416	Hs.124299	ESTs	3.53	6.00
60	316827	AI380429	Hs.172445	ESTs	0.72	1.56
	316891	AW298119	Hs.202536	ESTs	1.64	2.97
	316951	AA134365	Hs.57548	ESTs	1.45	1.08
	316970	AA860172	Hs.132406	ESTs	1.00	1.53
	316971	AA860212	Hs.170991	ESTs	1.08	1.96
	316990	AA861611	Hs.130643	ESTs	5.44	10.04
65	317001	AI627917	Hs.233694	hypothetical protein FLJ11350	3.56	4.37
	317008	AW051597	Hs.143707	ESTs	0.69	1.37
	317051	AA873253	Hs.126233	ESTs	6.18	12.72
	317128	AA971374	Hs.125674	ESTs	1.87	2.66
70	317129	H12523	Hs.78521	Homo sapiens cDNA: FLJ21193 fis, clone C	4.12	6.64
	317137	AW341567	Hs.125710	ESTs	2.82	5.12
	317196	AI348258	Hs.153412	ESTs	1.98	2.51
	317212	AI866468	Hs.148294	ESTs	1.86	2.83
	317223	AW297920	Hs.130054	ESTs	0.83	1.57
	317224	D56760	Hs.93029	sparc/osteonectin, cwcv and kazal-like d	2.74	0.86
75	317266	AA906289	Hs.203614	ESTs	1.00	1.00
	317282	AI807444	Hs.176101	ESTs	2.60	4.21
	317285	AW370882	Hs.222080	ESTs	1.96	3.49
	317302	AA908709	Hs.135564	ESTs	7.16	8.32
	317304	AW449899	Hs.130184	ESTs	1.38	2.28
80	317320	AA927151	Hs.130452	ESTs	3.58	8.13
	317413	AW341701	Hs.126622	ESTs	2.08	4.92
	317417	AA918420	Hs.145378	ESTs	3.06	4.79
	317452	AA972965	Hs.135568	ESTs	4.22	9.21
	317519	AI859695	Hs.126880	ESTs	1.88	4.15
85	317521	AI824338	Hs.126891	ESTs	3.12	4.55
	317529	AI916517	Hs.126865	ESTs	2.73	3.34

	317570	AI733361	Hs.127122	ESTs	1.00	2.43
	317571	AA938663	Hs.199828	ESTs	5.20	11.95
	317598	AW206035	Hs.192123	ESTs	0.33	1.55
5	317627	AI346110	Hs.132553	ESTs	1.50	1.39
	317650	AI733310	Hs.127346	ESTs	0.48	1.46
	317659	AA961216	Hs.127785	ESTs	4.18	7.14
	317674	AW294909	Hs.132208	ESTs	2.92	3.20
	317686	AA969051	Hs.187319	ESTs	1.00	1.01
10	317692	AI307659	Hs.174794	ESTs	5.33	9.59
	317701	AI674774	Hs.128014	ESTs	1.00	1.00
	317711	AI733015	Hs.272189	ESTs	5.13	7.81
	317722	AI733373	Hs.128119	ESTs	2.50	6.03
	317756	AA973667	Hs.128320	ESTs	1.59	1.30
15	317777	AI143525	Hs.47313	KIAA0258 gene product	1.00	2.48
	317799	AI498273	Hs.128808	ESTs	1.78	2.11
	317803	AA983251	Hs.128899	ESTs	0.80	1.06
	317821	AI368158	Hs.70983	PTPL1-associated RhoGAP 1	0.17	0.68
	317848	AI820575	Hs.129086	Homo sapiens cDNA FLJ12007 fis, clone HE	5.30	8.16
20	317850	N29974	Hs.152982	hypothetical protein FLJ13117	1.30	2.28
	317861	AW341064	Hs.129119	ESTs	2.18	5.93
	317865	AI298794	Hs.129130	ESTs	4.48	8.20
	317869	AW295184	Hs.129142	deoxyribonuclease II beta	0.44	0.99
	317881	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	4.06	2.23
25	317890	AI915599	Hs.129225	ESTs	4.68	7.48
	317899	AI952430	Hs.150614	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.14	3.37
	317986	AI005163	Hs.201378	ESTs, Weakly similar to T12545 hypotheli	0.28	1.66
	318001	AW235697	Hs.130980	ESTs	5.12	9.97
	318016	AI016694	Hs.256921	ESTs	1.86	4.50
30	318023	AW243058	Hs.131155	ESTs	2.92	5.22
	318054	AW449270	Hs.232140	ESTs	3.92	6.37
	318068	AI024540	Hs.131574	ESTs	1.21	1.27
	318117	AI208304	Hs.250114	ESTs	0.86	1.17
	318187	AI792585	Hs.133272	ESTs, Weakly similar to ALUC_HUMAN !!!!	5.90	6.98
35	318223	AI077540	Hs.134090	ESTs	1.05	0.90
	318240	AI085377	Hs.143610	ESTs	3.10	2.40
	318255	AI082692	Hs.134662	ESTs	0.02	1.05
	318266	AI554341	Hs.271443	ESTs	6.12	10.55
	318330	AI093840	Hs.143758	ESTs	4.98	7.90
40	318369	AI493501	Hs.170974	ESTs	2.46	5.62
	318428	AI949409	Hs.194591	ESTs	0.77	0.45
	318458	AI149783	Hs.158438	ESTs	3.54	4.92
	318467	AI151395	Hs.144834	ESTs	4.56	5.62
	318473	AI939339	Hs.146883	ESTs	2.08	4.05
45	318476	AI693927	Hs.265165	ESTs	4.22	8.07
	318487	AI167877	Hs.143716	ESTs	1.47	1.05
	318488	AI217431	Hs.144709	ESTs	1.40	4.14
	318491	T26477	Hs.22883	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.84	1.90
	318499	T25451		gb:PTH188 HTCDL1 Homo sapiens cDNA 5/3	2.58	5.20
50	318537	AA377908	Hs.13254	ESTs	3.26	4.18
	318538	N28625	Hs.74034	Homo sapiens clone 24651 mRNA sequence	0.35	1.07
	318547	R20578	Hs.90431	ESTs	3.22	4.60
	318552	R18364	Hs.90363	ESTs	4.87	9.06
	318575	R55102	Hs.107761	ESTs, Weakly similar to unnamed protein	1.91	1.98
55	318580	T34571	Hs.49007	poly(A) polymerase alpha	2.74	6.22
	318587	AA779704	Hs.168830	Homo sapiens cDNA FLJ12136 fis, clone MA	0.85	2.46
	318596	AI470235	Hs.172698	EST	4.88	4.93
	318622	T48325	Hs.237658	apolipoprotein A-II	4.80	12.51
	318629	N25163	Hs.8861	ESTs	0.39	1.04
60	318637	AA243539	Hs.9196	hypothetical protein	1.72	3.57
	318648	T77141	Hs.184411	albumin	6.27	9.91
	318650	AA393302	Hs.176626	hypothetical protein EDAG-1	3.96	8.84
	318671	AA188823	Hs.299254	Homo sapiens cDNA: FLJ23597 fis, clone L	1.53	0.81
	318679	T58115	Hs.10336	ESTs	1.00	2.19
65	318711	AI936475	Hs.101282	Homo sapiens cDNA: FLJ21238 fis, clone C	3.05	3.18
	318725	AI962487	Hs.242990	ESTs	1.08	2.46
	318728	Z30201	Hs.291289	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.77	1.33
	318740	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	0.25	1.49
	318776	R24963	Hs.23766	ESTs	1.00	3.01
70	318784	H00148	Hs.5181	proliferation-associated 2G4, 38kD	2.70	3.86
	318816	F07873	Hs.21273	ESTs	3.90	7.13
	318865	H10818		gb:ym04f10.r1 Soares infant brain 1N1B H	2.25	3.56
	318879	R56332	Hs.18268	adenylate kinase 5	1.78	5.00
	318881	Z43224	Hs.124952	ESTs	4.79	14.13
75	318894	F08138	Hs.7387	DKFZP564B116 protein	5.31	7.00
	318901	AW368520	Hs.301528	L-tyrosine/alpha-aminoacidipate aminotra	1.03	0.91
	318925	Z43577	Hs.21470	ESTs	2.23	3.80
	318936	AI219221	Hs.308298	ESTs	1.86	7.16
	318982	Z44140	Hs.269622	ESTs	5.84	9.79
80	318986	Z44186	Hs.169161	ESTs, Highly similar to MAON_HUMAN NADP-	1.00	1.00
	319041	Z44720	Hs.98365	ESTs, Weakly similar to weak similarity	3.38	6.11
	319103	H05896	Hs.4993	KIAA1313 protein	1.00	1.07
	319170	R13678	Hs.285306	putative selenocysteine lyase	3.79	5.03
	319196	F07953	Hs.16085	putative G-protein coupled receptor	1.00	2.98
85	319199	F07361	Hs.13306	ESTs	3.53	5.66
	319242	F11472	Hs.12839	ESTs	5.87	7.26

	319263	T65331	Hs.81360	Homo sapiens cDNA: FLJ21927 fis, clone H	1.81	1.57
	319267	F11802	Hs.6818	ESTs	1.10	4.72
	319270	R13474	Hs.290263	ESTs	4.80	10.40
5	319279	T65094	Hs.12677	CGI-147 protein	1.50	2.11
	319282	AA461358	Hs.12876	ESTs	1.00	1.00
	319289	W07304	Hs.79059	transforming growth factor, beta recepto	0.18	0.68
	319291	W86578	Hs.285243	hypothetical protein FLJ22029	0.26	0.62
	319293	F12119	Hs.12583	ESTs	3.13	4.50
10	319312	Z45481		gb:HSC2QE041 normalized infant brain cDN	1.10	1.00
	319370	H54254	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	0.16	0.73
	319391	R06304	Hs.13911	ESTs	1.26	2.43
	319396	H67130	Hs.301743	ESTs	0.70	0.76
	319398	AA359754	Hs.191196	ESTs	2.45	3.59
15	319407	R05329		gb:ye91b04.r1 Soares fetal liver spleen	2.00	3.54
	319425	T82930		gb:yd39f07.r1 Soares fetal liver spleen	4.28	8.81
	319433	R06050	Hs.191198	ESTs	6.15	14.13
	319437	AA282420	Hs.111991	ESTs, Weakly similar to Y48A5A.1 [C.eleg	3.26	5.68
	319466	Al809937	Hs.116417	ESTs	1.76	5.65
20	319471	R06546	Hs.19717	ESTs	4.29	4.84
	319480	R06933	Hs.184221	ESTs	1.00	1.00
	319484	T91772		gb:yd52a10.s1 Soares fetal liver spleen	2.81	4.88
	319486	Al382429	Hs.250799	ESTs	2.08	2.82
	319508	T99898	Hs.270104	ESTs, Moderately similar to ALU8_HUMAN A	2.80	4.39
25	319523	T69499	Hs.191184	ESTs	1.55	3.25
	319545	R83716	Hs.14355	Homo sapiens cDNA FLJ13207 fis, clone NT	1.65	1.19
	319546	R09692		gb:yf23b12.r1 Soares fetal liver spleen	5.11	8.54
	319552	AA086106	Hs.20403	ESTs	1.89	3.36
	319582	T82998	Hs.250154	hypothetical protein FLJ12973	3.48	4.82
30	319586	D78808	Hs.283683	chromosome 8 open reading frame 4	0.26	0.82
	319604	R11679	Hs.297753	vimentin	1.68	3.41
	319609	AW247514	Hs.12293	hypothetical protein FLJ21103	3.06	4.24
	319611	H14957		gb:ym19c10.r1 Soares infant brain 1N1B H	2.76	4.24
	319653	AA770183	Hs.173515	uncharacterized hypothalamus protein HTO	2.51	3.55
35	319657	R19897	Hs.106604	ESTs	5.32	7.68
	319658	R13432	Hs.167481	synthrophin, gamma 1	3.35	5.00
	319661	H08035	Hs.21398	ESTs, Moderately similar to A Chain A, H	5.18	12.55
	319662	H06382	Hs.21400	ESTs	1.58	1.56
	319708	R15372	Hs.22664	ESTs	1.00	1.22
40	319742	T77668	Hs.21162	ESTs	2.48	3.13
	319748	R18178	Hs.295866	Homo sapiens mRNA; cDNA DKFZp434N1923 (f	3.02	4.85
	319772	R76633	Hs.22646	ESTs	4.36	11.61
	319788	AA321932	Hs.117414	KIAA1320 protein	2.56	3.68
	319805	R92857	Hs.271350	likely ortholog of mouse polydom	4.63	6.56
45	319812	N74880	Hs.264330	N-acylsphingosine amidohydrolase (acid c	0.63	1.32
	319834	AA071267		gb:zm61g01.r1 Stratagene fibroblast (937	0.30	0.94
	319878	T78517	Hs.13941	ESTs	3.99	6.44
	319882	AA258981	Hs.291392	ESTs	5.09	7.36
	319912	T77559	Hs.94109	Homo sapiens cDNA FLJ13634 fis, clone PL	3.24	3.21
50	319935	H79460	Hs.271722	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.40	9.42
	319944	T79248	Hs.133510	ESTs	3.31	5.39
	319947	AA160967	Hs.14479	Homo sapiens cDNA FLJ14199 fis, clone NT	2.90	4.95
	319962	H06350	Hs.135056	Human DNA sequence from clone RP5-850E9	1.81	1.57
	320007	AA336314		gb:EST40943 Endometrial tumor Homo sapie	3.42	6.29
55	320018	T83263		gb:yd40h09.r1 Soares fetal liver spleen	2.77	5.14
	320030	H63789	Hs.296288	ESTs, Weakly similar to KIAA0638 protein	4.10	6.69
	320032	Al699772	Hs.292664	ESTs, Weakly similar to A46010 X-linked	3.27	3.27
	320040	AA233671	Hs.87164	hypothetical protein FLJ14001	1.81	1.64
	320047	T86564	Hs.302256	EST	3.38	7.36
60	320063	AA074108	Hs.120844	FOXJ2 forkhead factor	5.90	16.73
	320096	H58138	Hs.117915	ESTs	2.08	4.47
	320099	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	1.00	1.00
	320112	T92107	Hs.188489	ESTs	2.27	2.06
	320140	H94179	Hs.119023	SMC2 (structural maintenance of chromoso	1.00	1.00
65	320188	AW419200	Hs.172318	ESTs	1.26	1.00
	320193	AA831259	Hs.17132	ESTs	2.58	6.23
	320195	R62203	Hs.24321	Homo sapiens cDNA FLJ12028 fis, clone HE	2.85	4.53
	320199	R78659	Hs.29792	ESTs	0.40	0.94
	320203	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZp564N1116 (f	0.84	1.18
70	320219	AA327564	Hs.127011	tubulointerstitial nephritis antigen	1.00	1.17
	320220	AF054910	Hs.127111	tektin 2 (testicular)	0.18	1.09
	320225	AF058989	Hs.128231	G antigen, family B, 1 (prostate associa	5.26	13.75
	320231	H03139	Hs.24683	ESTs	1.59	1.93
	320260	NM_003608	Hs.131924	G protein-coupled receptor 65	1.38	4.56
75	320267	AL049337	Hs.132571	Homo sapiens mRNA; cDNA DKFZp564P016 (fr	1.00	1.92
	320268	H06019	Hs.151293	Homo sapiens cDNA FLJ10664 fis, clone NT	5.58	5.70
	320322	AF077374	Hs.139322	small proline-rich protein 3	1.41	1.01
	320325	Al167978	Hs.139851	caveolin 2	0.05	0.67
	320330	AF026004	Hs.141660	chloride channel 2	2.17	1.26
80	320339	H10807	Hs.281434	Homo sapiens cDNA FLJ14028 fis, clone HE	1.81	2.32
	320388	H16065	Hs.31286	ESTs	1.00	3.22
	320402	R22291	Hs.23368	Homo sapiens clone FLC0578 PRO2852 mRNA,	1.41	1.36
	320413	AA203711	Hs.173269	ESTs	2.31	3.61
	320432	R62786	Hs.124136	ESTs	11.25	20.78
	320436	AA253352	Hs.293663	ESTs	2.22	3.49
85	320438	W24548	Hs.5669	ESTs	3.53	8.14

	320448	AI240233	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	1.42	3.46
	320451	R26844	Hs.180777	Homo sapiens mRNA; cDNA DKFZp564M0264 (f	0.87	0.81
	320484	AA094436	Hs.296267	folliculin-like 1	0.65	1.18
5	320499	R32555	Hs.24321	Homo sapiens cDNA FLJ12028 fis, clone HE	3.44	7.15
	320514	AB007978	Hs.158278	KIAA0509 protein	6.44	13.62
	320521	N31464	Hs.24743	hypothetical protein FLJ20171	1.48	1.04
	320526	AW374205	Hs.111314	ESTs	3.66	7.87
	320527	R34672	Hs.324522	ESTs	3.16	5.63
10	320536	AA331732	Hs.137224	ESTs	2.83	5.83
	320556	AF054177	Hs.14570	hypothetical protein FLJ22530	1.28	1.00
	320564	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	1.22	0.81
	320587	Z44524	Hs.167456	Homo sapiens mRNA full length insert cDN	1.84	2.44
	320635	R54159	Hs.80506	small nuclear ribonucleoprotein polypept	1.00	6.25
15	320639	AA243258	Hs.7395	hypothetical protein FLJ23182	2.60	2.30
	320648	N48521	Hs.26549	Homo sapiens mRNA for KIAA1708 protein,	1.00	1.53
	320651	AA489268	Hs.111334	ferritin, light polypeptide	0.14	0.79
	320664	AI904216	Hs.91251	hypothetical protein FLJ11198	5.02	8.84
	320676	AA132650	Hs.300511	ESTs	3.63	5.37
20	320683	R59291	Hs.26638	ESTs, Weakly similar to unnamed protein	0.37	1.31
	320689	AA334609	Hs.171929	ESTs, Weakly similar to A54849 collagen	1.27	1.02
	320696	AW135016	Hs.172780	ESTs	3.53	4.60
	320714	AI445591		gb:yyq04a10.r1 Soares fetal liver spleen	1.06	0.85
	320727	U96044	Hs.181125	immunoglobulin lambda locus	1.35	1.49
25	320771	AI793266	Hs.117176	poly(A)-binding protein, nuclear 1	0.04	0.82
	320794	AA281993	Hs.91226	ESTs	2.96	4.33
	320822	AF100780	Hs.194679	WNT1 inducible signaling pathway protein	0.10	0.79
	320824	AF120274	Hs.194689	artemin	1.16	1.11
	320830	AJ132445	Hs.266416	claudin 14	1.06	1.75
30	320843	AA317372	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr	1.36	1.47
	320849	D60031	Hs.34771	ESTs	5.30	7.49
	320853	AI473796	Hs.135904	ESTs	1.00	1.00
	320896	AB002155	Hs.271580	uroplakin 1B	5.90	2.55
35	320921	R94038	Hs.199538	inhibin, beta C	2.20	1.17
	320927	AI205786	Hs.213923	ESTs	0.18	1.46
	320957	AI878933	Hs.92023	core histone macroH2A2.2	1.67	2.18
	320997	H22544		gb:yn69f11.r1 Soares adult brain N2b5HB5	3.26	3.62
	321045	W88483	Hs.293650	ESTs	2.25	4.55
40	321046	H27794	Hs.269055	ESTs	2.69	4.25
	321052	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	2.14	2.56
	321059	AI092824	Hs.126465	ESTs	1.69	0.53
	321062	R87955	Hs.241411	Homo sapiens mRNA full length insert cDN	2.76	5.20
	321067	AF131782	Hs.241438	Homo sapiens clone 24941 mRNA sequence	4.79	7.41
45	321102	AA018306		gb:ze40d08.r1 Soares retina N2b4HR Homo	1.79	4.27
	321130	H43750	Hs.125494	ESTs	1.00	3.14
	321142	AI817933	Hs.298351	ASPL protein	8.73	15.36
	321155	AA336635	Hs.99598	hypothetical protein MGC5338	3.04	5.03
	321158	AA700289		gb:yu76f11.r1 Soares fetal liver spleen	4.62	8.39
50	321170	N53742	Hs.172982	ESTs	2.21	4.46
	321199	AW385512		gb:yy56d10.s1 Soares_multiple_sclerosis_	5.69	8.01
	321206	H54178	Hs.226469	Homo sapiens cDNA FLJ12417 fis, clone MA	4.00	7.32
	321225	AL080073	Hs.251414	Homo sapiens mRNA; cDNA DKFZp564B1462 (f	4.17	4.63
	321236	AW371941	Hs.18192	Ser/Arg-related nuclear matrix protein (1.00	1.00
55	321244	AF068654		gb:Homo sapiens isolate AN.1 immunoglobu	2.18	9.13
	321270	R83560		gb:yv76c06.s1 Soares fetal liver spleen	3.80	5.26
	321317	AI937060	Hs.6298	KIAA1151 protein	1.81	1.65
	321318	AB033041	Hs.137507	KIAA1215 protein	1.00	1.00
	321325	AB033100	Hs.300546	KIAA protein (similar to mouse paladin)	0.44	0.93
60	321342	AA127984	Hs.222024	transcription factor BMAL2	4.94	4.93
	321356	R93443	Hs.271770	ESTs	3.10	4.66
	321418	AI739161	Hs.161075	ESTs	2.28	2.54
	321420	AI368667	Hs.132743	ESTs	1.13	0.97
65	321430	U05890		gb:H.sapiens (DIG3) mRNA for immunoglobu	2.42	3.35
	321453	N50080	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	1.60	3.11
	321467	X13075		gb:Human 2a12 mRNA for kappa-immunoglobu	0.42	0.72
	321468	AA514198	Hs.38540	ESTs	2.46	6.50
70	321491	H70665	Hs.292549	ESTs	1.00	1.25
	321498	AW295517	Hs.255436	ESTs	3.19	6.24
	321504	W02356	Hs.268980	ESTs	2.28	3.86
	321510	AA703650	Hs.255748	ESTs	2.14	3.94
	321513	H84972	Hs.108551	ESTs	2.78	5.37
	321516	AI382803	Hs.159235	ESTs	3.06	7.19
75	321565	AI525773	Hs.266514	hypothetical protein FLJ11342	4.89	7.82
	321577	H84260		gb:ys90g04.r1 Soares retina N2b5HR Homo	1.00	1.73
	321581	AA019964	Hs.28803	ESTs	4.88	6.73
	321582	AA143755	Hs.21858	trinucleotide repeat containing 3	1.00	2.08
	321587	H95531		gb:ys76e02.r1 Soares retina N2b4HR Homo	2.26	4.52
	321626	AA295430	Hs.96322	hypothetical protein FLJ23560	1.95	3.83
80	321628	H87064	Hs.161051	ESTs, Moderately similar to ALU6_HUMAN A	0.47	1.02
	321642	AW085917	Hs.247084	ESTs	1.52	1.38
	321669	H95404	Hs.294110	ESTs	2.17	2.45
	321687	AA625149		gb:af70c12.r1 Soares_NhHMPu_S1 Homo sapi	4.31	6.95
	321688	H97646	Hs.123158	Homo sapiens cDNA FLJ12830 fis, clone NT	2.82	3.28
	321693	AA700017	Hs.173737	ras-related C3 botulinum toxin substrate	0.51	1.08
85	321700	N55160	Hs.167260	ESTs	4.57	7.46
	321701	AW390923	Hs.42568	ESTs	1.00	1.00

	321709	N25847	Hs.108923	RAB38, member RAS oncogene family	1.00	1.00
	321710	N35682	Hs.259743	ESTs	2.97	5.26
	321775	AI694875	Hs.202312	Homo sapiens clone N11 NTera2D1 teratoca	1.00	1.00
5	321777	AI637993	Hs.202312	Homo sapiens clone N11 NTera2D1 teratoca	1.68	0.45
	321779	N42729	Hs.163835	ESTs	0.90	0.90
	321829	D81993	Hs.8966	tumor endothelial marker 8	2.69	3.89
	321846	AA281594	Hs.87902	ESTs	5.11	7.64
	321879	AL109670	Hs.302809	ESTs	6.49	9.58
10	321883	AA426494	Hs.46901	KIAA1462 protein	0.28	0.95
	321899	N55158	Hs.29468	ESTs	0.39	0.95
	321911	AF026944	Hs.293797	ESTs	6.20	10.76
	321949	R49202	Hs.181694	EST	4.62	10.51
	321955	AI651866	Hs.195689	ESTs	2.89	5.47
	321956	AL110177	Hs.132882	ESTs	0.32	1.25
15	321987	AL133612	Hs.272759	KIAA1457 protein	1.00	1.83
	321991	AL133627	Hs.158923	Homo sapiens mRNA; cDNA DKFZp434K0722 (f	4.00	6.47
	322002	AA328801	Hs.84522	ESTs	2.10	3.48
	322035	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	1.00	1.90
20	322044	AW340926		gb:xy51b10.x1 NCI_CGAP_Lu34.1 Homo sapie	3.20	9.67
	322057	N92197	Hs.154679	synaptotagmin 1	1.55	1.07
	322060	AI341937		gb:qt10e03.x1 NCI_CGAP_GC4 Homo sapiens	4.59	7.68
	322070	U80769	Hs.210322	Homo sapiens mRNA for KIAA1766 protein,	2.78	4.52
	322083	AF074982	Hs.226031	ESTs, Highly similar to KIAA0535 protein	3.10	5.52
25	322091	AI819863	Hs.106243	ESTs	1.59	1.75
	322125	R93901		gb:yq16c12.r1 Soares fetal liver spleen	2.06	5.27
	322130	R98978	Hs.117767	ESTs	10.12	16.49
	322147	AF085919	Hs.114176	ESTs	0.94	0.64
	322166	AF085958		gb:yr88b03.r1 Soares fetal liver spleen	4.09	6.67
30	322173	H52567		gb:yt85d04.r1 Soares_pineal_gland_N3HPG	3.46	4.85
	322178	H56535		gb:yt88g03.r1 Soares_pineal_gland_N3HPG	0.44	2.54
	322179	H92891		gb:yt84c02.s1 Soares_pineal_gland_N3HPG	4.52	7.50
	322186	H67346	Hs.269187	ESTs	0.15	0.98
	322196	W87895	Hs.211516	ESTs	2.20	5.04
35	322212	AF087995	Hs.134877	ESTs	3.42	4.84
	322221	AI890619	Hs.179562	nucleosome assembly protein 1-like 1	0.82	2.14
	322277	AI640193	Hs.226389	ESTs	3.62	3.98
	322278	AF086283		gb:zd46f01.r1 Soares_fetal_heart_NbHH19W	1.00	1.00
40	322284	AI792140	Hs.49265	ESTs	0.66	2.76
	322288	AL037273	Hs.7886	pellino (Drosophila) homolog 1	0.71	0.70
	322320	AF086419		gb:zd78d03.r1 Soares_fetal_heart_NbHH19W	2.02	2.76
	322336	AA308526	Hs.76152	decorin	2.92	4.44
	322339	W17348		gb:zb18c07.x5 Soares_fetal_lung_NbHL19W	8.50	11.56
	322366	AW404274	Hs.122492	hypothetical protein	0.61	1.34
45	322372	W25624	Hs.153943	ESTs	7.37	12.07
	322374	AI394663	Hs.122116	ESTs, Moderately similar to Osf2 [M.musc	4.78	10.50
	322378	AF064819	Hs.201877	DESC1 protein	1.00	1.00
	322388	AI815730	Hs.247474	hypothetical protein FLJ21032	7.09	8.49
	322416	AA223183	Hs.298442	adaptor-related protein complex 3, mu 1	3.20	5.80
50	322419	AA248987	Hs.14084	ring finger protein 7	1.64	1.57
	322425	W37943	Hs.34892	KIAA1323 protein	0.83	1.00
	322431	AA069222	Hs.141892	ESTs	3.96	5.22
	322450	AA040131	Hs.25144	ESTs	5.18	12.67
	322465	AA137152	Hs.286049	phosphoserine aminotransferase	3.41	2.23
55	322467	AF116826	Hs.180340	putative protein-tyrosine kinase	1.00	1.30
	322473	AA744286	Hs.266935	tRNA selenocysteine associated protein	1.75	2.03
	322509	T52172	Hs.302213	ESTs	1.00	2.27
	322523	W80398	Hs.193197	ESTs	2.75	5.49
	322527	AF147359		gb:Homo sapiens full length insert cDNA	1.25	1.27
60	322560	AI916847	Hs.270947	ESTs	4.57	8.81
	322566	W87285	Hs.269587	ESTs	1.00	1.42
	322585	AA837622		gb:zh69c01.r1 Soares_fetal_liver_spleen_	4.18	6.94
	322635	AA679084		gb:zh90h08.r1 Soares_fetal_liver_spleen_	2.40	4.85
	322641	AA007352	Hs.256042	ESTs	2.94	4.64
65	322653	AI828854	Hs.258538	striatin, calmodulin-binding protein	0.48	0.38
	322664	AA011522		gb:zi03g07.r1 Soares_fetal_liver_spleen_	1.92	2.18
	322687	AI110759		gb:AF074666 Human fetal liver cDNA libra	4.14	6.75
	322692	AA018117	Hs.60843	potassium voltage-gated channel, shaker-	3.50	5.00
70	322694	AI110872	Hs.279812	PRO0327 protein	1.80	1.72
	322708	AF113674	Hs.283773	clone FLB1727	1.00	3.43
	322712	AA021328	Hs.23607	hypothetical protein FLJ11109	3.28	3.86
	322766	AW068805	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MA	1.63	1.53
	322770	AA045796	Hs.122682	ESTs	1.53	1.06
	322794	AI608591	Hs.38991	S100 calcium-binding protein A2	12.06	1.94
75	322810	AI962276	Hs.127444	ESTs	4.09	6.90
	322818	AW043782	Hs.293616	ESTs	1.20	1.63
	322820	AI377755	Hs.120695	ESTs	0.21	1.93
	322872	AA827228	Hs.126943	ESTs	2.04	1.63
	322882	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	5.26	1.22
80	322887	AI986306	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.80	2.24
	322913	AI733737	Hs.68837	ESTs	2.38	6.61
	322926	AI825940	Hs.211192	ESTs	4.02	5.79
	322929	AI365585	Hs.146246	ESTs	0.30	1.14
	322968	AI905228	Hs.83484	SRY (sex determining region Y)-box 4	2.06	1.13
85	322971	C15953	Hs.212760	hypothetical protein FLJ13649	1.18	2.00
	322981	AA493252	Hs.159577	ESTs	2.28	2.61

	322988	C18727	Hs.171941	ESTs	0.39	2.00
	323003	AI733859	Hs.149089	ESTs	3.28	1.00
	323013	AA134042	Hs.191451	ESTs	3.38	5.68
5	323025	AL157565	Hs.315369	Homo sapiens cDNA: FLJ23075 fis, clone L	0.06	1.10
	323032	AW244073	Hs.145946	ESTs	10.18	21.27
	323052	R21124	Hs.85573	Homo sapiens DC29 mRNA, complete cds	1.46	1.90
	323064	AL119341	Hs.49359	Homo sapiens mRNA; cDNA DKFZp547E052 (fr	3.08	5.64
	323098	AI700025	Hs.270471	ESTs	2.31	4.49
10	323102	AL119913	Hs.163615	ESTs	5.38	11.64
	323155	AL135041		gb:DKFZp762K2310_r1 762 (synonym: hmel2)	2.38	5.56
	323176	AW071648	Hs.82101	pleckstrin homology-like domain, family	1.06	1.41
	323191	AA195600	Hs.301570	ESTs	0.73	1.24
	323225	AA205654	Hs.24790	KIAA1573 protein	5.25	11.95
15	323232	AA148722	Hs.224680	ESTs	0.45	1.35
	323266	AW003362	Hs.243886	nuclear autoantigenic sperm protein (his	1.71	1.83
	323281	AI697556	Hs.292659	ESTs	1.24	3.21
	323283	AA256014	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	12.68	15.05
	323314	AA226310	Hs.191501	ESTs	4.42	9.61
20	323316	AL134620	Hs.280175	ESTs	2.98	5.93
	323334	AI336501	Hs.77273	ras homolog gene family, member A	1.98	3.30
	323338	R74219	Hs.23348	S-phase kinase-associated protein 2 (p45	1.62	1.00
	323348	AA233056	Hs.191518	ESTs	1.00	1.07
	323351	AA704103	Hs.24049	ESTs	1.43	1.68
25	323359	AA234172	Hs.137418	ESTs	0.34	1.18
	323360	AA716061	Hs.161719	ESTs	3.01	3.71
	323405	AW139550	Hs.115173	ESTs	1.90	8.81
	323420	AI672386	Hs.263780	ESTs	0.29	1.01
	323434	AW081455	Hs.120219	ESTs	2.27	1.92
30	323445	AA253103	Hs.135569	ESTs, Weakly similar to NEUROD [H.sapien	0.43	0.80
	323449	AA282865	Hs.284153	Fanconi anemia, complementation group A	3.19	3.85
	323492	H00978	Hs.20887	hypothetical protein FLJ10392	2.70	3.20
	323501	AA182461	Hs.84520	ESTs	2.04	3.31
	323505	AI652287		gb:EST382593 MAGE resequences, MAGK Homo2.21		3.08
35	323515	AA282274	Hs.256083	ESTs	2.69	3.40
	323541	AI185116	Hs.104613	RP42 homolog	1.20	1.09
	323545	AI814405	Hs.224569	ESTs	1.25	1.55
	323635	R63117	Hs.9691	Homo sapiens cDNA: FLJ23249 fis, clone C	0.27	0.72
40	323675	AA984759	Hs.272168	tumor differentially expressed 1	3.70	5.80
	323678	AL042121	Hs.20880	ESTs	3.33	5.10
	323691	AA317561	Hs.145599	ESTs	1.00	1.00
	323693	AW297758	Hs.249721	ESTs	2.01	1.54
	323746	AW298611	Hs.12808	MARK	4.11	5.53
	323774	AA329806	Hs.321056	Homo sapiens mRNA; cDNA DKFZp586F1322 (f	2.06	3.70
45	323856	AA355264	Hs.267604	hypothetical protein FLJ10450	3.42	8.13
	323857	T18988	Hs.293668	ESTs	5.97	12.51
	323870	AA341774	Hs.129212	ESTs	3.17	4.52
	323876	AL042492	Hs.147313	ESTs	0.36	1.00
	323885	AA344308	Hs.128427	Homo sapiens BAC clone RP11-335J18 from	2.31	3.33
50	323911	AL043212	Hs.92550	ESTs	4.38	5.41
	323919	AA862973	Hs.220704	ESTs	5.80	10.20
	323972	AI869964	Hs.182906	ESTs	3.10	5.14
	324005	AA610011	Hs.208021	ESTs	5.34	10.07
	324036	AI472078	Hs.303662	ESTs	1.00	5.03
55	324055	AA528794	Hs.128644	ESTs	0.86	1.00
	324063	AW292740	Hs.272813	dual oxidase 1	0.45	0.91
	324072	AA381829		gb:EST94855 Activated T-cells I Homo sap	2.82	5.12
	324092	AW269931	Hs.202473	Homo sapiens cDNA: FLJ22278 fis, clone H	2.40	2.52
	324095	AW377983	Hs.298140	Homo sapiens cDNA: FLJ22502 fis, clone H	1.32	4.30
60	324129	AI381918	Hs.285833	Homo sapiens cDNA: FLJ22135 fis, clone H	1.40	1.77
	324132	AW504860	Hs.288836	hypothetical protein FLJ12673	4.24	6.21
	324214	AA412395	Hs.225740	ESTs	6.96	10.69
	324227	AA295552	Hs.28631	Homo sapiens cDNA: FLJ22141 fis, clone H	0.81	0.53
	324266	AL047634	Hs.231913	ESTs	2.42	4.05
	324275	AA429088	Hs.98523	ESTs	3.62	5.38
65	324281	AL048026	Hs.124675	ESTs, Weakly similar to T14742 hypotheti	0.14	0.70
	324290	AA432032	Hs.304420	ESTs	3.71	4.34
	324303	AL118754		gb:DKFZp761P1910_r1 761 (synonym: hamy2)	0.95	0.91
70	324312	AI198841	Hs.128173	ESTs	4.06	5.91
	324325	AL138153	Hs.300410	ESTs	5.88	8.25
	324338	AL138357	Hs.145078	regulator of differentiation (in S. pomb	0.87	1.25
	324341	AW197734	Hs.99807	ESTs, Weakly similar to unnamed protein	1.28	1.00
	324343	AW452016	Hs.293232	ESTs	2.54	3.46
	324371	AA452305	Hs.270319	ESTs	5.85	8.36
75	324382	AW502749	Hs.24724	MFH-amplified sequences with leucine-ric	0.76	1.64
	324384	AA453396	Hs.127656	KIAA1349 protein	2.88	5.69
	324385	F28212	Hs.284247	KIAA1491 protein	1.81	1.99
	324388	AI924963	Hs.306206	hypothetical protein FLJ11215	1.00	1.00
	324432	AA464510	Hs.152812	ESTs	2.73	2.17
	324497	AW152624	Hs.136340	ESTs, Weakly similar to unnamed protein	0.71	1.90
80	324510	AI148353	Hs.287425	Homo sapiens cDNA FLJ11569 fis, clone HE	1.00	1.00
	324580	AA492588		gb:ng99c08.s1 NCL_CGAP_Thy1 Homo sapiens	2.18	3.50
	324582	AA506935	Hs.132036	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.96	11.36
	324633	AA572994	Hs.325489	ESTs	2.92	4.22
	324640	AW295832	Hs.134798	ESTs, Moderately similar to TTL MOUSE TU	5.48	11.74
85	324675	AW014734	Hs.157969	ESTs	0.39	0.73

	324699	AW504732	Hs.21275	hypothetical protein FLJ11011	0.93	0.93
	324747	AA603532	Hs.130807	ESTs	1.57	1.81
	324748	AA657457	Hs.292385	ESTs	1.55	1.34
5	324801	AI819924	Hs.14553	sterol O-acyltransferase (acyl-Coenzyme	1.00	6.56
	324804	AI692552		gb:wd73f12.x1 NCI_CGAP_Lu24 Homo sapiens	1.00	7.53
	324828	AA843926	Hs.124434	ESTs	2.00	3.25
	324855	AW152305	Hs.122364	ESTs	2.74	3.43
	324866	AI541214	Hs.46320	Small proline-rich protein SPRK (human,	1.07	0.95
10	324871	AW297755	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	1.68	1.21
	324886	AA806794	Hs.131511	ESTs	2.56	5.61
	324889	D31010		gb:HUML12147 Human fetal lung Homo sapie	2.20	4.65
	324948	AW383618	Hs.265459	ESTs, Moderately similar to ALU2_HUMAN A	5.28	7.05
	324953	AI264628	Hs.125428	ESTs	3.37	5.51
15	324958	AA625076	Hs.132892	protocadherin 20	5.12	9.81
	324988	T06997	Hs.121028	hypothetical protein FLJ10549	2.52	1.08
	325024	F13254	Hs.78672	laminin, alpha 4	5.24	10.22
	325105	H97109	Hs.105421	ESTs	1.00	1.00
	325108	AA401863	Hs.22380	ESTs	1.99	2.14
20	325114	D83901	Hs.315562	ESTs	2.73	3.17
	325146	AI064690	Hs.171176	ESTs	1.86	3.41
	325149	D61117	Hs.187646	ESTs	0.42	0.93
	325187	AI653682	Hs.197812	ESTs	6.50	11.31
	325228				6.18	15.76
25	325235				2.64	4.12
	325328				2.87	4.42
	325340				0.29	0.33
	325367				16.56	24.29
	325373				0.63	1.22
30	325389				0.88	1.05
	325436				5.75	14.14
	325471				8.46	17.82
	325498				3.32	6.42
	325557				5.51	8.28
35	325559				7.48	21.40
	325560				4.08	6.25
	325569				4.20	5.24
	325585				1.10	1.13
	325587				1.00	1.00
40	325597				2.98	13.40
	325639				0.78	0.78
	325685				0.46	0.66
	325686				0.95	1.55
	325735				4.48	9.20
45	325739				0.59	0.88
	325740				2.42	6.61
	325792				7.88	9.83
	325819				4.74	7.18
	325883				2.02	2.64
50	325895				7.78	15.98
	325925				2.04	10.60
	325932				4.18	7.36
	325941				3.66	9.03
	325969				0.61	0.80
55	325971				4.88	7.42
	326025				0.55	1.07
	326046				7.21	14.72
	326099				3.60	5.98
	326108				1.27	1.06
60	326163				3.27	5.70
	326165				0.45	1.11
	326189				0.13	0.45
	326204				5.60	9.00
	326230				7.00	12.01
65	326274				1.00	8.09
	326360				9.86	15.35
	326393				0.52	0.77
	326505				1.00	1.42
	326515				1.24	5.84
70	326589				9.20	13.49
	326592				2.77	4.01
	326605				2.01	2.53
	326692				1.00	1.00
	326693				1.00	1.31
75	326720				0.19	0.65
	326742				2.34	7.20
	326770				0.25	0.83
	326818				3.09	4.56
	326936				2.08	3.45
80	326964				0.41	1.70
	326983				2.02	3.80
	326991				1.09	1.20
	327036				1.00	8.04
	327040				3.05	4.22
85	327053				3.55	6.31
	327075				1.59	1.40

	327085	2.50	12.57
	327130	5.38	8.04
	327156	3.74	6.58
5	327220	1.28	1.54
	327224	6.56	12.91
	327288	2.61	5.40
	327321	2.42	3.11
	327332	6.62	10.58
10	327361	2.69	4.41
	327377	2.04	6.72
	327396	2.61	4.50
	327414	1.00	8.01
	327442	5.91	9.65
15	327467	6.58	18.01
	327473	3.79	7.48
	327483	4.08	8.87
	327562	0.68	2.86
	327568	1.00	2.00
20	327606	2.06	3.61
	327611	5.90	14.26
	327642	4.06	8.74
	327654	1.05	2.08
	327734	1.00	1.00
	327775	1.46	11.79
25	327796	3.47	5.65
	327840	3.26	6.64
	327940	5.84	15.58
	327984	0.36	1.50
30	328004	1.87	1.42
	328021	0.42	0.59
	328068	2.83	4.68
	328100	3.04	5.39
	328101	3.54	5.20
35	328113	0.72	0.91
	328157	5.58	5.16
	328196	5.76	11.13
	328197	5.98	10.58
	328264	3.11	4.88
40	328299	2.20	3.06
	328342	1.49	1.94
	328365	1.00	1.00
	328369	4.40	7.36
	328381	1.86	4.93
45	328451	5.51	7.56
	328481	0.13	0.72
	328500	2.71	3.97
	328530	5.41	7.62
	328600	3.14	10.68
50	328608	4.56	8.17
	328616	2.24	11.91
	328623	3.04	5.46
	328632	0.70	1.19
	328664	3.48	6.80
55	328666	10.42	26.47
	328698	9.68	14.56
	328700	2.74	10.22
	328708	0.15	0.57
	328735	6.23	8.91
60	328743	3.62	6.54
	328806	0.22	0.78
	328861	3.68	10.54
	328908	5.42	16.36
	328933	2.02	5.29
	328934	1.73	4.45
65	328949	3.34	5.41
	329005	2.88	7.26
	329011	2.52	3.72
	329033	1.00	1.03
70	329037	5.07	8.16
	329067	1.98	2.41
	329134	2.24	3.25
	329157	2.30	11.04
	329178	2.64	5.02
75	329192	6.41	15.27
	329194	0.31	0.79
	329204	1.60	3.75
	329224	2.99	6.11
	329228	0.83	0.83
80	329288	0.63	1.01
	329337	1.00	1.00
	329541	0.76	1.68
	329560	1.34	2.02
	329588	1.68	2.22
85	329643	4.18	11.77
	329703	1.00	1.00

	329764			5.78	15.50	
	329816			2.09	5.44	
	329860			3.13	10.77	
	329993			7.83	14.21	
5	330020			5.58	13.12	
	330036			3.32	5.57	
	330052			4.31	7.97	
	330085			1.34	1.76	
	330088			4.70	12.46	
10	330093			0.44	1.06	
	330100			3.47	4.83	
	330106			2.14	3.61	
	330107			3.17	6.87	
	330120			5.61	11.89	
15	330123			4.50	12.74	
	330208			1.55	7.62	
	330263			13.10	23.38	
	330300			2.81	4.98	
	330313			3.00	4.41	
20	330366			0.67	0.76	
	330372			4.76	11.82	
	330385	AA449749	Hs.182971	karyopherin alpha 5 (importin alpha 6)	2.14	2.15
	330397	D14659	Hs.154387	KIAA0103 gene product	0.40	1.15
25	330468	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	1.11	0.94
	330472	L24203	Hs.82237	ataxia-telangiectasia group D-associated	1.67	1.17
	330478	L38486	Hs.296049	microfibrillar-associated protein 4	0.46	1.07
	330493	M27826	Hs.267319	endogenous retroviral protease	1.07	0.95
	330495	M31328	Hs.71642	guanine nucleotide binding protein (G pr	0.97	0.96
30	330506	M61906	Hs.6241	phosphoinositide-3-kinase, regulatory su	0.17	3.66
	330512	M80563	Hs.81256	S100 calcium-binding protein A4 (calcium	0.60	1.06
	330537	U19765	Hs.2110	zinc finger protein 9 (a cellular retrov	2.81	2.07
	330547	U32989	Hs.183671	tryptophan 2,3-dioxygenase	3.91	1.49
	330551	U39840	Hs.299867	hepatocyte nuclear factor 3, alpha	1.15	1.03
35	330568	U56244		(NONE)	2.83	4.79
	330599	U90437		gb:Human RP1 homolog mRNA, 3'UTR region	2.08	1.54
	330601	U90916	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	0.89	1.35
	330605	X02419	Hs.77274	plasminogen activator, urokinase	1.87	1.55
	330609	X04741	Hs.76118	ubiquitin carboxyl-terminal esterase L1	1.83	1.30
40	330617	X53587	Hs.85266	integrin, beta 4	1.54	1.15
	330630	X78669	Hs.79088	reticulocalbin 2, EF-hand calcium bindin	1.39	1.19
	330644	Y07755	Hs.38991	S100 calcium-binding protein A2	3.83	1.13
	330650	Z68228	Hs.2340	junction plakoglobin	1.25	0.95
	330660	AA347868	Hs.139293	ESTs, Weakly similar to ALU7_HUMAN ALU S	15.50	29.07
	330692	AA017045	Hs.6702	ESTs	1.00	1.00
45	330707	AA133891	Hs.293690	ESTs	0.20	1.35
	330715	AA233707	Hs.11571	Homo sapiens cDNA FLJ11570 fis, clone HE	0.12	1.40
	330717	AA233926	Hs.52620	integrin, beta 8	6.62	5.42
	330722	AA243560	Hs.34382	ESTs	1.40	1.65
50	330740	AA297746	Hs.22654	Homo sapiens voltage-gated sodium channe	0.27	2.04
	330742	AA400979	Hs.25691	receptor (calcitonin) activity modifying	0.44	0.90
	330744	AA406142	Hs.12393	dTDP-D-glucose 4,6-dehydratase	0.71	3.23
	330751	AA428286	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	1.66	1.52
	330760	AA448663	Hs.30469	ESTs	0.52	0.90
55	330763	AA450200	Hs.274337	hypothetical protein FLJ20666	0.37	0.97
	330786	D60374	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	0.78	0.84
	330790	T48536	Hs.105807	ESTs	0.23	3.17
	330814	AA015730	Hs.265398	ESTs, Weakly similar to transformation-r	0.37	2.07
	330827	AA040332	Hs.12744	ESTs	1.60	1.00
60	330844	AA063037	Hs.66803	ESTs	0.93	1.16
	330901	AA157818	Hs.267319	endogenous retroviral protease	1.02	1.03
	330931	F01443	Hs.284256	hypothetical protein FLJ14033 similar to	0.24	0.88
	330952	H02855	Hs.29567	ESTs	0.08	1.31
	330961	H10998	Hs.7164	a disintegrin and metalloproteinase doma	1.29	1.26
65	330968	H16568	Hs.23748	ESTs	0.48	0.96
	331014	H98597	Hs.30340	hypothetical protein KIAA1165	0.29	0.74
	331046	N66563	Hs.191358	ESTs	0.99	8.56
	331060	N75081	Hs.157148	Homo sapiens cDNA FLJ11883 fis, clone HE	1.24	1.00
	331099	R36671	Hs.83937	hypothetical protein	0.75	1.03
70	331108	R41408	Hs.21983	ESTs	1.00	2.75
	331131	R54797		gb:yg87b07.s1 Soares infant brain 1N1B H	6.04	10.68
	331135	R61398	Hs.4197	ESTs	0.80	0.96
	331170	T23461	Hs.159293	ESTs	2.63	4.29
	331180	T32446	Hs.6640	Human DNA sequence from PAC 75N13 on chr	1.78	2.71
75	331183	T40769	Hs.8469	ESTs	1.00	3.01
	331203	T82310		(NONE)	1.70	3.80
	331271	AA059347	Hs.82226	glycoprotein (transmembrane) nmb	1.20	3.19
	331306	AA252079	Hs.63931	dachshund (Drosophila) homolog	0.31	1.30
	331327	AA281076	Hs.109221	ESTs	2.09	2.41
80	331341	AA303125	Hs.23240	Homo sapiens cDNA FLJ13496 fis, clone PL	0.72	2.43
	331359	AA416979	Hs.46901	KIAA1462 protein	0.09	0.91
	331363	AA421562	Hs.91011	anterior gradient 2 (Xenopus laevis) hom	1.02	0.87
	331378	AA448881	Hs.49282	hypothetical protein FLJ11088	1.03	1.23
	331384	AA456001	Hs.93847	NADPH oxidase 4	1.40	1.00
85	331402	AA505135	Hs.44037	ESTs	1.80	3.93
	331422	F10802	Hs.163628	ESTs, Moderately similar to ALU7_HUMAN	1.65	1.89

	331490	N32912	Hs.26813	CDA14	2.48	1.73
	331531	N51343		gb:yz15g04.s1 Soares_multiple_sclerosis_	0.98	1.68
	331547	N54811		gb:xd74f04.s1 NCI_CGAP_Ov2 Homo sapiens	3.80	5.75
5	331578	N67960	Hs.249989	ESTs	0.11	0.67
	331589	N71027	Hs.152618	ESTs	1.09	1.38
	331608	N89861	Hs.112110	PTD007 protein	0.93	0.76
	331614	N92293	Hs.240272	EST	0.17	1.34
	331668	W69707	Hs.58030	EST	2.24	3.82
10	331671	W72033	Hs.194695	ras homolog gene family, member l	1.00	1.24
	331676	W79834	Hs.58559	ESTs, Weakly similar to rhoteikin [M.musc	0.08	1.07
	331681	W85712	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl	8.72	4.27
	331692	W93592	Hs.152213	wingless-type MMTV integration site fami	0.94	0.54
	331717	AA190888	Hs.153881	Homo sapiens NY-REN-62 antigen mRNA, par	1.57	1.34
15	331718	AA191404	Hs.104072	ESTs	6.80	11.77
	331811	AA404500	Hs.301570	ESTs	1.10	1.00
	331820	AA405970	Hs.97996	transcription termination factor, mitoc	0.73	0.59
	331831	AA412031	Hs.97901	EST	2.77	4.08
	331852	AA418988	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	0.23	0.93
20	331943	AA453418	Hs.21275	hypothetical protein FLJ11011	0.36	1.88
	331969	AA460702	Hs.82772	collagen, type XI, alpha 1	1.00	1.00
	331990	AA478102	Hs.139631	ESTs	3.04	3.87
	332002	AA482009	Hs.105104	ESTs	1.19	0.78
	332027	AA489671	Hs.65641	hypothetical protein FLJ20073	1.27	1.03
25	332029	AA489697	Hs.145053	ESTs	0.30	1.62
	332033	AA489840	Hs.251014	EST	2.30	3.70
	332048	AA496019	Hs.201591	ESTs	0.17	0.52
	332071	AA598594	Hs.205293	KIAA1211 protein	1.35	1.23
30	332074	AA599012		gb:ae41e11.s1 Gessler Wilms tumor Homo s	0.19	2.00
	332083	AA600200	Hs.155546	KIAA1080 protein; Golgi-associated, gamm	0.31	1.18
	332085	AA600353	Hs.173933	nuclear factor I/A	0.30	1.50
	332125	AA609861	Hs.312447	ESTs	0.22	0.62
	332177	F10812	Hs.101433	ESTs	8.21	18.03
	332180	H03348	Hs.7327	claudin 1	2.27	1.57
35	332185	H10356	Hs.101689	ESTs	0.09	1.18
	332203	H49388	Hs.317769	EST	8.05	5.02
	332232	N48891	Hs.101915	Stargardt disease 3 (autosomal dominant)	0.78	0.85
	332240	N54803	Hs.324267	ESTs, Weakly similar to putative p150 [0.96	1.23
	332261	N70294	Hs.269137	ESTs	2.40	3.74
40	332275	R08838	Hs.26530	serum deprivation response (phosphatidyl	0.27	0.75
	332280	R38100	Hs.146381	RNA binding motif protein, X chromosome	0.39	1.88
	332299	R69250	Hs.21201	neclin 3; DKFZP566B0846 protein	5.24	12.76
	332304	R74041	Hs.101539	ESTs	1.44	3.18
	332314	T25862	Hs.101774	hypothetical protein FLJ23045	0.68	1.32
45	332384	M11433	Hs.101850	retinol-binding protein 1, cellular	1.71	0.88
	332434	N75542	Hs.289068	Homo sapiens cDNA FLJ11918 fis, clone HE	0.43	0.86
	332445	T63781	Hs.11112	ESTs	0.68	1.00
	332453	L00205	Hs.111758	keratin 6A	31.54	1.00
	332458	M33493	Hs.250700	trypsin beta 1	0.51	1.00
50	332504	AA053917	Hs.15106	chromosome 14 open reading frame 1	0.79	1.24
	332525	M17252	Hs.278430	cytochrome P450, subfamily XXIA (steroid	0.98	1.70
	332530	M31682	Hs.1735	inhibin, beta B (activin AB beta polypep	0.88	0.66
	332535	N20284	Hs.19280	cysteine-rich motor neuron 1	0.22	1.46
	332539	AA412528	Hs.20183	ESTs, Weakly similar to AF164793 1 prote	0.93	1.49
55	332559	M13955	Hs.166189	cytokeratin 2	0.35	1.13
	332563	N92924	Hs.274407	protease, serine, 16 (thymus)	1.00	1.00
	332565	AA234896	Hs.25272	E1A binding protein p300	0.36	1.05
	332594	AA279313	Hs.3239	methyl CpG binding protein 2 (Rett syndr	0.53	0.59
	332634	S38953	Hs.283750	tenascin XA	0.38	1.16
60	332638	AA283034	Hs.50640	JAK binding protein	1.00	1.70
	332640	AA417152	Hs.5101	protein regulator of cytokinesis 1	6.15	1.16
	332654	AA001296	Hs.288217	hypothetical protein MGC2941	1.50	2.73
	332665	AA223335	Hs.63788	propionyl Coenzyme A carboxylase, beta p	1.20	0.91
	332692	AA496035	Hs.247926	gap junction protein, alpha 5, 40kD (con	0.17	1.12
65	332716	L00058	Hs.79070	v-myc avian myelocytomatosis viral oncog	1.00	1.44
	332736	L13773	Hs.114765	myeloid/lymphoid or mixed-lineage leukem	1.00	1.81
	332758	X93921	Hs.296938	dual specificity phosphatase 7	0.53	0.78
	332781	AA233258	Hs.247112	hypothetical protein FLJ10902	1.44	1.56
	332792				1.70	1.19
70	332816				1.85	2.47
	332858				1.04	1.57
	332906				3.48	8.04
	332911				1.00	1.00
	332912				1.06	4.40
75	332922				1.00	1.00
	332956				0.42	0.88
	332959				1.96	6.34
	332982				0.56	0.99
	332984				0.30	0.78
80	332998				1.47	2.01
	333058				0.47	1.38
	333097				2.14	3.19
	333121				2.76	3.70
	333122				1.92	1.21
85	333123				1.85	1.39
	333138				0.47	0.52

	333139	1.88	0.84
	333140	0.21	0.64
	333221	1.51	1.11
5	333260	0.75	1.01
	333380	6.68	15.75
	333387	4.56	12.61
	333512	5.05	8.01
	333524	2.28	3.98
10	333585	2.31	1.53
	333603	2.23	1.17
	333604	2.51	1.58
	333618	0.52	0.98
	333627	1.44	1.36
15	333628	1.90	1.90
	333650	1.85	2.10
	333678	1.85	2.35
	333750	2.18	5.67
	333763	1.99	2.60
20	333767	1.02	0.96
	333768	1.78	1.65
	333769	2.15	2.13
	333772	1.46	2.53
	333777	1.00	1.42
25	333846	2.99	4.50
	333884	0.47	0.94
	333887	0.50	1.00
	333891	0.43	0.89
	333892	0.51	0.91
30	333904	0.26	1.13
	333906	0.55	0.98
	333948	1.70	2.15
	333954	0.37	1.09
	333966	8.10	14.30
35	333968	0.63	1.38
	334061	4.24	12.30
	334094	1.30	12.03
	334113	4.55	8.63
	334161	0.82	1.59
40	334183	0.47	0.76
	334187	1.36	3.70
	334219	0.69	1.04
	334222	1.88	1.70
	334223	4.72	3.14
45	334239	0.79	0.62
	334255	0.45	1.10
	334333	1.00	3.56
	334378	3.98	5.76
	334382	1.50	1.31
50	334492	3.59	4.75
	334562	5.94	15.40
	334588	8.14	19.53
	334616	1.55	1.56
	334633	5.16	8.07
55	334648	0.59	2.13
	334787	3.70	7.15
	334866	8.13	10.60
	334891	0.32	1.14
	334933	1.00	3.84
60	334934	4.01	7.43
	334945	1.04	2.96
	334967	0.29	1.14
	334990	1.50	1.39
	335015	5.88	18.65
65	335093	0.55	1.75
	335120	4.31	8.01
	335125	0.38	1.97
	335179	1.24	1.98
	335188	0.46	1.47
70	335211	1.61	1.42
	335288	0.73	0.97
	335289	0.20	0.26
	335361	2.18	1.58
	335379	0.50	0.71
75	335414	3.64	14.94
	335416	2.93	3.98
	335496	0.96	0.91
	335497	1.71	1.92
	335548	1.15	2.40
80	335551	3.22	10.54
	335558	3.42	4.89
	335586	5.50	12.75
	335619	2.99	3.07
	335620	3.80	8.29
85	335621	0.28	0.57
	335682	0.46	1.17

	335686	2.55	3.81
	335755	2.24	1.07
	335784	0.20	0.97
5	335814	1.13	1.48
	335815	2.45	3.51
	335823	1.00	4.16
	335835	0.49	1.70
	335851	1.66	1.39
10	335868	2.98	6.43
	335896	0.98	0.99
	335936	12.10	21.93
	335948	1.00	1.64
	335983	1.00	4.21
	335995	0.37	1.17
15	336021	1.04	0.84
	336034	11.40	23.54
	336038	1.19	1.21
	336066	0.54	1.63
20	336107	0.95	0.70
	336205	3.13	6.29
	336275	3.20	10.10
	336292	2.34	3.09
	336331	1.00	1.00
25	336419	0.65	0.79
	336632	2.33	2.16
	336633	2.55	2.23
	336634	2.19	2.03
	336635	2.69	2.48
30	336636	2.13	1.83
	336637	2.43	2.24
	336638	2.31	2.03
	336659	0.60	1.31
	336675	0.31	1.18
35	336684	1.50	1.14
	336694	4.74	7.10
	336716	4.43	6.37
	336721	2.20	0.74
	336798	1.64	2.14
40	336900	6.14	12.73
	336948	1.00	1.00
	337028	1.30	2.09
	337043	4.01	11.53
	337046	1.67	1.84
45	337054	2.78	7.35
	337128	7.20	16.14
	337162	3.45	5.34
	337183	5.72	11.41
	337184	3.72	5.90
50	337192	1.27	1.06
	337194	1.88	1.68
	337229	0.22	1.03
	337268	1.00	3.31
	337299	3.23	5.14
55	337325	2.76	3.72
	337389	5.80	10.42
	337493	2.06	6.30
	337497	7.88	20.29
	337500	3.80	4.48
60	337549	1.66	2.31
	337603	1.27	8.54
	337605	5.76	7.16
	337671	0.73	0.97
	337755	1.54	0.92
65	337786	5.07	9.73
	337809	6.18	12.87
	337862	3.78	12.97
	337871	2.66	8.16
	337958	0.26	1.34
70	338008	1.48	1.12
	338033	2.38	14.59
	338083	0.65	2.16
	338110	1.00	1.61
	338112	5.86	8.25
75	338145	1.70	1.97
	338148	8.07	18.19
	338158	1.30	4.55
	338161	2.58	3.57
	338179	1.00	1.00
80	338182	3.32	4.63
	338189	1.00	3.34
	338197	0.99	1.69
	338199	4.58	7.62
	338215	6.01	15.85
85	338279	0.53	0.95
	338316	20.58	38.66

	338322	3.23	7.39
	338357	4.10	11.39
	338359	10.12	21.59
5	338366	0.69	1.02
	338374	0.40	1.18
	338414	0.47	1.06
	338418	6.12	13.86
	338469	3.09	5.11
10	338501	6.28	10.32
	338506	6.97	12.41
	338523	3.10	5.84
	338549	1.70	2.70
	338561	0.79	0.81
15	338662	1.72	1.46
	338671	0.17	0.91
	338676	2.10	15.86
	338726	1.20	1.09
	338779	0.12	0.57
20	338804	0.99	1.67
	338836	1.00	1.00
	338871	4.30	9.81
	338872	5.02	12.81
	338879	0.23	1.12
25	338937	6.55	12.26
	338966	1.76	5.42
	338993	1.00	2.40
	339047	5.26	10.81
	339100	5.10	6.88
30	339114	1.00	1.70
	339121	1.00	3.75
	339170	10.36	19.67
	339229	4.08	13.48
	339264	2.64	3.83
35	339293	1.73	1.94

TABLE 8B shows the accession numbers for those Pkeys in Table 8A lacking unigenelD's. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

	Pkey	CAT number	Accessions
	322044	187363_1	AW340926 AA249063 N86075
	322060	44320_1	AI341937 AW003063 U34725 AA904742
50	321430	42705_1	X57414 X57415
	321467	43034_1	X13075 X13076
	322125	46779_1	R93901 AF075073 R93902
	322166	46861_1	H69434 AF085958 H69846
55	322173	46873_1	H52567 H52557 AF085970 H52164
	322178	46882_1	H56535 AF085980 H56712
	322179	46885_1	H92891 AF085982 H92777
	321577	1615102_1	H84849 H84252 H84260 H86664 H85320
	321587	1615333_1	H95531 H95521 H84529
60	313723	111953_1	AA070412 AA102346 AA081885
	320997	627492_1	H22544 H46842 AI204929
	322278	47271_1	W69304 AF086283 W69200
	321687	218439_1	AA625149 AA313030 AA313052 H97463
	313883	129439_1	AA665089 AA135130 AA484059 AA102419 AW877765
	322320	47422_1	W79150 AF086419
65	322339	814584_1	AI668646 AI734214 W17348
	314648	293660_1	AW979268 AA878419 AA431342 AA431628
	300201	682222_1	AI308300 AI308296
	306897	25196_2	AI093967
70	323155	979809_1	AL120701 AL135041 AL121524
	322527	38927_1	AF147359 T58511 T58560
	322585	473768_2	W88919 W89125
	300362	1574395_1	Z42308 H23514
	322635	82296_1	AA005129 AA679084 AA694399
75	322664	85042_1	AA011522 AA702841 AA011691 AA330797
	315454	380580_1	AI239464 AI239473 AA625812 AI208703
	322687	37372_1	AF074666 AI110759 AF090902
	314852	327472_1	AI903735 AA491283 AI694953 AW976903 AA761362
	307783	697809_1	AI347274 AW844024
	324072	269032_1	AA381722 AA381829 AW963906 AW963902 AA381242
80	300627	221345_1	AA488472 W27363 AA317053 BE082689 AW967036 BE079872
	323505	196389_1	AW970512 AA280251 AI652287 BE466438 AI650725 AA551854 AA281574 AW571481
	315791	403558_1	AA678177 AA677034
	324303	233842_1	AL118754 AA333202 H38001
	316519	442885_1	AA847835 AA768376
85	300926	333127_1	AA504860 AA504911

	324580	328264_1	AA492588 AA492498 AA492571
	301882	275087_1	T78054 T79888 AA398185
	324804	398093_1	AI692552 AI393343 AI800510 AI377711 F24263 AA661876
5	324889	1515978_1	D31010 D30991 D31168 D31166 D31465
	302697	43219_1	AJ001409 AJ001410
	302711	45419_1	L08442 D51348
	302742	458_39	L12061
	318499	364430_1	T25451 AA585296 AA585305
10	310624	34624_4	U88896 U88898 AA916056 T03285 AI341594 AI359534 AI634031 U88897
	302847	458_105	X98941 X98942 X98943 X98953 X98949
	304122	77271_5	H28966
	303598	270283_1	AA382814 AA402411 AA412355
	311409	837264_1	AI698839 AI909260 AI909259
15	312094	797889_1	Z78390 T97427
	319312	1540116_1	Z45481 F12393 T74437
	319407	1688823_1	R05329 R01555 R08276
	319425	1689571_1	T82930 R02424 T85145
	320007	229683_1	AA336314 T82938 AA327744 AW967388 AA639967 T10753
20	320018	1815987_1	T83263 T85731 T85730
	319484	1691553_1	T91772 R07257 R07098
	318865	1535937_1	H10818 F07831 Z43072
	312220	1671607_1	N74613 T98756 T98589
	319546	243305_1	R09692 R09414 AA346353
25	312389	902067_1	AI863140 W80703 R43474
	319611	1566863_1	H14957 R56522 R11908
	312437	291472_1	BE080180 AW827313 AW231970 AA995028 AA428584 AW872716 AW892508 AW854593 AA578441 AW975234 AA664937 AA984131 AA528743 AA552874 AA564758 AW063245 AI267534 AW070190 AW893483 AA770330 AA906928 AA906582 AA758746 AA551717 AW063311 AA429538
30	311896	579192_1	AW206447 AI248530 AI084433 AI400976 R16553
	319834	112523_1	AA071267 T65940 T64515 AA071334
	321102	80531_1	AA018306 H38925 AA001221
	321158	410938_1	H79670 H47798 AA700289
	321199	212379_1	N34524 AA305071 AW954803 AA502335 AI433430 AI203597 AW026670 AW265323 AW850787 AA317554 AW993643 AW835572 AW385512 AI334966 W32951 H62656 H53902 R88904 AW835732
35	305528	28832_3	AA769156
	321270	1662057_1	N59537 N78278 R83560
	314126	177666_1	AA226431 AA226569 AA488748
	320714	743644_1	R91883 AI445591
40	306442	AA976899	
	306446	AA977348	
	306458	AA978186	
	306510	AA988546	
	306557	AA994530	
45	306572	AA995686	
	306582	AA996248	
	306656	AI004024	
	306686	AI015615	
	306751	AI032589	
50	308011	AI439473	
	306892	AI092465	
	308106	AI476803	
	308154	AI500600	
	306956	AI125111	
55	306958	AI125152	
	308213	AI557041	
	308216	AI557135	
	308219	AI557246	
	308588	AI718299	
60	308599	AI719893	
	308643	AI745040	
	308673	AI760864	
	308697	AI767143	
	308778	AI811109	
	308808	AI818289	
65	308875	AI832332	
	308886	AI833240	
	308898	AI858845	
	308966	AI870704	
	308979	AI873111	
70	303011	41689_1	AF090405 AF090407 AF090406
	303077	44060_1	AF163305 AF163307 AF163303
	305016	AA626876	
	305034	AA630128	
75	305072	AA641012	
	305148	AA654070	
	305190	AA665955	
	303978	AW513315	
	303990	AW515465	
80	303998	AW516449	
	303999	AW516611	
	305235	AA670480	
	305312	AA700201	
	305413	AA724659	
85	305447	AA737856	
	321244	29327_1	AF068654 AF068656 AF068655

	305614	AA782866	
	305637	AA806124	
	305639	AA806138	
5	305650	AA807709	
	305690	AA813477	
	305728	AA828209	
	305759	AA835353	
	305792	AA845256	
10	307041	AI144243	
	307091	AI167439	
	307181	AI189251	
	305901	AA872968	
	305910	AA875981	
15	307415	AI242118	
	307426	AI243364	
	307517	AI275055	
	307551	AI281556	
	307561	AI282207	
20	307608	AI290295	
	307691	AI318285	
	307730	AI336092	
	307760	AI342387	
	307764	AI342731	
25	307796	AI350556	
	309045	AI910902	
	309051	AI911975	
	307807	AI351799	
	307808	AI351826	
30	307820	AI355761	
	307852	AI365541	
	309122	AI928178	
	309164	AI937761	
	309177	AI951118	
35	307902	AI380462	
	309299	AW003478	
	309303	AW004823	
	309476	AW129368	
	309532	AW151119	
40	309747	AW264889	
	309769	AW272346	
	309799	AW276964	
	309866	AW299916	
45	302679	311853_1	H65022 AA186889
	309923	AW340684	
	309928	AW341418	
	309931	AW341683	
	309933	AW341936	
50	302705	31765_1	U09060 U09061
	302789	34161_1	AJ245067 AJ245070
	304006	AW517947	
	304024	T03036	
	304026	T03160	
	304028	T03266	
55	304046	T54803	
	304061	T61521	
	304063	T62536	
	302802	34487_1	Y08250 Y08245
	304114	R78946	
60	304155	H68696	
	304203	N56929	
	304234	W81608	
	304348	AA179868	
	304430	AA347682	
65	304456	AA411240	
	304521	AA464716	
	304526	AA476427	
	304607	AA513322	
	304735	AA576453	
70	304760	AA580401	
	306015	AA897116	
	306063	AA906316	
	306065	AA906725	
	306104	AA910956	
75	306109	AA911861	
	306242	AA932805	
	306288	AA936900	
	306396	AA970223	
80	330568	NOT_FOUND_entrez	U56244
	330599	15323_-12	U90437
	331131	genbank_R54797	R54797
	331203	NOT_FOUND_entrez	T82310
	331531	genbank_N51343	N51343
	331547	467396_1	AA828597 N54811
85	332074	genbank_AA599012	AA599012

TABLE 8C shows the genomic position for those Pkeys in Table 8A lacking unigene ID's and accession numbers. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

5	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
10	Nt_position:	Indicates nucleotide positions of predicted exons.		
	Pkey	Ref	Strand	Nt_position
	332792	Dunham, I. et.al.	Plus	73381-73768
	332816	Dunham, I. et.al.	Plus	359844-360030
15	332906	Dunham, I. et.al.	Plus	1923101-1923205
	332911	Dunham, I. et.al.	Plus	1961767-1961858
	332912	Dunham, I. et.al.	Plus	1962120-1962246
	332922	Dunham, I. et.al.	Plus	2009620-2009738
	332956	Dunham, I. et.al.	Plus	2510528-2510658
20	332959	Dunham, I. et.al.	Plus	2518145-2518213
	333138	Dunham, I. et.al.	Plus	3369205-3369323
	333139	Dunham, I. et.al.	Plus	3369495-3369571
	333221	Dunham, I. et.al.	Plus	3978070-3978187
	333380	Dunham, I. et.al.	Plus	4904775-4904846
25	333387	Dunham, I. et.al.	Plus	4910935-4910997
	333512	Dunham, I. et.al.	Plus	5560510-5560564
	333524	Dunham, I. et.al.	Plus	5612620-5612780
	333585	Dunham, I. et.al.	Plus	6234778-6234894
	333618	Dunham, I. et.al.	Plus	6562391-6562566
30	333627	Dunham, I. et.al.	Plus	6620584-6620903
	333628	Dunham, I. et.al.	Plus	6629004-6629233
	333650	Dunham, I. et.al.	Plus	6796852-6797128
	333678	Dunham, I. et.al.	Plus	7068223-7068288
	333750	Dunham, I. et.al.	Plus	7608165-7608234
35	333763	Dunham, I. et.al.	Plus	7692491-7692630
	333767	Dunham, I. et.al.	Plus	7694407-7694623
	333768	Dunham, I. et.al.	Plus	7695440-7695697
	333769	Dunham, I. et.al.	Plus	7696625-7696707
	333772	Dunham, I. et.al.	Plus	7706773-7706902
40	333777	Dunham, I. et.al.	Plus	7746805-7746916
	333846	Dunham, I. et.al.	Plus	8008623-8008757
	333884	Dunham, I. et.al.	Plus	8153960-8154161
	333887	Dunham, I. et.al.	Plus	8154882-8155025
	333891	Dunham, I. et.al.	Plus	8156437-8156709
45	333892	Dunham, I. et.al.	Plus	8156825-8157001
	333948	Dunham, I. et.al.	Plus	8583497-8583627
	333954	Dunham, I. et.al.	Plus	8563186-8563335
	333966	Dunham, I. et.al.	Plus	8655643-8655826
	333968	Dunham, I. et.al.	Plus	8681004-8681241
50	334061	Dunham, I. et.al.	Plus	9686941-9687077
	334094	Dunham, I. et.al.	Plus	9889953-9890105
	334113	Dunham, I. et.al.	Plus	10282459-10282597
	334161	Dunham, I. et.al.	Plus	10599033-10599180
55	334219	Dunham, I. et.al.	Plus	12716160-12716384
	334239	Dunham, I. et.al.	Plus	13056569-13056693
	334333	Dunham, I. et.al.	Plus	13603544-13603657
	334378	Dunham, I. et.al.	Plus	13907239-13907370
	334382	Dunham, I. et.al.	Plus	13915866-13916036
60	334562	Dunham, I. et.al.	Plus	14987847-14987940
	334588	Dunham, I. et.al.	Plus	15032740-15032817
	334616	Dunham, I. et.al.	Plus	15176123-15176470
	334633	Dunham, I. et.al.	Plus	15333206-15333305
	334866	Dunham, I. et.al.	Plus	18872214-18872317
	334891	Dunham, I. et.al.	Plus	19299770-19299944
65	334934	Dunham, I. et.al.	Plus	20103970-20104058
	335015	Dunham, I. et.al.	Plus	20682792-20682945
	335120	Dunham, I. et.al.	Plus	21436286-21436384
	335125	Dunham, I. et.al.	Plus	21441390-21441471
70	335179	Dunham, I. et.al.	Plus	21634405-21634526
	335188	Dunham, I. et.al.	Plus	21669118-21669328
	335211	Dunham, I. et.al.	Plus	21774611-21774680
	335361	Dunham, I. et.al.	Plus	22807292-22807445
	335379	Dunham, I. et.al.	Plus	22899306-22899420
75	335414	Dunham, I. et.al.	Plus	23235546-23235684
	335416	Dunham, I. et.al.	Plus	23237354-23237465
	335496	Dunham, I. et.al.	Plus	24164386-24164545
	335497	Dunham, I. et.al.	Plus	24167666-24167869
	335558	Dunham, I. et.al.	Plus	24740167-24740347
	335586	Dunham, I. et.al.	Plus	24990333-24990497
80	335686	Dunham, I. et.al.	Plus	25439839-25439920
	335784	Dunham, I. et.al.	Plus	25942710-25942792
	335823	Dunham, I. et.al.	Plus	26365925-26366004
	335983	Dunham, I. et.al.	Plus	27938968-27939070
	335995	Dunham, I. et.al.	Plus	28009044-28009184
85	336021	Dunham, I. et.al.	Plus	28686482-28686559

	336034	Dunham, I. et.al.	Plus	29014404-29014590
	336038	Dunham, I. et.al.	Plus	29022963-29023165
	336107	Dunham, I. et.al.	Plus	29987731-29987869
5	336632	Dunham, I. et.al.	Plus	983890-985529
	336633	Dunham, I. et.al.	Plus	985591-986221
	336634	Dunham, I. et.al.	Plus	986296-986670
	336635	Dunham, I. et.al.	Plus	987908-988364
	336636	Dunham, I. et.al.	Plus	988418-989185
10	336637	Dunham, I. et.al.	Plus	989276-990813
	336638	Dunham, I. et.al.	Plus	991906-993240
	336659	Dunham, I. et.al.	Plus	1896402-1896478
	336694	Dunham, I. et.al.	Plus	2420546-2420616
	336721	Dunham, I. et.al.	Plus	3371522-3371586
15	336900	Dunham, I. et.al.	Plus	10236423-10236523
	336948	Dunham, I. et.al.	Plus	12692290-12692381
	337028	Dunham, I. et.al.	Plus	16644817-16644942
	337054	Dunham, I. et.al.	Plus	17821742-17821922
	337162	Dunham, I. et.al.	Plus	23478943-23479145
20	337183	Dunham, I. et.al.	Plus	23943606-23943696
	337184	Dunham, I. et.al.	Plus	23973949-23974016
	337268	Dunham, I. et.al.	Plus	28011979-28012034
	337299	Dunham, I. et.al.	Plus	29022656-29022775
	337389	Dunham, I. et.al.	Plus	31401509-31401579
25	337493	Dunham, I. et.al.	Plus	33330760-33330981
	337549	Dunham, I. et.al.	Plus	34474472-34474531
	337755	Dunham, I. et.al.	Plus	3971764-3971900
	337809	Dunham, I. et.al.	Plus	4449069-4449193
	337871	Dunham, I. et.al.	Plus	5443027-5443101
30	337958	Dunham, I. et.al.	Plus	6969162-6969270
	338008	Dunham, I. et.al.	Plus	7697068-7697236
	338033	Dunham, I. et.al.	Plus	8092128-8092271
	338110	Dunham, I. et.al.	Plus	10384481-10384621
	338112	Dunham, I. et.al.	Plus	10391398-10391600
35	338145	Dunham, I. et.al.	Plus	11386629-11386692
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	338179	Dunham, I. et.al.	Plus	12808775-12808833
	338197	Dunham, I. et.al.	Plus	13638107-13638181
	338279	Dunham, I. et.al.	Plus	16168944-16169091
40	338316	Dunham, I. et.al.	Plus	17089711-17089988
	338322	Dunham, I. et.al.	Plus	17132477-17132547
	338357	Dunham, I. et.al.	Plus	18062184-18062402
	338359	Dunham, I. et.al.	Plus	18074402-18074501
	338366	Dunham, I. et.al.	Plus	18252026-18252189
45	338374	Dunham, I. et.al.	Plus	18371200-18371282
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	338418	Dunham, I. et.al.	Plus	19435506-19435596
	338501	Dunham, I. et.al.	Plus	21244713-21244828
	338506	Dunham, I. et.al.	Plus	21221871-21221953
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	338836	Dunham, I. et.al.	Plus	27792166-27792272
	338879	Dunham, I. et.al.	Plus	28410653-28410734
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	338993	Dunham, I. et.al.	Plus	30077787-30078184
	339047	Dunham, I. et.al.	Plus	30760793-30760968
	339100	Dunham, I. et.al.	Plus	31141580-31141765
	339114	Dunham, I. et.al.	Plus	31456454-31456519
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	339170	Dunham, I. et.al.	Plus	32216399-32216527
	339293	Dunham, I. et.al.	Plus	33223671-33223819
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	332982	Dunham, I. et.al.	Minus	2628296-2628109
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	334187	Dunham, I. et.al.	Minus	11921456-11921205
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	334223	Dunham, I. et.al.	Minus	12734365-12734269
	334255	Dunham, I. et.al.	Minus	13200776-13200692
	334492	Dunham, I. et.al.	Minus	14478333-14478172
	334648	Dunham, I. et.al.	Minus	15363301-15363222
85	334787	Dunham, I. et.al.	Minus	16299093-16298937
	334933	Dunham, I. et.al.	Minus	20078117-20077991

	334945	Dunham, I. et.al.	Minus	20138885-20138637
	334967	Dunham, I. et.al.	Minus	20173311-20173218
	334990	Dunham, I. et.al.	Minus	20341159-20341087
5	335093	Dunham, I. et.al.	Minus	21297367-21297214
	335288	Dunham, I. et.al.	Minus	22304275-22303770
	335289	Dunham, I. et.al.	Minus	22305950-22305708
	335548	Dunham, I. et.al.	Minus	24662773-24662673
	335551	Dunham, I. et.al.	Minus	24679828-24678961
10	335619	Dunham, I. et.al.	Minus	25082677-25082498
	335620	Dunham, I. et.al.	Minus	25092561-25092434
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	335682	Dunham, I. et.al.	Minus	25421215-25421093
	335755	Dunham, I. et.al.	Minus	25763806-25763747
15	335814	Dunham, I. et.al.	Minus	26320043-26319845
	335815	Dunham, I. et.al.	Minus	26320518-26320421
	335835	Dunham, I. et.al.	Minus	26393311-26393245
	335851	Dunham, I. et.al.	Minus	26604863-26604742
	335868	Dunham, I. et.al.	Minus	26711437-26711300
20	335896	Dunham, I. et.al.	Minus	26977639-26977558
	335936	Dunham, I. et.al.	Minus	27360474-27360400
	335948	Dunham, I. et.al.	Minus	27555924-27555788
	336066	Dunham, I. et.al.	Minus	29241080-29240842
	336205	Dunham, I. et.al.	Minus	30477456-30477311
25	336275	Dunham, I. et.al.	Minus	32086675-32086536
	336292	Dunham, I. et.al.	Minus	32818035-32817927
	336331	Dunham, I. et.al.	Minus	33594527-33594371
	336419	Dunham, I. et.al.	Minus	34052568-34052445
	336675	Dunham, I. et.al.	Minus	2020758-2020664
30	336684	Dunham, I. et.al.	Minus	2158060-2157993
	336716	Dunham, I. et.al.	Minus	3259952-3259862
	336798	Dunham, I. et.al.	Minus	5888954-5888757
	337043	Dunham, I. et.al.	Minus	17407330-17407251
	337046	Dunham, I. et.al.	Minus	17610892-17610821
35	337128	Dunham, I. et.al.	Minus	22215251-22215034
	337192	Dunham, I. et.al.	Minus	24591853-24591771
	337194	Dunham, I. et.al.	Minus	24610510-24610359
	337229	Dunham, I. et.al.	Minus	26716579-26716481
	337325	Dunham, I. et.al.	Minus	30015948-30015800
40	337497	Dunham, I. et.al.	Minus	33371317-33371258
	337500	Dunham, I. et.al.	Minus	33376212-33376158
	337603	Dunham, I. et.al.	Minus	1299296-1299194
	337605	Dunham, I. et.al.	Minus	1346555-1346397
	337671	Dunham, I. et.al.	Minus	3260634-3260547
45	337786	Dunham, I. et.al.	Minus	4133203-4133081
	337862	Dunham, I. et.al.	Minus	5347658-5347550
	338083	Dunham, I. et.al.	Minus	9318438-9318301
	338158	Dunham, I. et.al.	Minus	11794465-11794343
50	338161	Dunham, I. et.al.	Minus	12124716-12124658
	338182	Dunham, I. et.al.	Minus	12824919-12824827
	338189	Dunham, I. et.al.	Minus	12878594-12878478
	338199	Dunham, I. et.al.	Minus	13760865-13760780
	338215	Dunham, I. et.al.	Minus	14055447-14055355
	338469	Dunham, I. et.al.	Minus	20520387-20520242
55	338549	Dunham, I. et.al.	Minus	22049171-22049081
	338561	Dunham, I. et.al.	Minus	22311966-22311856
	338671	Dunham, I. et.al.	Minus	24508421-24508346
	338676	Dunham, I. et.al.	Minus	24637427-24637369
	338726	Dunham, I. et.al.	Minus	25926206-25925618
50	338779	Dunham, I. et.al.	Minus	27030151-27029795
	338871	Dunham, I. et.al.	Minus	28301708-28301611
	338872	Dunham, I. et.al.	Minus	28300921-28300790
	338966	Dunham, I. et.al.	Minus	29614876-29614749
	339229	Dunham, I. et.al.	Minus	32722330-32722199
55	339264	Dunham, I. et.al.	Minus	32975145-32975053
	325228	6381940	Plus	2630-2694
	325235	6381943	Minus	162154-162264
	329588	3962484	Plus	1169-1619
	329560	3962491	Plus	2095-2990
70	329541	3983503	Minus	2765-3059
	325328	5866875	Plus	86780-86854
	325340	6017033	Minus	166656-166819
	325373	5866920	Minus	1136686-1136777
	325367	5866920	Minus	922881-922958
75	325389	5866921	Plus	239672-239759
	325436	5866939	Minus	29778-29907
	325498	5866967	Plus	173372-173930
	325471	6017034	Minus	289268-289342
	325557	6056302	Plus	50921-51050
30	325559	6249595	Minus	118590-119172
	325560	6249595	Minus	133794-133981
	325569	6249599	Plus	79927-80217
	325587	6682462	Plus	126724-126967
	325585	6682462	Plus	73476-73574
35	325597	5866992	Plus	1065020-1065089
	325639	5867002	Plus	253525-253608

	325739	5867038	Minus	205138-205269
	325740	5867038	Minus	207533-207690
	325792	6469828	Minus	1018-1176
5	325735	6552447	Minus	269122-269190
	325685	6682468	Plus	117397-117483
	325686	6682468	Plus	118337-118439
	325819	6682490	Minus	130314-130370
	329764	6048195	Minus	109733-109968
10	329703	6065793	Minus	139994-140138
	329643	6448539	Plus	53403-53537
	329816	6624888	Minus	70296-70423
	329860	6687260	Minus	163474-163605
	325883	5867087	Plus	22498-22663
15	325895	5867097	Plus	358317-358476
	325925	5867124	Plus	115749-115962
	325932	5867127	Plus	7369-7441
	325941	5867133	Minus	64228-64402
	325969	5867153	Plus	101911-102081
20	325971	5867153	Plus	105841-106035
	329993	4567166	Minus	101307-101434
	330020	6671887	Plus	172397-172491
	326163	5867168	Minus	7831-8035
	326274	5867171	Minus	410289-410404
25	326025	5867176	Plus	70854-70915
	326046	5867182	Minus	62668-62825
	326099	5867186	Minus	661381-661510
	326108	5867187	Minus	23784-23903
	326165	5867208	Minus	62787-62929
30	326189	5867212	Plus	69288-69413
	326204	5867218	Minus	148088-148200
	326230	5867230	Minus	301868-301972
	330052	4567182	Plus	352560-352963
	330036	6042048	Plus	117120-117216
35	326360	5867293	Plus	13627-13844
	326589	5867320	Plus	22760-22919
	326393	5867341	Plus	41702-41841
	326505	5867435	Minus	8818-8949
	326515	5867439	Plus	36683-36809
40	326592	6138928	Plus	23689-23828
	330107	6015249	Minus	100091-100282
	330106	6015249	Minus	99443-99778
	330100	6015253	Plus	21166-21301
	330093	6015278	Plus	1043-1199
45	330088	6015293	Plus	37517-37638
	330085	6015302	Minus	59613-59770
	330120	6671864	Minus	127553-127656
	330123	6671869	Minus	35311-35406
50	326742	5867611	Minus	95187-95248
	326605	5867637	Plus	24656-24749
	326818	6117831	Minus	15199-15309
	326720	6552456	Plus	84525-84677
	326770	6598307	Minus	513603-513668
	326692	6682502	Plus	117697-117899
55	326693	6682502	Minus	335002-335095
	326983	5867657	Minus	16023-16581
	326991	5867660	Plus	18147-18339
	326936	6004446	Minus	10217-10357
	326964	6469836	Plus	75340-75456
60	327040	6531965	Plus	783670-783817
	327053	6531965	Plus	2247267-2247437
	327075	6531965	Plus	4041318-4041431
	327085	6531965	Plus	4734947-4735069
	327036	6531965	Plus	319951-320040
65	327130	6531976	Plus	20247-22343
	327156	5866841	Minus	2462-2620
	327288	5867481	Plus	48583-48773
	327332	5867516	Minus	56361-56532
	327220	5867525	Minus	65701-65781
70	327224	5867534	Plus	188468-188544
	327321	6249562	Minus	99745-99836
	327361	6552412	Minus	61013-62130
	327396	5867743	Plus	8702-8820
75	327414	5867750	Plus	102461-102586
	327442	5867759	Plus	111483-111618
	327467	5867772	Plus	88030-88151
	327473	5867775	Plus	75101-75181
	327483	5867783	Plus	181573-181662
80	327377	5867793	Minus	37610-37676
	327562	5867804	Minus	343989-344474
	327568	5867811	Minus	46152-46287
	327606	6004463	Plus	200262-200495
	327611	5867868	Minus	175063-175392
	327642	5867891	Minus	2513-2743
85	327654	5867910	Minus	97564-97710
	327734	5867940	Minus	31003-31583

	327775	5867964	Minus	130791-130871
	327796	5867982	Plus	85267-85405
	327840	6249578	Minus	73065-73206
5	330208	6013599	Plus	66517-66931
	330263	6671884	Minus	101503-101634
	328004	5867993	Minus	157407-157887
	328101	5868020	Plus	289920-290014
	328100	5868020	Minus	263545-263635
10	328113	5868024	Minus	80378-80491
	328157	5868064	Plus	73326-73615
	328196	5868080	Minus	16551-16729
	328197	5868081	Minus	42133-42438
	327940	5868197	Minus	95240-95428
15	327984	5868216	Plus	66611-66677
	328021	5902482	Plus	713478-714590
	328068	6117819	Plus	253903-254022
	328264	6381912	Plus	55086-55404
	330300	2905862	Minus	3246-3302
20	328608	5868222	Minus	87770-87953
	328600	5868229	Minus	38889-40010
	328616	5868239	Plus	293920-294224
	328623	5868246	Minus	120020-120126
	328632	5868247	Plus	76734-76853
25	328666	5868254	Minus	778-901
	328698	5868264	Minus	625555-625633
	328700	5868264	Plus	764089-764203
	328708	5868271	Minus	68114-68854
	328735	5868289	Plus	89389-89455
30	328743	5868289	Plus	274638-274726
	328806	5868324	Plus	29408-29684
	328299	5868366	Minus	149708-149889
	328342	5868383	Plus	59955-60094
	328365	5868387	Minus	270724-270798
35	328369	5868388	Plus	75371-75583
	328381	5868392	Plus	662758-662848
	328451	5868425	Minus	217275-217336
	328481	5868449	Minus	8987-9180
	328500	5868464	Plus	59098-59481
40	328530	5868482	Plus	334973-335406
	328664	6004473	Plus	1193739-1193866
	328861	6381928	Minus	108317-108403
	328908	5868493	Plus	117002-117059
	328933	5868500	Plus	771755-771889
45	328934	5868500	Plus	846342-846448
	328949	6456765	Minus	43552-43619
	330313	6042030	Minus	33642-33775
	329005	5868542	Plus	85470-85673
	330366	2944106	Plus	151837-151914
50	330372	6580495	Minus	317461-317688
	329033	5868561	Minus	5390-5479
	329037	5868562	Minus	32466-32562
	329067	5868591	Minus	146417-147652
	329134	5868679	Plus	29959-30018
55	329157	5868687	Minus	145940-146155
	329178	5868704	Plus	179177-179463
	329192	5868716	Plus	166936-167020
	329194	5868716	Minus	304450-304559
	329204	5868720	Minus	3050-3190
60	329224	5868728	Plus	27422-27664
	329228	5868728	Minus	50118-50287
	329288	5868771	Plus	25554-26299
	329337	5868806	Minus	467155-467222
	329011	6682532	Plus	48658-48741

TABLE 9A: Potential Therapeutic, Diagnostic and Prognostic targets for Therapy of Lung Cancer

Table 9A shows about 1312 genes up-regulated in lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) relative to normal body tissues. These genes were selected from about 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

Table 9B show the accession numbers for those Pkey's lacking UnigenelD's for table 9A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 9C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 9A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the average of normal lung samples
 R2: Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples

Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
400195			NM_007057*:Homo sapiens ZW10 interactor	1.00	1.00
400205			NM_006265*:Homo sapiens RAD21 (S. pombe)	15.80	396.00
400220			Eos Control	2.28	2.84
400277			Eos Control	7.68	9.72
400285			Eos Control	1.00	1.00
400288	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor,	1.04	2.24
400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	132.45	4.00
400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	43.86	74.00
400301	X03635	Hs.1657	estrogen receptor 1	1.00	1.00
400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	1.75	1.65
400328	X87344	Hs.180062	transporter 2, ATP-binding cassette, sub	0.87	1.80
400419	AF084545		Target	156.55	253.00
400512			NM_030878*:Homo sapiens cytochrome P450,	1.00	2.00
400517	AF242388		lengsin	3.67	87.00
400560			NM_030878*:Homo sapiens cytochrome P450,	1.00	1.00
400664			NM_002425:Homo sapiens matrix metallopro	20.26	45.00
400665			NM_002425:Homo sapiens matrix metallopro	1.36	1.07
400666			NM_002425:Homo sapiens matrix metallopro	3.26	3.22
400749			NM_003105*:Homo sapiens sortilin-related	1.00	91.00
400763			Target Exon	7.63	24.00
401027			Target Exon	1.00	1.00
401093			C12000586*:gi 6330167 dbj BAA86477.1 (A	1.00	155.00
401203			Target Exon	1.00	86.00
401212			C12000457*:gi 7512178 pir T30337 polypr	1.00	400.00
401411			ENSP00000247172*:HYPOTHETICAL 126.2 kDa	1.00	72.00
401435			C14000397*:gi 7498898 pir T33295 hypoth	1.00	64.00
401464	AF039241		histone deacetylase 5	3.82	49.00
401714			ENSP00000241802*:CDNA FLJ11007 FIS, CLON	2.02	40.00
401747			Homo sapiens keratin 17 (KRT17)	128.43	68.00
401760			Target Exon	1.74	35.00
401780			NM_005557*:Homo sapiens keratin 16 (foca	26.47	10.50
401781			Target Exon	10.33	4.61
401785			NM_002275*:Homo sapiens keratin 15 (KRT1	4.13	2.70
401797			Target Exon	1.44	2.10
401961			NM_021626:Homo sapiens serine carboxypep	1.41	1.86
401985	AF053004		class I cytokine receptor	1.00	177.00
401994			Target Exon	61.84	47.00
402075			ENSP00000251056*:Plasma membrane calcium	1.00	1.00
402260			NM_001436*:Homo sapiens fibrillarlin (FBL	1.58	1.39
402265			Target Exon	2.09	35.00
402297			Target Exon	1.00	92.00
402408			NM_030920*:Homo sapiens hypothetical pro	28.87	13.00
402420			C1000823*:gi 10432400 emb CAC10290.1 (A	1.00	1.44
402674			Target Exon	7.44	243.00
402802			NM_001397:Homo sapiens endothelin conver	1.00	70.00
402994			NM_002463*:Homo sapiens myxovirus (influ	1.37	1.43
403137			NM_005381*:Homo sapiens nucleolin (NCL),	1.00	19.00
403306	NM_006825		transmembrane protein (63kD), endoplasmic	1.00	43.00
403329			Target Exon	1.00	61.00
403381			ENSP00000231844*:Ecotropic virus integra	1.00	119.00
403478			NM_022342:Homo sapiens kinesin protein 9	28.13	136.00
403485			C3001813*:gi 12737279 ref XP_012163.1 k	20.23	76.00
403627			Target Exon	6.30	29.33
403715			Target Exon	1.30	35.00
404044			ENSP00000237855*:DJ398G3.2 (NOVEL PROTEI	1.00	54.00
404076			NM_016020*:Homo sapiens CGI-75 protein (14.29	91.00
404101			C8000950:gi 423560 pir A47318 RNA-bindi	1.00	1.00
404140			NM_006510:Homo sapiens ret finger protei	1.42	1.44
404165			ENSP00000244562:NRH dehydrogenase [quino	1.00	54.00
404185			Target Exon	1.00	117.00
404210			NM_005936:Homo sapiens myeloid/lymphoid	5.93	13.77
404253			NM_021058*:Homo sapiens H2B histone fami	1.00	1.00

	404287		C6001909:gi 704441 dbj BAA18909.1 (D298	29.71	42.00
	404298		C6001238*:gi 121715 sp P26697 GTA3_CHICK	1.30	1.00
	404347		Target Exon	1.00	1.00
5	404440		NM_021048:Homo sapiens melanoma antigen,	1.00	15.00
	404721		NM_005596*:Homo sapiens nuclear factor I	1.00	60.00
	404794	NM_000078	cholesteryl ester transfer protein, plas	1.07	1.38
	404854		Target Exon	1.61	2.01
	404877		NM_005365:Homo sapiens melanoma antigen,	1.00	1.00
10	404927		Target Exon	1.00	1.00
	404996		Target Exon	1.00	1.00
	405449		CY000047*:gi 11427234 ref XP_009399.1 z	1.00	1.00
	405568		NM_031413*:Homo sapiens cat eye syndrome	1.00	78.00
	405572		Target Exon	0.76	1.14
15	405646		C12000200:gi 4557225 ref NP_000005.1 al	1.01	1.28
	405676	BE336714	cytochrome c-1	1.13	2.89
	405770		NM_002362:Homo sapiens melanoma antigen,	45.52	37.00
	405932		C15000305:gi 3806122 gb AAC69198.1 (AF0	1.99	1.99
	406137		NM_000179*:Homo sapiens mutS (E. coli) h	2.77	2.38
	406360		Target Exon	1.00	35.00
20	406399		NM_003122*:Homo sapiens serine protease	1.00	39.00
	406467		Target Exon	1.00	1.00
	406621	X57809 Hs.181125	immunoglobulin lambda locus	1.41	1.74
	406642	AJ245210	gb:Homo sapiens mRNA for immunoglobulin	2.16	3.91
25	406663	U24683 Hs.293441	immunoglobulin heavy constant mu	2.07	2.93
	406671	AA129547 Hs.285754	met proto-oncogene (hepatocyte growth fa	15.00	51.00
	406673	M34996 Hs.198253	major histocompatibility complex, class	0.98	3.09
	406676	X58399 Hs.81221	Human L2-9 transcript of unrearranged im,	1.30	1.53
	406678	U77534	gb:Human clone 1A11 immunoglobulin varia	1.33	1.45
30	406685	M18728	gb:Human nonspecific crossreacting antig	1.46	2.85
	406687	M31126 Hs.272822	pregnancy specific beta-1-glycoprotein 9	8.61	8.50
	406690	M29540 Hs.220529	carcinoembryonic antigen-related cell ad	226.37	350.00
	406698	X03068 Hs.73931	major histocompatibility complex, class	1.01	2.52
	406815	AA833930 Hs.288036	tRNA isopentenylpyrophosphate transferas	20.25	32.00
35	406861	AA609784	major histocompatibility complex, class	0.75	1.91
	406964	M21305	gb:Human alpha satellite and satellite 3	38.15	1114.00
	406967	M24349	gb:Human parathyroid hormone-like protei	1.00	1.00
	406974	M57293	gb:Human parathyroid hormone-related pep	1.00	1.00
	407103	AA424881 Hs.256301	hypothetical protein MGC13170	1.77	1.10
40	407128	R83312 Hs.237260	EST	1.00	1.00
	407137	T97307	gb:ye53h05.s1 Soares fetal liver spleen	142.70	135.00
	407168	R45175 Hs.117183	ESTs	2.16	18.00
	407239	AA076350 Hs.67846	leukocyte immunoglobulin-like receptor,	1.10	1.57
	407242	M18728	gb:Human nonspecific crossreacting antig	1.12	2.85
45	407244	M10014 Hs.75431	fibrinogen, gamma polypeptide	3.24	15.38
	407289	AA135159 Hs.203349	Homo sapiens cDNA FLJ12149 fis, clone MA	3.53	3.68
	407300	AA102616 Hs.120769	gb:zn43e07.s1 Stratagene HeLa cell s3 93	19.74	73.00
	407366	AF026942 Hs.271530	gb:Homo sapiens cig33 mRNA, partial sequ	0.06	8.25
	407378	AA299264 Hs.57776	ESTs, Moderately similar to I38022 hypot	1.00	26.00
50	407430	AF169351	gb:Homo sapiens protein tyrosine phospho	1.00	25.00
	407453	AJ132087	gb:Homo sapiens mRNA for axonemal dynein	1.00	75.00
	407577	AW131324 Hs.246759	hypothetical protein MGC12538	1.00	1.00
	407634	AW016569 Hs.136414	UDP-GlcNAc:betaGal beta-1,3-N-acetylgluc	111.20	228.00
	407710	AW022727 Hs.23616	ESTs	1.00	28.00
55	407720	AB037776 Hs.38002	KIAA1355 protein	1.89	1.31
	407746	AK001962	hypothetical protein FLJ11100	1.00	1.00
	407756	AA116021 Hs.38260	ubiquitin specific protease 18	4.51	5.00
	407758	D50915 Hs.38365	KIAA0125 gene product	1.00	28.00
	407782	AA608956 Hs.112619	ESTs, Moderately similar to PURKINJE CEL	0.97	1.14
60	407788	BE514982 Hs.38991	S100 calcium-binding protein A2	7.88	3.83
	407790	AI027274 Hs.288941	Homo sapiens cDNA FLJ14866 fis, clone PL	3.63	42.00
	407811	AW190902 Hs.40098	cysteine knot superfamily 1, BMP antagon	89.96	109.00
	407839	AA045144 Hs.161566	ESTs	173.91	108.00
	407944	R34008 Hs.239727	desmocollin 2	111.30	70.00
65	408000	L11690 Hs.620	bullous pemphigoid antigen 1 (230/240kD)	151.17	8.00
	408031	AA081395 Hs.42173	Homo sapiens cDNA FLJ10366 fis, clone NT	9.91	93.00
	408063	BE086548 Hs.42346	calcineurin-binding protein calsarcin-1	195.78	231.00
	408070	AW148852	gb:xf05d05.x1 NCI_CGAP_Brn35 Homo sapien	1.00	1.00
70	408101	AW968504 Hs.123073	CDC2-related protein kinase 7	37.84	61.00
	408122	AI432652 Hs.42824	hypothetical protein FLJ10718	0.85	1.71
	408212	AA297567 Hs.43728	hypothetical protein	5.88	7.91
	408243	Y00787 Hs.624	interleukin 8	4.27	9.98
	408349	BE546947 Hs.44276	homeo box C10	3.79	3.46
	408353	BE439838 Hs.44298	mitochondrial ribosomal protein S17	1.88	1.65
75	408354	AI382803 Hs.159235	ESTs	1.00	73.00
	408369	R38438 Hs.182575	solute carrier family 15 (H??? transport	1.41	16.50
	408380	AF123050 Hs.44532	diubiquitin	15.19	37.22
	408482	NM_000676 Hs.45743	adenosine A2b receptor	1.65	1.19
	408522	AI541214 Hs.46320	Small proline-rich protein SPRK [human,	1.98	1.24
80	408536	AW381532 Hs.135188	ESTs	1.55	1.50
	408545	AW235405 Hs.253690	ESTs	1.00	1.00
	408572	AA055611 Hs.226568	ESTs, Moderately similar to ALU4_HUMAN A	1.00	44.00
	408633	AW963372 Hs.46677	PRO2000 protein	107.16	56.00
	408660	AA525775	ESTs, Moderately similar to PC4259 ferri	1.00	1.00
85	408761	AA057264 Hs.238936	ESTs, Weakly similar to (define not ava	52.24	141.00
	408771	AW732573 Hs.47584	potassium voltage-gated channel, delayed	3.05	109.00

	408783	AF192522	Hs.47701	NPC1 (Niemann-Pick disease, type C1, gen	1.02	1.07
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	41.19	61.00
	408805	H69912	Hs.48269	vaccinia related kinase 1	24.67	45.00
5	408841	AW438865	Hs.256862	ESTs	1.00	58.00
	408873	AL046017	Hs.182278	calmodulin 2 (phosphorylase kinase, delt	1.00	89.00
	408908	BE296227	Hs.250822	serine/threonine kinase 15	7.76	1.00
	408992	AA059325	Hs.71642	guanine nucleotide binding protein (G pr	1.00	1.00
	408996	AI979168	Hs.344096	glycoprotein (transmembrane) nmb	3.71	5.50
10	409015	BE389387	Hs.49767	NM_004553:Homo sapiens NADH dehydrogenas	1.44	1.24
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	4.28	5.32
	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	112.42	195.00
	409077	AA401369	Hs.190721	ESTs	1.00	17.00
	409093	BE243834	Hs.50441	CGI-04 protein	2.02	1.93
15	409103	AF251237	Hs.112208	XAGE-1 protein	80.44	40.00
	409142	AL136877	Hs.50758	SMC4 (structural maintenance of chromoso	14.87	6.00
	409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitoch	1.00	1.00
	409228	AI654298	Hs.271695	ESTs, Weakly similar to 2109260A B cell	1.22	1.00
	409234	AI879419	Hs.27206	ESTs	1.00	1.00
20	409268	AA625304	Hs.187579	ESTs	11.90	23.00
	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	1.00	1.00
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	168.91	35.00
	409404	BE220053	Hs.129056	ESTs	1.00	1.00
	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	79.74	96.00
25	409430	R21945	Hs.346735	splicing factor, arginine/serine-rich 5	1.45	2.10
	409446	AI561173	Hs.67688	ESTs	1.00	4.00
	409506	NM_006153	Hs.54589	NCK adaptor protein 1	3.97	28.00
	409522	AA075382		gb:zm87b03.s1 Stratagene ovarian cancer	15.98	141.00
	409582	AA401369	Hs.190721	ESTs	1.00	17.00
30	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	292.12	79.00
	409705	M37762	Hs.56023	brain-derived neurotrophic factor	1.00	82.00
	409719	AI769160	Hs.108681	Homo sapiens brain tumor associated prot	1.00	1.00
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	0.12	18.12
	409744	AW675258	Hs.56265	Homo sapiens mRNA; cDNA DKFZp586P2321 (f	20.75	51.00
35	409757	NM_001898	Hs.123114	cystatin SN	22.46	15.80
	409866	AW502152		gb:U1-HF-BR0p-ajr-f-11-0-U1.r1 NIH_MGC_5	1.00	1.00
	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	1.50	1.09
	409902	AI337658	Hs.156351	ESTs	25.92	50.00
	409935	AW511413	Hs.278025	ESTs	2.63	2.11
40	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	2.17	4.01
	409958	NM_001523	Hs.57697	hyaluronan synthase 1	0.91	2.07
	410001	AB041036	Hs.57771	kallikrein 11	1.04	2.28
	410032	BE065985		gb:RC3-BT0319-120200-014-a09 BT0319 Homo	1.00	58.00
	410037	AB020725	Hs.58009	KIAA0918 protein	1.00	34.00
45	410044	BE566742	Hs.58169	highly expressed in cancer, rich in leuc	1.00	1.00
	410048	W76467	Hs.58218	proline oxidase homolog	1.03	1.44
	410076	T05387	Hs.7991	ESTs	1.12	1.50
	410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	9.89	1.00
	410153	BE311926	Hs.15830	hypothetical protein FLJ12691	1.00	1.00
50	410166	AK001376	Hs.59346	hypothetical protein FLJ10514	1.00	1.00
	410193	AJ132592	Hs.59757	zinc finger protein 281	42.01	51.00
	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	1.72	1.32
	410309	BE043077	Hs.278153	ESTs	1.00	2.00
	410340	AW182833	Hs.112188	hypothetical protein FLJ13149	32.08	75.00
55	410348	AW182663	Hs.95469	ESTs	1.00	1.00
	410407	X66839	Hs.63287	carbonic anhydrase IX	1.40	1.11
	410418	D31382	Hs.63325	transmembrane protease, serine 4	4.30	2.03
	410438	AB037756	Hs.45207	hypothetical protein KIAA1335	1.00	18.00
	410553	AW016824	Hs.255527	hypothetical protein MGC14128	1.34	1.04
60	410555	W27235	Hs.64311	a disintegrin and metalloproteinase doma	23.99	1.41
	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	10.04	1.00
	410681	AW246890	Hs.65425	calbindin 1, (28kD)	10.88	18.92
	410781	AI375672	Hs.165028	ESTs	1.00	57.00
	411027	AF072099	Hs.67846	leukocyte immunoglobulin-like receptor,	1.62	3.78
65	411074	X60435	Hs.68137	adenylate cyclase activating polypeptide	1.00	1.15
	411089	AA456454		cell division cycle 2-like 1 (PITSLRE pr	1.56	1.58
	411152	BE069199		gb:QV3-BT0379-010300-105-g03 BT0379 Homo	1.00	84.00
	411248	AA551538	Hs.334605	Homo sapiens cDNA FLJ14408 fis, clone HE	1.82	1.45
	411252	AB018549	Hs.69328	MD-2 protein	7.32	12.74
70	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-assoc	3.44	2.55
	411365	M76477	Hs.289082	GM2 ganglioside activator protein	1.35	2.02
	411402	BE297855	Hs.69855	NRAS-related gene	1.00	46.00
	411573	AB029000	Hs.70823	KIAA1077 protein	11.40	11.35
	411579	AC005258	Hs.70830	U6 snRNA-associated Sm-like protein LSm7	1.08	1.90
75	411617	AA247994	Hs.90063	neurocalcin delta	1.74	2.57
	411732	AA059325	Hs.71642	guanine nucleotide binding protein (G pr	1.02	1.00
	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	1.34	2.19
	411789	AF245505	Hs.72157	Adican	2.19	2.79
	411800	N39342	Hs.103042	microtubule-associated protein 1B	23.34	34.00
80	411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral oncog	1.00	8.00
	412115	AK001763	Hs.73239	hypothetical protein FLJ10901	2.07	1.64
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	118.48	92.00
	412276	BE262621	Hs.73798	macrophage migration inhibitory factor (1.98	1.49
	412464	T78141	Hs.22826	ESTs, Weakly similar to I55214 salivary	1.16	1.34
85	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	41.52	84.00
	412537	AL031778		nuclear transcription factor Y, alpha	17.90	55.00

	412659	AW753865	Hs.74376	olfactomedin related ER localized protei	14.65	47.00
	412719	AW016610	Hs.816	ESTs	382.46	128.00
	412723	AA648459	Hs.335951	hypothetical protein AF301222	54.90	1.00
5	412811	H06382		ESTs	1.00	11.00
	412817	AL037159	Hs.74619	proteasome (prosome, macropain) 26S subu	1.63	1.42
	412863	AA121673	Hs.59757	zinc finger protein 281	17.63	56.00
	412924	BE018422	Hs.75258	H2A histone family, member Y	1.00	22.00
	413004	T35901	Hs.75117	interleukin enhancer binding factor 2, 4	2.19	2.05
10	413011	AW068115	Hs.821	biglycan	1.22	1.88
	413048	M93221	Hs.75182	mannose receptor, C type 1	0.30	6.23
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	3.43	8.71
	413129	AF292100	Hs.104613	RP42 homolog	4.67	4.77
	413142	M81740	Hs.75212	ornithine decarboxylase 1	1.92	2.59
15	413223	AI732182	Hs.191866	ESTs	5.73	27.00
	413248	T64858	Hs.21433	hypothetical protein DKFZp547J036	0.99	1.06
	413273	U75679	Hs.75257	stem-loop (histone) binding protein	1.00	18.00
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	1.10	1.09
	413281	AA861271	Hs.222024	transcription factor BMAL2	95.94	69.00
20	413364	BE536218	Hs.137516	fidgulin-like 1	1.00	1.00
	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	0.95	2.09
	413409	AI638418	Hs.1440	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	1.00	1.00
	413453	AA129640	Hs.128065	ESTs	1.00	31.00
	413527	BE250788	Hs.179882	hypothetical protein FLJ12443	1.08	1.46
25	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	79.15	114.00
	413573	AI733859	Hs.149089	ESTs	1.00	1.00
	413582	AW295647	Hs.71331	hypothetical protein MGC5350	8.80	10.00
	413597	AW302885	Hs.117183	ESTs	1.00	1.00
30	413690	BE157489		gb:RC1-HT0375-120200-011-e06 HT0375 Homo	1.00	1.00
	413691	AB023173	Hs.75478	ATPase, Class VI, type 11B	3.16	2.32
	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	2.88	9.52
	413753	U17760	Hs.75517	laminin, beta 3 (niclin (125kD), kalinin	144.10	108.00
	413801	M62246	Hs.35406	ESTs, Highly similar to unnamed protein	1.00	17.00
	413833	Z15005	Hs.75573	centromere protein E (312kD)	1.00	1.00
35	413882	AA132973	Hs.184492	ESTs	64.24	148.00
	413926	AA133338	Hs.54310	ESTs	1.00	67.00
	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT	43.42	42.00
	413995	BE048146	Hs.75671	syntaxin 1A (brain)	1.23	1.11
40	414035	Y00630	Hs.75716	serine (or cysteine) proteinase inhibito	2.02	2.51
	414142	AW368397	Hs.334485	Homo sapiens cDNA FLJ14438 fis, clone HE	1.00	102.00
	414180	AI863304	Hs.120905	Homo sapiens cDNA FLJ11448 fis, clone HE	6.92	77.00
	414245	BE148072	Hs.75850	WAS protein family, member 1	1.00	1.00
	414275	AW970254	Hs.889	Charot-Leyden crystal protein	1.00	59.00
45	414317	BE263280	Hs.75888	phosphogluconate dehydrogenase	1.52	1.73
	414334	AA824298	Hs.21331	hypothetical protein FLJ10036	1.78	1.72
	414341	D80004	Hs.75909	KIAA0182 protein	33.90	151.00
	414368	W70171	Hs.75939	uridine monophosphate kinase	171.60	97.00
	414416	AW409985	Hs.76084	hypothetical protein MGC2721	2.32	1.85
	414430	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	226.15	66.00
50	414570	Y00285	Hs.76473	insulin-like growth factor 2 receptor	1.64	1.98
	414618	AI204600	Hs.96978	hypothetical protein MGC10764	1.87	72.00
	414675	R79015	Hs.296281	Interleukin enhancer binding factor 1	1.51	1.39
	414683	S78296	Hs.76888	hypothetical protein MGC12702	43.61	64.00
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	28.63	71.00
55	414711	AI310440	Hs.288735	Homo sapiens cDNA FLJ13522 fis, clone PL	14.86	42.00
	414718	H95348	Hs.107987	ESTs	1.00	5.00
	414732	AW410976	Hs.77152	minichromosome maintenance deficient (S.	1.64	1.44
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitosi	65.01	74.00
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	130.35	121.00
60	414774	X02419	Hs.77274	plasminogen activator, urokinase	2.24	2.19
	414806	D14694	Hs.77329	phosphatidylserine synthase 1	1.63	1.53
	414809	AI434699	Hs.77356	transferrin receptor (p90, CD71)	1.97	2.60
	414812	X72755	Hs.77367	monokine induced by gamma interferon	3.48	10.60
	414825	X06370	Hs.77432	epidermal growth factor receptor (avian	103.22	143.00
65	414839	X63692	Hs.77462	DNA (cytosine-5-)-methyltransferase 1	1.80	1.69
	414883	AA926960		CDC28 protein kinase 1	14.29	10.06
	414907	X90725	Hs.77597	polo (Drosophila)-like kinase	1.95	2.20
	414914	U49844	Hs.77613	ataxia telangiectasia and Rad3 related	3.00	2.90
70	414945	BE076358	Hs.77667	lymphocyte antigen 6 complex, locus E	1.02	1.21
	414972	BE263782	Hs.77695	KIAA0008 gene product	1.00	1.00
	415014	AW954064	Hs.24951	ESTs	1.42	2.84
	415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	1.00	30.00
	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	34.72	107.00
75	415227	AW821113	Hs.72402	ESTs	1.87	49.00
	415238	R37780	Hs.21422	ESTs	1.00	1.00
	415263	AA948033	Hs.130853	ESTs	1.00	1.00
	415295	R41450	Hs.6546	ESTs	1.00	1.00
80	415339	NM_015156	Hs.78398	KIAA0071 protein	51.18	166.00
	415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	30.84	63.00
	415674	BE394784	Hs.78596	proteasome (prosome, macropain) subunit,	1.48	1.39
	415709	AA649850	Hs.278558	ESTs	1.00	1.00
	415735	AA704162	Hs.120811	ESTs, Weakly similar to I38022 hypotheti	1.00	72.00
	415799	AA653718	Hs.225841	DKFZP434D193 protein	6.23	31.00
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	24.30	1.00
85	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	32.51	35.00
	415989	AI267700		ESTs	78.89	1.00

	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin t	1.00	1.00
	416065	BE267931	Hs.78996	proliferating cell nuclear antigen	3.35	2.32
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (39.03	3.00
	416177	AA174069	Hs.187607	ESTs	1.00	9.00
5	416178	AI808527	Hs.192822	serologically defined breast cancer anti	3.83	3.76
	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	3.67	1.00
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	9.70	1.00
	416239	AL038450	Hs.48948	ESTs	83.87	129.00
10	416250	AA581386	Hs.73452	hypothetical protein MGC10791	1.96	2.12
	416322	BE019494	Hs.79217	pyrroline-5-carboxylate reductase 1	2.08	1.73
	416423	H54375	Hs.268921	ESTs	1.00	89.00
	416448	L13210	Hs.79339	lectin, galactoside-binding, soluble, 3	1.28	1.54
	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	27.29	67.00
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	53.29	51.00
15	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	9.96	5.00
	416722	AA354604	Hs.122546	hypothetical protein FLJ23017	3.68	33.00
	416819	U77735	Hs.80205	pim-2 oncogene	1.59	1.84
	416936	N21352	Hs.42987	ESTs, Weakly similar to S21348 probable	1.00	1.00
20	417034	NM_006183	Hs.80962	neurotensin	1.00	1.00
	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	32.95	156.00
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	3.91	4.93
	417218	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	1.00	51.00
	417233	W25005	Hs.24395	small inducible cytokine subfamily B (Cy	3.38	2.05
25	417308	H60720	Hs.81892	KIAA0101 gene product	82.94	25.36
	417315	AI080042	Hs.180450	ribosomal protein S24	106.61	121.00
	417324	AW265494		ESTs	1.20	1.28
	417366	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)	8.97	3.27
	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	2.69	1.82
30	417428	N87579	Hs.278871	gb:LL2030F Human fetal heart, Lambda ZAP	1.00	52.00
	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	304.75	173.00
	417466	AI681547	Hs.59457	hypothetical protein FLJ22127	1.24	1.34
	417512	AI979168	Hs.344096	glycoprotein (transmembrane) nmb	2.14	5.50
	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	2.66	1.68
35	417542	J04129	Hs.82269	progesterone-associated endometrial prote	1.28	1.35
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	42.76	51.00
	417715	AW969587	Hs.86366	ESTs	6.35	2.75
	417720	AA205625	Hs.208067	ESTs	113.31	56.00
	417791	AW965339	Hs.111471	ESTs	39.98	16.00
40	417830	AW504786	Hs.122579	hypothetical protein FLJ10461	2.61	31.00
	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	2.35	2.44
	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	1.52	1.11
	417933	X02308	Hs.82962	thymidylate synthetase	4.74	2.55
	417944	AU077196	Hs.82985	collagen, type V, alpha 2	3.61	5.21
45	417975	AA641836	Hs.30085	hypothetical protein FLJ23186	12.49	38.00
	417991	AA731452	Hs.190008	ESTs	1.00	26.00
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	3.02	2.12
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	187.59	1.00
	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	2.85	2.63
50	418057	NM_012151	Hs.83363	coagulation factor VIII-associated (intr	1.54	1.69
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	6.82	5.22
	418140	BE613836	Hs.83551	microfibrillar-associated protein 2	1.26	1.46
	418203	X54942	Hs.83758	CDC28 protein kinase 2	134.19	144.00
	418207	C14685	Hs.34772	ESTs	1.00	1.00
55	418216	AA662240	Hs.283099	AF15q14 protein	64.66	61.00
	418236	AW994005	Hs.337534	ESTs	18.53	147.00
	418249	H89226	Hs.34892	KIAA1323 protein	30.53	106.00
	418281	U09550	Hs.1154	oviductal glycoprotein 1, 120kD (mucin 9	1.00	3.00
	418283	S79895	Hs.83942	cathepsin K (pseudosclerosis)	3.96	5.16
60	418300	AI433074	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	3.18	2.91
	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	11.96	6.68
	418327	U70370	Hs.84136	paired-like homeodomain transcription fa	9.23	2.22
	418345	AJ001696	Hs.241407	serine (or cysteine) proteinase inhibito	1.00	1.00
	418379	AA218940	Hs.137516	fidgetin-like 1	21.68	44.00
65	418397	NM_001269	Hs.84746	chromosome condensation 1	1.00	8.00
	418403	D86978	Hs.84790	KIAA0225 protein	16.91	18.98
	418462	BE001596	Hs.85266	integrin, beta 4	1.56	1.16
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	3.22	2.38
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	2.66	2.22
70	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	2.04	2.21
	418538	BE244323	Hs.85951	exportin, tRNA (nuclear export receptor	1.33	37.00
	418543	NM_005329	Hs.85962	hyaluronan synthase 3	1.04	1.23
	418574	N28754		M-phase phosphoprotein 9	48.60	85.00
	418592	X99226	Hs.284153	Fanconi anemia, complementation group A	18.24	26.00
75	418641	BE243136	Hs.86947	a disintegrin and metalloproteinase doma	1.19	1.41
	418661	NM_001949	Hs.1189	E2F transcription factor 3	29.05	43.00
	418663	AK001100	Hs.41690	desmocollin 3	112.17	19.00
	418678	NM_001327	Hs.87225	cancer/testis antigen	1.18	1.10
	418686	Z36830	Hs.87268	annexin A8	1.54	1.98
80	418689	AI360883	Hs.274448	hypothetical protein FLJ11029	1.19	1.04
	418712	Z42183		gb:HSC0BF041 normalized infant brain cDN	1.00	12.00
	418727	AA227609	Hs.94834	ESTs	1.00	49.00
	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	49.85	1.00
	418819	AA228776	Hs.191721	ESTs	1.00	140.00
85	418830	BE513731	Hs.88959	hypothetical protein MGC4816	20.97	23.00
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	57.09	35.00

	418971	AA360392	Hs.87113	ESTs	1.00	12.00
	418973	AA233056	Hs.191518	ESTs	4.89	28.00
	419078	M93119	Hs.89584	insulinoma-associated 1	1.00	10.00
5	419079	AW014836	Hs.18844	ESTs	1.09	1.98
	419080	AW150835	Hs.18878	hypothetical protein FLJ21620	2.06	1.68
	419088	AI538323	Hs.52620	integrin, beta 8	15.60	51.00
	419092	J05581	Hs.89603	mucin 1, transmembrane	1.11	1.83
	419121	AA374372	Hs.89626	parathyroid hormone-like hormone	1.00	1.00
10	419171	NM_002846	Hs.89655	protein tyrosine phosphatase, receptor t	1.10	1.14
	419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	1.00	1.00
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	3.18	2.43
	419288	AA256106	Hs.87507	ESTs	1.00	34.00
	419335	AW960146	Hs.284137	hypothetical protein FLJ12888	1.00	8.00
15	419354	M62839	Hs.1252	apolipoprotein H (beta-2-glycoprotein I)	22.63	54.00
	419359	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	2.50	1.98
	419423	D26488	Hs.90315	KIAA0007 protein	1.00	7.00
	419443	D62703		gb:HUM316G10B Clontech human aorta polyA	1.00	12.00
	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	1.64	1.84
20	419474	AW968619	Hs.155849	ESTs	13.63	62.00
	419485	AA489023	Hs.99807	ESTs, Weakly similar to unnamed protein	4.27	2.26
	419488	AA316241	Hs.90691	nucleophosmin/nucleoplasm 3	3.66	3.63
	419502	AU076704		fibrinogen, A alpha polypeptide	13.05	115.00
	419539	AF070590	Hs.90869	Homo sapiens clones 24622 and 24623 mRNA	74.60	117.00
25	419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	1.47	4.98
	419569	AI971651	Hs.91143	jagged 1 (Alagille syndrome)	1.00	4.00
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	94.30	94.00
	419703	AI793257	Hs.128151	ESTs	15.26	50.00
	419721	NM_001650	Hs.288650	aquaporin 4	1.00	191.00
30	419729	AA586442	Hs.21411	gb:nc53a03.s1 NCL_CGAP_SS1 Homo sapiens	1.00	59.00
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	2.02	1.08
	419745	AF042001	Hs.93005	slug (chicken homolog), zinc finger prot	1.00	1.00
	419752	AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z	29.87	77.00
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	50.99	214.00
35	419936	AI792788		gb:ol91d05.y5 NCL_CGAP_Kid5 Homo sapiens	1.00	1.00
	419937	AB040959	Hs.93836	DKFZP434N014 protein	1.64	2.47
	419983	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f	15.72	94.00
	420005	AW271106	Hs.133294	ESTs	3.15	1.43
	420047	AI478658	Hs.94631	brefeldin A-inhibited guanine nucleotide	12.45	39.00
40	420058	AK001423	Hs.94694	Homo sapiens cDNA FLJ10561 fis, clone NT	1.00	117.00
	420162	BE378432	Hs.95577	cyclin-dependent kinase 4	1.43	1.21
	420251	AW374968	Hs.348112	Human DNA sequence from clone RP5-1103G7	2.35	3.23
	420259	AF004884	Hs.96253	calcium channel, voltage-dependent, P/Q	0.77	1.15
	420281	AI623693	Hs.323494	ESTs	45.04	54.00
45	420309	AW043637	Hs.21766	ESTs, Weakly similar to ALU5_HUMAN ALU S	49.22	31.00
	420332	NM_001756	Hs.1305	serine (or cysteine) proteinase inhibito	0.05	2.82
	420380	AA640891	Hs.102406	ESTs	0.99	2.74
	420462	AF050147	Hs.97932	chondromodulin 1 precursor	1.00	1.00
	420520	AK001978	Hs.98510	similar to rab11-binding protein	49.74	133.00
50	420552	AK000492	Hs.98806	hypothetical protein	94.65	88.00
	420560	AW207748	Hs.59115	ESTs	1.00	17.00
	420610	AI683183	Hs.99348	distal-less homeo box 5	1.00	13.00
	420689	H79979	Hs.88678	ESTs	50.09	95.00
	420721	AA927802	Hs.159471	ZAP3 protein	1.00	31.00
55	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	1.00	48.00
	420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	3.04	1.25
	420900	AL045633	Hs.44269	ESTs	2.24	7.00
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	1.00	8.00
	421002	AF116030	Hs.100932	transcription factor 17	1.00	27.00
60	421027	AA761198	Hs.55254	ESTs	2.87	38.00
	421037	AI684808	Hs.197653	ESTs	1.00	46.00
	421041	N36914	Hs.14691	ESTs, Moderately similar to I38022 hypot	1.00	98.00
	421073	NM_004689	Hs.101448	metastasis associated 1	1.34	1.46
	421110	AJ250717	Hs.1355	cathepsin E	119.47	427.00
65	421133	AA401369	Hs.190721	ESTs	1.10	17.00
	421150	AI913562	Hs.189902	ESTs	1.45	1.63
	421155	H87879	Hs.102267	lysyl oxidase	1.00	15.00
	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	1.37	1.10
	421316	AA287203	Hs.324728	SMA5	1.00	21.00
70	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	1.92	3.94
	421451	AA291377	Hs.50831	ESTs	5.89	14.00
	421474	U76362	Hs.104637	solute carrier family 1 (glutamate trans	1.46	1.76
	421506	BE302796	Hs.105097	thymidine kinase 1, soluble	1.56	1.08
	421508	NM_004833	Hs.105115	absent in melanoma 2	5.11	5.23
75	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase 1, I	1.00	3.00
	421524	AA312082	Hs.105445	GDNF family receptor alpha 1	2.63	10.58
	421526	AL080121	Hs.105460	DKFZP564O0823 protein	1.46	1.88
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	30.21	50.32
	421574	AJ000152	Hs.105924	defensin, beta 2	1.67	1.74
80	421582	AI910275		trefoil factor 1 (breast cancer, estroge	1.23	1.00
	421633	AF121860	Hs.106260	sorting nexin 10	1.00	116.00
	421659	NM_014459	Hs.106511	protocadherin 17	0.05	6.33
	421677	H64092	Hs.38282	ESTs	1.31	1.42
	421753	BE314828	Hs.107911	ATP-binding cassette, sub-family B (MDR/	1.41	1.20
85	421773	W69233	Hs.112457	ESTs	1.12	1.14
	421777	BE562088	Hs.108196	HSPC037 protein	1.97	1.29

	421800	AA298151	Hs.222969	ESTs	1.03	1.30
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	1.88	1.59
	421896	N62293	Hs.45107	ESTs	11.84	22.80
5	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	45.89	90.00
	421931	NM_000814	Hs.1440	gamma-aminobutyric acid (GABA) A recepto	1.13	1.49
	421948	L42583	Hs.334309	keratin 6A	51.83	20.25
	421975	AW961017	Hs.6459	hypothetical protein FLJ11856	1.17	1.15
	422026	U80736	Hs.110826	trinucleotide repeat containing 9	1.00	52.00
10	422094	AF129535	Hs.272027	F-box only protein 5	67.61	62.00
	422095	AI868872	Hs.282804	hypothetical protein FLJ22704	4.37	2.34
	422109	S73265	Hs.1473	gastrin-releasing peptide	4.18	95.50
	422128	AW881145		gb:QV0-OT0033-010400-182-a07 OT0033 Homo	40.89	71.00
	422129	AU076635	Hs.1478	serine (or cysteine) proteinase inhibito	1.13	1.38
	422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	41.59	96.00
15	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	2.37	1.10
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	3.29	1.68
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	4.93	5.73
	422282	AF019225	Hs.114309	apolipoprotein L	1.49	1.71
20	422283	AW411307	Hs.114311	CD45 (cell division cycle 45, S.cerevis	25.99	10.91
	422310	AA316622	Hs.98370	cytochrome P450, subfamily IIS, polypept	1.54	1.41
	422311	AF073515	Hs.114948	cytokine receptor-like factor 1	1.15	1.78
	422330	D30783	Hs.115263	epiregulin	1.00	112.00
	422364	AF067800	Hs.115515	C-type (calcium dependent, carbohydrate-	9.39	60.00
25	422406	AF025441	Hs.116206	Opa-interacting protein 5	18.33	53.00
	422424	AI186431	Hs.296638	prostate differentiation factor	1.71	3.21
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	47.53	32.00
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	73.68	35.54
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	173.97	26.00
30	422515	AW500470	Hs.117950	multifunctional polypeptide similar to S	4.68	2.92
	422656	AI870435	Hs.1569	LIM homeobox protein 2	1.00	1.00
	422737	M26939	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl	3.89	4.55
	422756	AA441787	Hs.119689	glycoprotein hormones, alpha polypeptide	1.05	1.46
	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	3.88	1.53
35	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	99.56	53.00
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	1.69	3.17
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	70.46	61.00
	422966	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	77.74	3.00
	422960	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)	5.88	8.55
40	422963	AA401369	Hs.190721	ESTs	171.41	17.00
	422976	AU076657	Hs.1600	chaperonin containing TCP1, subunit 5 (e	2.12	1.62
	422981	AF026445	Hs.122752	TATA box binding protein (TBP)-associate	10.49	35.00
	422986	AA319777	Hs.221974	ESTs	12.40	32.47
	423034	AL119930		gb:DKFZp761A092_r1 761 (synonym: hamy2)	16.41	60.00
45	423049	X59373	Hs.188023	ESTs, Moderately similar to HXDA_HUMAN H	1.00	1.00
	423081	AF262992	Hs.123159	sperm associated antigen 4	1.82	2.96
	423184	NM_004428	Hs.1624	ephrin-A1	1.14	1.53
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	2.14	1.69
	423248	AA380177	Hs.125845	ribulose-5-phosphate-3-epimerase	7.18	14.00
50	423309	BE006775	Hs.126782	sushi-repeat protein	21.90	64.00
	423361	AW170055	Hs.47628	ESTs	1.00	1.00
	423453	AW450737	Hs.128791	CGI-09 protein	55.52	66.00
	423511	AF036329	Hs.129715	gonadotropin-releasing hormone 2	0.88	1.17
	423516	AB007933	Hs.129729	ligand of neuronal nitric oxide synthase	1.76	5.40
55	423551	AA327598	Hs.233785	ESTs	3.54	4.33
	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	1.00	50.00
	423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	38.88	70.00
	423624	AI807408	Hs.166368	ESTs	1.00	67.00
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	76.02	1.00
60	423642	AW452650	Hs.167148	hypothetical protein MGC13204	19.14	58.00
	423662	AA642452	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro	3.61	13.57
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	240.73	40.00
	423698	AA329796	Hs.1098	DKFZp434J1813 protein	1.00	59.00
	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	4.20	1.00
65	423761	NM_006194	Hs.132576	paired box gene 9	1.00	1.00
	423787	AJ295745	Hs.236204	nuclear pore complex protein	7.18	6.64
	423816	AF151064		hypothetical protein	1.00	44.00
	423826	U20325	Hs.1707	cocaine- and amphetamine-regulated trans	1.00	1.00
	423849	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	1.00	1.00
70	423887	AL080207	Hs.134585	DKFZP434G232 protein	1.00	1.00
	423934	U89995	Hs.159234	forkhead box E1 (thyroid transcription f	31.33	31.00
	423954	AW753164	Hs.288604	KIAA1632 protein	5.81	10.87
	423961	D13666	Hs.136348	osteoblast specific factor 2 (fasciclin	3.55	3.30
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	233.42	68.00
75	424016	AW163729	Hs.6140	hypothetical protein MGC15730	0.93	1.01
	424028	AF055084	Hs.153692	Homo sapiens cDNA FLJ14354 fis, clone Y7	21.30	52.00
	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	1.00	1.00
	424086	AI351010	Hs.102267	lysyl oxidase	21.91	70.00
	424098	AF077374	Hs.139322	small proline-rich protein 3	137.82	54.00
80	424120	T80579	Hs.290270	ESTs	1.00	1.00
	424165	AW582904	Hs.142255	islet amyloid polypeptide	1.00	34.00
	424200	AA337221		gb:EST41944 Endometrial tumor Homo sapie	13.06	48.00
	424279	L29306	Hs.171814	tryptophan hydroxylase (tryptophan 5-mon	1.00	1.00
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	164.58	87.00
	424326	NM_014479	Hs.145296	disintegrin protease	53.72	302.00
85	424340	AA339036	Hs.7033	ESTs	0.88	1.15

	424351	BE622117	Hs.145567	hypothetical protein	0.93	1.03
	424364	AW383226	Hs.201189	ESTs, Weakly similar to G01763 atrophin-	7.02	3.24
	424381	AA285249	Hs.146329	protein kinase Chk2	95.55	92.00
5	424411	NM_005209	Hs.146549	crystallin, beta A2	1.63	3.25
	424420	BE614743	Hs.146688	prostaglandin E synthase	1.63	1.33
	424441	X14850	Hs.147097	H2A histone family, member X	1.82	1.29
	424502	AF242388	Hs.149585	lengsin	1.00	1.00
	424503	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor,	1.02	2.24
10	424513	BE385864	Hs.149894	mitochondrial translational initiation f	1.00	17.00
	424539	L02911	Hs.150402	Activin A receptor, type I (ACVR1) (ALK	32.46	108.00
	424568	AF005418	Hs.150595	cytochrome P450, subfamily XXVIA, polype	3.40	2.58
	424602	AK002055	Hs.151046	hypothetical protein FLJ11193	31.87	25.00
	424629	M90656	Hs.151393	glutamate-cysteine ligase, catalytic sub	3.58	2.37
15	424645	NM_014682	Hs.151449	KIAA0535 gene product	1.00	1.00
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.12	2.23
	424717	AW992292	Hs.152213	wingless-type MMTV integration site fami	1.00	1.00
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	56.19	12.00
	424840	D79987	Hs.153479	extra spindle poles, S. cerevisiae, homo	2.65	1.30
20	424867	AI024860	Hs.153591	Not56 (D. melanogaster)-like protein	1.23	1.05
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	21.35	1.00
	424979	D87989	Hs.154073	UDP-galactose transporter related	1.36	1.35
	424999	AW953120		gb:EST365190 MAGE resequences, MAGB Homo	1.24	1.41
	425048	H05468	Hs.164502	ESTs	1.00	11.00
25	425057	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol	7.46	87.00
	425081	X74794	Hs.154443	minichromosome maintenance deficient (S.	2.52	3.82
	425118	AU076611	Hs.154672	methylene tetrahydrofolate dehydrogenase	4.84	4.03
	425159	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspart	3.62	2.73
	425202	AW962282	Hs.152049	ESTs, Weakly similar to I38022 hypotheti	1.00	53.00
30	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	100.77	44.00
	425236	AW067800	Hs.155223	stanniocalcin 2	3.30	2.90
	425245	AI751768	Hs.155314	KIAA0095 gene product	1.91	2.32
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	1.41	1.49
	425266	J00077	Hs.155421	alpha-fetoprotein	1.00	68.00
35	425274	BE281191	Hs.155462	minichromosome maintenance deficient (mi	1.97	1.63
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	141.49	123.00
	425349	AA425234	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	1.00	84.00
	425371	D49441	Hs.155981	mesothelin	0.87	1.59
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	14.90	5.76
40	425420	BE536911	Hs.234545	hypothetical protein NUF2R	1.00	1.00
	425424	NM_004954	Hs.157199	ELKL motif kinase	10.58	9.74
	425483	AF231022	Hs.158159	FAT tumor suppressor (Drosophila) homolo	1.74	1.40
	425566	AW162943	Hs.250618	UL16 binding protein 2	1.49	1.14
	425580	L11144	Hs.1907	galanin	53.29	233.00
45	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	33.45	1.00
	425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	1.00	55.00
	425695	NM_005401	Hs.159238	protein tyrosine phosphatase, non-recept	1.00	10.00
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	1.00	41.00
	425776	U25128	Hs.159499	parathyroid hormone receptor 2	1.00	48.00
50	425810	AI923627	Hs.31903	ESTs	27.39	98.00
	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	1.99	1.58
	425849	AI077288	Hs.296323	serum/glucocorticoid regulated kinase	71.16	3.42
	425852	AK001504	Hs.159561	death receptor 6, TNF superfamily member	1.35	1.34
	426067	AA401369	Hs.190721	ESTs	1.01	17.00
55	426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	26.26	47.00
	426215	AW067800	Hs.155223	stanniocalcin 2	1.91	2.90
	426227	U67058	Hs.154299	Human proteinase activated receptor-2 mR	22.40	25.00
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	1.00	1.00
	426283	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	91.39	229.00
60	426329	AL389951	Hs.271623	nucleoporin 50kD	4.34	4.08
	426427	M86699	Hs.169840	TTK protein kinase	7.02	1.00
	426432	AF001601	Hs.169857	paraoxonase 2	1.16	1.68
	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu	2.59	1.71
	426459	AF151812	Hs.169992	hypothetical 43.2 Kd protein	1.56	1.66
65	426471	M22440	Hs.170009	transforming growth factor, alpha	20.60	26.00
	426496	D31765	Hs.170114	KIAA0061 protein	9.81	22.00
	426501	AA401369	Hs.190721	ESTs	19.23	17.00
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	103.74	41.00
	426536	AI949749	Hs.44441	ESTs	4.65	23.00
70	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	1.00	43.00
	426582	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	160.06	8.00
	426691	NM_006201	Hs.171834	PCTAIRE protein kinase 1	1.51	1.35
	426746	J03626	Hs.2057	uridine monophosphate synthetase (orotat	2.13	1.68
	426752	X69490	Hs.172004	titin	0.02	5.14
75	426784	U03749	Hs.172216	chromogranin A (parathyroid secretory pr	1.72	1.71
	426807	AA385315	Hs.156682	ESTs	1.30	1.64
	426812	AF105365	Hs.172613	solute carrier family 12 (potassium/chlo	1.47	1.53
	426814	AF036943	Hs.172619	myelin transcription factor 1-like	1.00	1.00
	426831	BE296216	Hs.172673	S-adenosylhomocysteine hydrolase	1.51	1.25
80	426897	AA401369	Hs.190721	ESTs	141.56	17.00
	426925	NM_001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fis, clone H	32.61	38.00
	426935	NM_000088	Hs.172928	collagen, type I, alpha 1	2.65	3.16
	426964	AA393739	Hs.287416	Homo sapiens cDNA FLJ11439 fis, clone HE	1.97	3.49
	426966	AI493134		sclerostin	1.00	1.00
85	426991	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	3.39	2.28
	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	4.24	17.00

	427239	BE270447	Hs.174070	ubiquitin carrier protein	1.58	1.05
	427260	AA663848		gb:ae70b06.s1 Stratagene schizo brain S1	1.34	1.60
	427281	AA906147	Hs.102869	ESTs	1.00	66.00
	427335	AA448542	Hs.251677	G antigen 7B	51.83	4.00
5	427354	T57896	Hs.191095	ESTs	1.17	1.95
	427356	AW023482	Hs.97849	ESTs	7.31	41.00
	427376	AA401533	Hs.19440	ESTs	1.00	57.00
	427383	NM_005411	Hs.177582	surfactant, pulmonary-associated protein	0.42	1.32
10	427427	AF077345	Hs.177936	lectin, superfamily member 1 (cartilage- SPANX family, member C	1.00	20.00
	427441	AA412605	Hs.343879	glutamate receptor, metabotropic 4	1.00	1.00
	427445	X80818	Hs.178078	26S proteasome-associated pad1 homolog	0.97	1.03
	427505	AA361562	Hs.178761	small nuclear RNA activating complex, po	4.60	4.04
	427510	Z47542	Hs.179312	minichromosome maintenance deficient (S.	22.00	45.00
15	427528	AU077143	Hs.179565	hypothetical protein FLJ23188	97.45	92.00
	427546	AA188763	Hs.36793	ESTs	1.50	3.24
	427562	R56424	Hs.26534	collagen, type X, alpha 1 (Schmid metaph	6.81	40.00
	427585	D31152	Hs.179729	Homo sapiens cDNA: FLJ23228 fis, clone C	69.91	62.00
	427660	AI741320	Hs.114121	calmodulin-like skin protein	2.70	49.00
20	427666	AI791495	Hs.180142	hypothetical protein FLJ14904	1.37	1.88
	427668	AA298760	Hs.180191	FGFR1 oncogene partner	29.55	67.00
	427677	NM_007045	Hs.180296	nuclear autoantigenic sperm protein (his	3.52	2.63
	427711	AA411101	Hs.243886	solute carrier family 25 (mitochondrial	7.41	34.00
	427719	M31659	Hs.180408	ESTs	15.84	70.00
25	427722	AI393122	Hs.134726	hypothetical protein FLJ20116	7.03	4.52
	427747	AW411425	Hs.180479	serine/threonine kinase 12	2.92	1.74
	427912	AL022310	Hs.181097	tumor necrosis factor (ligand) superfam	1.76	1.26
	427961	AW293165	Hs.143134	ESTs	9.63	59.00
	428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	41.97	118.00
30	428023	AL038843		Homo sapiens cDNA: FLJ23602 fis, clone L	23.82	1.00
	428046	AW812795	Hs.337534	ESTs, Moderately similar to I38022 hypot	1.40	1.33
	428093	AW594506	Hs.104830	ESTs	96.28	167.00
	428098	AU077258	Hs.182429	protein disulfide isomerase-related prot	1.25	1.29
35	428129	AI244311	Hs.26912	ESTs	1.86	1.60
	428169	AI928984	Hs.182793	golgi phosphoprotein 2	1.00	42.00
	428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT	2.76	2.11
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	1.00	1.00
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	85.59	181.00
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	8.57	21.64
40	428434	AI909935	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	7.77	15.90
	428450	NM_014791	Hs.184339	KIAA0175 gene product	0.58	1.43
	428471	X57348	Hs.184510	stratifin	237.53	204.00
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	6.00	4.60
45	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	56.54	16.00
	428505	AL035461	Hs.2281	chromogranin B (secretogranin 1)	3.53	2.15
	428532	AF157326	Hs.184786	TBP-interacting protein	1.00	1.00
	428645	AA431400	Hs.98729	ESTs, Weakly similar to 2017205A dihydro	1.00	58.00
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	1.00	16.00
50	428698	AA852773	Hs.334838	KIAA1866 protein	1.00	1.00
	428728	NM_016625	Hs.191381	hypothetical protein	187.37	255.00
	428748	AW593206	Hs.98785	Ksp37 protein	47.24	80.00
	428758	AA433988	Hs.98502	hypothetical protein FLJ14303	1.00	87.00
	428771	AB028992	Hs.193143	KIAA1069 protein	1.06	1.13
55	428801	AW277121	Hs.254881	ESTs	1.98	92.00
	428810	AF068236	Hs.193788	nitric oxide synthase 2A (inducible, hep	1.67	6.15
	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	1.03	1.27
	428845	AL157579	Hs.153610	KIAA0751 gene product	124.17	43.00
	428959	AF100779	Hs.194680	WNT1 inducible signaling pathway protein	1.00	1.00
60	428969	AF120274	Hs.194689	artemin	15.16	27.00
	429038	AL023513	Hs.194766	seizure related gene 6 (mouse)-like	1.36	1.24
	429065	AI753247	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	0.97	3.31
	429164	AI688663	Hs.116586	ESTs	6.82	16.47
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	19.08	67.00
65	429183	AB014604	Hs.197955	KIAA0704 protein	16.18	105.00
	429201	X03178	Hs.198246	group-specific component (vitamin D bind	79.72	104.00
	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	1.00	1.00
	429220	AW207206		ESTs	1.33	1.09
	429228	AI553633	Hs.326447	ESTs	1.00	7.00
70	429259	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	39.47	29.25
	429263	AA019004	Hs.198396	ATP-binding cassette, sub-family A (ABC1	2.01	1.18
	429276	AF056085	Hs.198612	G protein-coupled receptor 51	1.07	1.00
	429359	W00482	Hs.2399	matrix metalloproteinase 14 (membrane-in	3.70	142.00
	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	1.30	1.94
75	429413	NM_014058	Hs.201877	DESC1 protein	94.09	86.00
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	41.91	10.00
	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	12.19	1.00
	429538	BE182592	Hs.11261	small proline-rich protein 2A	1.61	1.08
	429547	AA401369	Hs.190721	ESTs	4.43	2.90
	429551	AW450624	Hs.220931	ESTs	1.06	17.00
80	429563	BE619413	Hs.2437	eukaryotic translation initiation factor	2.89	65.00
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	1.49	1.37
	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	61.86	100.00
	429612	AF062649	Hs.252587	pituitary tumor-transforming 1	1.59	1.69
	429616	AI982722	Hs.120845	ESTs	2.78	1.74
85	429656	X05608	Hs.211584	neurofilament, light polypeptide (68kD)	1.00	1.00

5	429663	M68874	Hs.211587	phospholipase A2, group IVA (cytosolic,	69.95	104.00
	429736	AF125304	Hs.212680	tumor necrosis factor receptor superfam	1.25	1.21
	429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain	1.00	7.00
	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	11.80	1.00
	429918	AW873986	Hs.119383	ESTs	1.00	78.00
10	429978	AA249027		ribosomal protein S6	1.98	3.09
	429986	AF092047	Hs.227277	sine oculis homeobox (Drosophila) homolo	1.00	48.00
	430044	AA464510	Hs.152812	ESTs	69.27	59.00
	430114	AA847744	Hs.99640	ESTs	1.00	1.00
	430134	BE380149	Hs.105223	ESTs, Weakly similar to T33188 hypotheti	1.00	51.00
15	430147	R60704	Hs.234434	hairly/enhancer-of-split related with YRP	1.10	2.22
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	1.00	127.00
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	3.80	1.47
	430300	U60805	Hs.238648	oncostatin M receptor	1.00	35.00
	430315	NM_004293	Hs.239147	guanine deaminase	92.31	28.00
20	430337	M36707	Hs.239600	calmodulin-like 3	1.18	1.08
	430378	Z29572	Hs.2556	tumor necrosis factor receptor superfam	5.28	66.00
	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	16.76	38.00
	430393	BE185030	Hs.241305	estrogen-responsive B box protein	1.63	1.50
	430439	AL133561		DKFZP434B061 protein	1.00	1.00
25	430451	AA836472	Hs.297939	cathepsin B	1.64	2.12
	430454	AW469011	Hs.105635	ESTs	63.35	44.00
	430466	AF052573	Hs.241517	polymerase (DNA directed), theta	2.47	1.91
	430481	AA479678	Hs.203269	ESTs, Moderately similar to ALU8_HUMAN A	1.00	31.00
	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	12.28	41.00
30	430508	AI015435	Hs.104637	ESTs	4.75	7.27
	430533	AA480895	Hs.57749	ESTs, Weakly similar to T17288 hypotheti	1.00	1.00
	430563	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	1.00	1.59
	430677	Z26317	Hs.94560	desmoglein 2	1.72	1.30
	430678	AA401369	Hs.190721	ESTs	0.90	17.00
35	430686	NM_001942	Hs.2633	desmoglein 1	1.00	1.00
	430788	AI742925	Hs.7179	ESTs, Weakly similar to 2004399A chromos	1.62	1.84
	430890	X54232	Hs.2699	glypican 1	1.58	1.40
	430935	AW072916		zinc finger protein 131 (clone pHZ-10)	90.28	132.00
	430985	AA490232	Hs.27323	ESTs, Weakly similar to I78885 serine/th	0.94	1.28
40	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	60.25	28.00
	431089	BE041395		ESTs, Weakly similar to unknown protein	23.32	941.00
	431092	AI332764	Hs.125757	ESTs	13.46	63.00
	431124	AF284221	Hs.59506	doublesex and mab-3 related transcriptio	49.43	62.00
	431164	AA493650	Hs.94367	Homo sapiens cDNA: FLJ23494 fis, clone L	0.44	2.20
45	431211	M66849	Hs.323733	gap junction protein, beta 2, 26kD (conn	182.26	101.00
	431221	AW207837	Hs.286145	SRB7 (suppressor of RNA polymerase B, ye	4.15	13.97
	431277	AA501806	Hs.345824	ESTs	1.00	86.00
	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	40.55	200.00
	431342	AW971018	Hs.21659	ESTs	1.00	53.00
50	431384	BE158000	Hs.285026	gb:MR2-HT0377-150200-202-e03 HT0377 Homo	0.94	1.14
	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	1.30	1.25
	431494	AA991355	Hs.298312	hypothetical protein DKFZp434A1315	3.90	26.00
	431515	NM_012152	Hs.258583	endothelial differentiation, lysophospha	1.41	1.87
	431548	AI834273	Hs.9711	novel protein	5.66	15.00
55	431630	NM_002204	Hs.265829	integrin, alpha 3 (antigen CD49C, alpha	0.99	1.44
	431745	AW972448	Hs.163425	ESTs	0.99	3.51
	431770	BE221880	Hs.268555	5'-3' exoribonuclease 2	67.12	91.00
	431830	Y16645	Hs.271387	small inducible cytokine subfamily A (Cy	3.36	4.71
	431846	BE019924	Hs.271580	uropalakin 1B	4.49	2.51
60	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	2.20	3.32
	431934	AB031481	Hs.272214	STG protein	1.01	1.04
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	51.17	46.35
	432006	AL137382	Hs.272320	Homo sapiens mRNA; cDNA DKFZp434L1226 (f	0.94	1.65
	432023	R43020	Hs.236223	EST	0.94	47.00
65	432201	AI538613	Hs.298241	Transmembrane protease, serine 3	1.10	2.24
	432210	AI567421	Hs.273330	Homo sapiens, clone IMAGE:3544662, mRNA,	1.42	1.45
	432226	AW182766	Hs.273558	phosphate cytidyltransferase 1, cholin	1.00	1.00
	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	18.67	1.00
	432265	BE382679	Hs.285753	SCG10-like-protein	1.09	1.21
70	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	40.98	58.00
	432365	AK001106	Hs.274419	hypothetical protein FLJ10244	1.00	214.00
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	157.34	37.00
	432375	BE536069	Hs.2962	S100 calcium-binding protein P	1.65	1.06
	432407	AA221036		gb:zr03f12.r1 Stratagene NT2 neuronal pr	73.71	75.00
75	432441	AW292425	Hs.163484	ESTs	56.35	72.00
	432489	AI804855	Hs.207530	ESTs	1.00	24.00
	432543	AA552690	Hs.152423	Homo sapiens cDNA: FLJ21274 fis, clone C	137.72	98.00
	432552	AI537170	Hs.173725	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.00	31.00
	432583	AW023624	Hs.162282	potassium channel TASK-4; potassium chan	0.27	35.18
80	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	2.87	6.22
	432625	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	26.63	56.00
	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	1.92	5.29
	432677	NM_004482	Hs.278611	UDP-N-acetyl-alpha-D-galactosamine:polyp	1.00	48.00
	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	45.13	31.00
85	432753	NM_014075	Hs.336938	Homo sapiens PRO0593 mRNA, complete cds	1.00	68.00
	432788	AA521091	Hs.178499	Homo sapiens cDNA: FLJ23117 fis, clone L	2.69	3.67
	432842	AW674093	Hs.334822	hypothetical protein MGC4485	1.22	1.34
	432867	AW016936	Hs.233364	ESTs	1.00	1.00
	432917	NM_014125	Hs.241517	PRO0327 protein	10.25	6.62

	432920	U37689	Hs.3128	polymerase (RNA) II (DNA directed) polyp	1.44	1.30
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	154.79	85.64
	433023	AW864793	Hs.87409	thrombospondin 1	20.96	100.00
5	433042	AW193534	Hs.281895	Homo sapiens cDNA FLJ11660 fis, clone HE	1.00	10.00
	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	1.20	1.09
	433159	AB035898	Hs.150587	kinesin-like protein 2	13.82	39.00
	433183	AF231338	Hs.222024	transcription factor BMAL2	1.00	69.00
	433258	AA622788	Hs.203613	ESTs, Weakly similar to ALUB_HUMAN !!!!	1.00	1.25
10	433409	AI278802	Hs.25661	ESTs	44.81	117.00
	433437	U20536	Hs.3280	caspase 6, apoptosis-related cysteine pr	70.39	105.00
	433485	AI493076	Hs.201967	aldo-keto reductase family 1, member C2	11.55	2.00
	433537	AI733692	Hs.112488	ESTs	8.66	55.00
	433547	W04978	Hs.303023	beta tubulin 1, class VI	25.16	83.00
15	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	1.00	19.00
	433647	AA603367	Hs.222294	ESTs	20.30	49.00
	433658	L03678	Hs.155110	immunoglobulin kappa constant	5.92	10.03
	433800	AI094221	Hs.135150	lung type-I cell membrane-associated gly	2.29	2.22
	433819	AW511097	Hs.112765	ESTs	3.71	8.00
20	433862	D86960	Hs.3610	KIAA0205 gene product	62.08	104.00
	433980	AA137152	Hs.286049	phosphoserine aminotransferase	108.91	47.00
	434088	AF116677	Hs.249270	hypothetical protein PRO1966	1.00	1.00
	434094	AA305599	Hs.238205	hypothetical protein PRO2013	121.27	87.00
	434105	AW952124	Hs.13094	presenilins associated rhomboid-like pro	1.22	1.23
25	434217	AW014795	Hs.23349	ESTs	14.11	57.00
	434340	AI193043	Hs.128685	ESTs, Weakly similar to T17226 hypotheti	2.10	2.56
	434360	AA401369	Hs.190721	ESTs	40.98	17.00
	434414	AI798376		gb:tr34b07.x1 NCL_CGAP_Ov23 Homo sapiens	1.48	1.56
	434424	AI811202	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	1.00	64.00
30	434467	BE552368	Hs.231853	Homo sapiens cDNA FLJ13445 fis, clone PL	54.91	85.00
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	2.46	2.00
	434627	AI221894	Hs.39311	ESTs	1.00	1.00
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	1.00	23.00
	434769	AA648884	Hs.134278	Homo sapiens cDNA FLJ12676 fis, clone NT	7.08	56.00
35	434792	AA649253	Hs.132458	ESTs	8.52	44.00
	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	11.33	1.00
	434828	D90070	Hs.96	phorbol-12-myristate-13-acetate-induced	1.00	1.00
	434876	AF160477	Hs.61460	Ig superfamily receptor LNIR	1.25	1.29
	434891	AA814309	Hs.123583	ESTs	1.00	6.00
40	434928	AW015595	Hs.4267	Homo sapiens clones 24714 and 24715 mRNA	1.00	1.00
	435013	H91923	Hs.110024	Target CAT	1.26	1.10
	435066	BE261750	Hs.4747	dyskeratosis congenita 1, dyskerin	1.69	1.37
	435087	AW975241	Hs.23567	ESTs	1.00	1.00
	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	2.90	1.93
45	435159	AA668879	Hs.116649	ESTs	1.00	1.00
	435205	X54136	Hs.181125	immunoglobulin lambda locus	1.02	1.46
	435232	NM_001262	Hs.4854	cyclin-dependent kinase inhibitor 2C (p1	2.04	2.70
	435304	H10709	Hs.269524	ESTs	27.58	139.00
	435313	AI769400	Hs.189729	ESTs	1.00	14.00
50	435505	AF200492	Hs.211238	interleukin-1 homolog 1	1.00	38.00
	435509	AI458679	Hs.181915	ESTs	1.00	1.00
	435525	AI831297	Hs.123310	ESTs	1.00	56.00
	435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	1.00	2.00
	435550	AI224456	Hs.324507	H.sapiens polyA site DNA	3.42	3.92
55	435602	AF217515	Hs.283532	uncharacterized bone marrow protein BM03	3.95	1.80
	435766	R11673	Hs.186498	ESTs	1.00	28.00
	435793	AB037734	Hs.4993	KIAA1313 protein	23.68	42.00
	436069	AI056879	Hs.263209	ESTs	1.00	58.00
	436170	AW450381	Hs.14529	ESTs	1.00	18.00
60	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	5.84	22.00
	436213	AA325512	Hs.71472	hypothetical protein FLJ10774; KIAA1709	1.42	1.27
	436217	T53925	Hs.107	fibrinogen-like 1	57.97	31.00
	436238	AK002163	Hs.301724	hypothetical protein FLJ11301	2.51	1.71
	436251	BE515065	Hs.296585	nucleolar protein (KKE/D repeat)	2.33	1.64
65	436291	BE568452	Hs.344037	protein regulator of cytokinesis 1	108.99	52.00
	436302	AL355841	Hs.99330	hypothetical protein FLJ23588	0.75	2.81
	436396	AW992292	Hs.152213	wingless-type MMTV integration site fami	60.01	1.00
	436414	BE264633	Hs.143638	WD repeat domain 4	2.50	2.19
	436419	AI948626	Hs.171356	ESTs	0.95	1.33
70	436443	AW138211	Hs.128746	ESTs	1.12	9.26
	436474	AJ270693	Hs.199887	ESTs	1.00	1.00
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	3.28	1.56
	436486	AA742221	Hs.120633	ESTs	1.00	19.00
	436511	AA721252	Hs.291502	ESTs	16.76	14.00
75	436553	X57809	Hs.181125	immunoglobulin lambda locus	1.08	1.74
	436557	W15573	Hs.5027	ESTs, Weakly similar to A47582 B-cell gr	19.20	9.75
	436608	AA628980		down syndrome critical region protein DS	33.92	25.00
	436667	AW025183	Hs.127680	ESTs	0.89	1.19
	436771	AW975687	Hs.292979	ESTs	1.00	10.00
80	436839	AA401369	Hs.190721	ESTs	1.00	17.00
	436887	AW953157	Hs.193235	hypothetical protein DKFZp547D155	1.06	1.15
	436944	AW268614	Hs.5840	ESTs	1.00	1.00
	436961	AW375974	Hs.156704	ESTs	25.13	25.00
	436972	AA284679	Hs.25640	claudin 3	1.59	1.46
	437016	AU076916	Hs.5398	guanine monophosphate synthetase	2.35	1.78
85	437044	AL035864	Hs.69517	cDNA for differentially expressed CO16 g	1.34	1.13

	437181	AI306615	Hs.125343	ESTs, Weakly similar to KIAA0758 protein	1.00	17.00
	437204	AL110216	Hs.22826	ESTs, Weakly similar to I55214 salivary	40.55	82.00
	437205	AL110232	Hs.279243	Homo sapiens mRNA; cDNA DKFZp564D2071 (f	1.00	112.00
	437259	AI377755	Hs.120695	ESTs	1.00	205.00
5	437270	R18087	Hs.323769	cisplatin resistance related protein CRR	1.56	1.54
	437271	AL137445	Hs.28846	Homo sapiens mRNA; cDNA DKFZp566O134 (fr	113.25	125.00
	437370	AL359567	Hs.161962	Homo sapiens mRNA; cDNA DKFZp547D023 (fr	1.82	4.57
	437390	AI125859	Hs.112607	ESTs	1.35	1.75
10	437412	BE069288	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr	3.58	3.20
	437435	AI306152	Hs.27027	hypothetical protein DKFZp762H1311	3.03	1.08
	437444	H46008	Hs.31518	ESTs	1.00	39.00
	437568	AI954795	Hs.156135	ESTs	1.00	19.00
	437623	D63880	Hs.5719	chromosome condensation-related SMC-asso	1.95	1.57
15	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	1.00	3.00
	437814	AI088192	Hs.135474	ESTs, Weakly similar to DDx9_HUMAN ATP-D	1.00	45.00
	437840	AA884836	Hs.292014	ESTs	1.07	1.78
	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365O12.1 [H.sa	1.68	3.26
	437879	BE262082	Hs.5894	hypothetical protein FLJ10305	1.87	2.52
20	437915	AI637993	Hs.202312	Homo sapiens clone N11 NTera2D1 teratoca	74.05	35.00
	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	23.15	89.00
	437937	AI917222	Hs.121655	ESTs	1.00	1.00
	437942	AI888256	Hs.307526	ESTs	12.28	31.00
	438091	AW373062		nuclear receptor subfamily 1, group 1, m	1.53	10.85
25	438113	AI467908	Hs.8882	ESTs	1.80	2.39
	438119	AW963217	Hs.203961	ESTs, Moderately similar to AF116721 89	22.67	36.90
	438274	AI918906	Hs.55080	ESTs	1.00	1.00
	438378	AW970529	Hs.86434	hypothetical protein FLJ21816	38.92	38.00
	438403	AA806607	Hs.292206	ESTs	1.00	1.00
30	438494	AA908678	Hs.130183	ESTs	2.05	80.00
	438546	AW297204	Hs.125811	ESTs	1.00	131.00
	438552	AJ245820	Hs.6314	type 1 transmembrane receptor (seizure-r	1.43	1.45
	438702	AI879054	Hs.54618	ESTs	1.00	34.00
	438724	AW612553	Hs.114670	Human DNA sequence from clone RP11-16L21	1.33	1.10
35	438746	AI885815	Hs.184727	Human melanoma-associated antigen p97 (m	2.42	1.59
	438779	NM_003787	Hs.6414	nucleolar protein 4	1.00	18.00
	438821	AA826425	Hs.192375	ESTs	2.03	2.57
	438885	AI886558	Hs.184987	ESTs	6.42	88.00
	438898	AA401369	Hs.190721	ESTs	22.41	17.00
40	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	1.00	1.00
	438956	W00847	Hs.135056	Human DNA sequence from clone RP5-850E9	2.20	1.88
	439000	AW979121		gb:EST391231 MAGE resequences, MAGP Homo	2.78	4.81
	439023	AA745978	Hs.28273	ESTs	1.17	1.31
45	439024	R96696	Hs.35598	ESTs	1.00	28.00
	439128	AI949371	Hs.153089	ESTs	1.00	67.00
	439146	AW138909	Hs.156110	immunoglobulin kappa constant	1.38	1.41
	439223	AW238299	Hs.250618	UL16 binding protein 2	1.93	1.64
	439285	AL133916		hypothetical protein FLJ20093	46.23	139.00
	439318	AW837046	Hs.6527	G protein-coupled receptor 56	2.00	2.20
50	439343	AF086161	Hs.114611	hypothetical protein FLJ11808	6.10	7.37
	439394	AA401369	Hs.190721	ESTs	3.39	17.00
	439410	AA632012	Hs.188746	ESTs	1.83	3.07
	439451	AF086270	Hs.278554	heterochromatin-like protein 1	23.28	52.00
	439452	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	18.76	122.00
55	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	2.78	1.58
	439477	W69813	Hs.58042	ESTs, Moderately similar to GFR3_HUMAN G	1.22	1.44
	439492	AF086310	Hs.103159	ESTs	7.46	39.00
	439523	W72348	Hs.185029	ESTs	1.00	1.19
	439592	AF086413	Hs.58399	ESTs	1.00	1.00
60	439606	W79123	Hs.58561	G protein-coupled receptor 87	33.61	1.00
	439670	AF088076	Hs.59507	ESTs, Weakly similar to AC004858 3 U1 sm	1.00	1.00
	439702	AW085525	Hs.134182	ESTs	4.30	10.00
	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	86.55	11.00
	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	2.36	1.88
65	439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDN	2.02	6.08
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	1.00	21.00
	439780	AL109688		gb:Homo sapiens mRNA full length insert	7.27	25.00
	439840	AW449211	Hs.105445	GDNF family receptor alpha 1	1.00	1.00
	439926	AW014875	Hs.137007	ESTs	32.58	71.00
70	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	21.28	9.55
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	68.83	61.00
	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	1.83	4.02
	440028	AW473675	Hs.125843	ESTs, Weakly similar to T17227 hypotheti	1.42	2.54
75	440106	AA864968	Hs.127699	KIAA1603 protein	1.00	54.00
	440138	AB033023	Hs.318127	hypothetical protein FLJ10201	24.18	52.00
	440273	AI805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	3.21	4.72
	440289	AW450991	Hs.192071	ESTs	38.63	113.00
	440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma	62.88	147.00
	440492	R39127	Hs.21433	hypothetical protein DKFZp547J036	2.35	3.62
80	440527	AV657117	Hs.184164	ESTs, Moderately similar to S65657 alpha	10.84	57.00
	440659	AF134160	Hs.7327	claudin 1	3.18	2.37
	440704	M69241	Hs.162	insulin-like growth factor binding prote	2.89	2.09
	440943	AW082298	Hs.146161	hypothetical protein MGC2408	2.02	1.41
	440994	AI160011	Hs.272068	ESTs	1.29	1.14
85	441020	AA401369	Hs.190721	ESTs	142.99	17.00
	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	1.41	99.00

	441128	AA570256		ESTs, Weakly similar to T23273 hypotheti	4.13	3.50
	441290	W27501	Hs.89605	cholinergic receptor, nicotinic, alpha p	1.00	1.00
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	130.23	43.00
	441377	BE218239	Hs.202656	ESTs	22.03	1.00
5	441390	AI692560	Hs.131175	ESTs	3.65	7.70
	441497	R51064	Hs.23172	ESTs	1.00	1.00
	441525	AW241867	Hs.127728	ESTs	1.53	1.42
	441553	AA281219	Hs.121296	ESTs	1.89	1.57
10	441607	NM_005010	Hs.7912	neuronal cell adhesion molecule	1.47	2.11
	441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	216.22	363.00
	441636	AA081846	Hs.7921	Homo sapiens mRNA; cDNA DKFZp566E183 (fr	2.31	2.05
	441737	X79449	Hs.7957	adenosine deaminase, RNA-specific	1.30	1.49
	441790	AA401369	Hs.190721	ESTs	44.15	17.00
15	441801	AW242799	Hs.86366	ESTs	1.00	1.00
	441919	AI553802	Hs.128121	ESTs	1.00	122.00
	441937	R41782	Hs.22279	ESTs	0.86	1.37
	441954	AI744935	Hs.8047	Fanconi anemia, complementation group G	1.48	1.39
	442025	AW887434	Hs.11810	CDA11 protein	1.00	46.00
20	442029	AW956698	Hs.14456	neural precursor cell expressed, develop	9.92	45.00
	442072	AI740832	Hs.12311	Homo sapiens clone 23570 mRNA sequence	25.05	77.00
	442108	AW452649	Hs.166314	ESTs	3.61	3.14
	442117	AW664964	Hs.128899	ESTs	3.00	5.49
	442137	AA977235	Hs.128830	ESTs, Weakly similar to Z192_HUMAN ZINC	1.00	1.00
25	442159	AW163390	Hs.278554	heterochromatin-like protein 1	1.92	1.66
	442179	AA983842	Hs.333555	chromosome 2 open reading frame 2	27.22	50.00
	442328	AI952430	Hs.150614	ESTs, Weakly similar to ALU4_HUMAN ALU S	5.00	3.42
	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	181.59	76.00
	442530	AI580830	Hs.176508	Homo sapiens cDNA FLJ14712 fis, clone NT	10.59	144.00
30	442547	AA306997	Hs.217484	ESTs, Weakly similar to ALU1_HUMAN ALU S	109.23	98.00
	442556	AL137761	Hs.8379	Homo sapiens mRNA; cDNA DKFZp586L2424 (f	1.00	53.00
	442619	AA447492	Hs.20183	ESTs, Weakly similar to AF164793 1 prote	29.02	50.00
	442710	AI015631	Hs.23210	ESTs	1.00	19.00
	442717	R88362	Hs.180591	ESTs, Weakly similar to T23976 hypotheti	1.00	5.00
35	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	22.85	50.00
	442914	AW188551	Hs.99519	hypothetical protein FLJ14007	25.33	82.00
	442932	AA457211	Hs.8868	bromodomain adjacent to zinc finger doma	3.18	4.41
	442942	AW167087	Hs.131562	ESTs	8.45	64.00
	443068	AI188710		ESTs	1.00	27.00
40	443204	AW205878	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	1.00	24.00
	443211	AI128388	Hs.143655	ESTs	12.42	2.00
	443247	BE614387	Hs.333893	c-Myc target JPO1	128.84	96.00
	443324	R44013	Hs.164225	ESTs	0.02	4.59
	443383	AI792453	Hs.166507	ESTs	1.00	47.00
45	443400	R28424	Hs.250648	ESTs	18.52	61.00
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	4.02	1.75
	443572	AA025610	Hs.9605	cleavage and polyadenylation specific fa	2.98	2.57
	443575	AI078022	Hs.269636	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.00	29.00
	443614	AV655386	Hs.7645	fibrinogen, B beta polypeptide	1.00	16.00
50	443633	AL031290	Hs.9654	similar to pregnancy-associated plasma p	1.00	39.00
	443648	AI085377	Hs.143610	ESTs	39.81	70.00
	443715	AI583187	Hs.9700	cyclin E1	48.74	7.00
	443723	AI144442	Hs.157144	syntaxin 6	1.29	1.30
	443802	AW504924	Hs.9805	KIAA1291 protein	1.75	1.61
55	443859	NM_013409	Hs.9914	folistatin	1.35	1.13
	443892	AA401369	Hs.190721	ESTs	1.00	17.00
	443947	W24187		gb:zb47f09.r1 Soares_fetal_lung_NbHL19W	1.33	1.64
	443991	NM_002250	Hs.10082	potassium intermediate/small conductance	5.71	6.87
60	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	1.47	1.92
	444009	AI380792	Hs.135104	ESTs	1.00	77.00
	444017	U04840	Hs.214	neuro-oncological ventral antigen 1	1.00	1.00
	444127	N63620	Hs.13281	ESTs	1.00	29.00
	444129	AW294292	Hs.256212	ESTs	1.00	1.00
	444279	U62432	Hs.89605	cholinergic receptor, nicotinic, alpha p	0.60	7.80
65	444371	BE540274	Hs.239	forkhead box M1	2.91	1.14
	444378	R41339	Hs.12569	ESTs	1.00	1.00
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	469.00	556.00
	444461	R53734	Hs.25978	ESTs, Weakly similar to 2109260A B cell	12.88	105.00
	444471	AB020684	Hs.11217	KIAA0877 protein	24.91	90.00
70	444489	AI151010	Hs.157774	ESTs	1.00	111.00
	444619	BE538082	Hs.8172	ESTs, Moderately similar to A46010 X-in	1.00	70.00
	444665	BE613126	Hs.47783	B aggressive lymphoma gene	30.56	139.00
	444707	AI188613	Hs.41690	desmocollin 3	1.00	1.00
	444735	BE019923	Hs.243122	hypothetical protein FLJ13057 similar to	77.02	90.00
75	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	1.57	1.31
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	77.55	2.00
	445236	AK001676	Hs.12457	hypothetical protein FLJ10814	1.00	27.00
	445258	AI635931	Hs.147613	ESTs	1.00	73.00
	445413	AA151342	Hs.12677	CGI-147 protein	28.14	50.00
80	445417	AK001058	Hs.12680	Homo sapiens cDNA FLJ10196 fis, clone HE	1.81	2.62
	445443	AV653838	Hs.322971	ESTs	1.00	1.00
	445462	AA378776	Hs.288649	hypothetical protein MGC3077	2.09	1.70
	445517	AF208855	Hs.12830	hypothetical protein	1.87	70.00
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	1.71	2.72
	445580	AF167572	Hs.12912	skb1 (S. pombe) homolog	1.52	1.34
85	445654	X91247	Hs.13046	thioredoxin reductase 1	1.51	1.52

	445669	AI570830	Hs.174870	ESTs	10.95	11.45
	445818	BE045321	Hs.136017	ESTs	1.00	1.00
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-l	49.42	54.00
	445885	AI734009	Hs.127699	KIAA1603 protein	1.00	132.00
5	445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	1.00	1.00
	445903	AI347487	Hs.132781	class I cytokine receptor	1.00	36.00
	445932	BE046441	Hs.333555	Homo sapiens clone 24859 mRNA sequence	2.41	2.88
	445982	BE410233	Hs.13501	pescadillo (zebrafish) homolog 1, contai	1.60	1.35
	446078	AI339982	Hs.156061	ESTs	1.00	42.00
10	446102	AW168067	Hs.317694	ESTs	1.00	1.00
	446157	BE270828	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H	1.70	1.53
	446269	AW263155	Hs.14559	hypothetical protein FLJ10540	73.01	48.00
	446292	AF081497	Hs.279682	Rh type C glycoprotein	1.55	1.26
	446293	AI420213	Hs.149722	ESTs	1.00	2.00
15	446423	AW139655	Hs.150120	ESTs	1.10	4.19
	446428	AW082270	Hs.12496	ESTs, Weakly similar to ALU4_HUMAN ALU S	0.53	3.26
	446432	AI377320	Hs.150058	ESTs	1.00	5.00
	446528	AU076640	Hs.15243	nucleolar protein 1 (120kD)	1.36	1.31
	446574	AI310135	Hs.335933	ESTs	3.89	72.00
20	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	32.03	20.23
	446636	AC002563	Hs.15767	citron (rho-interacting, serine/threonin	4.19	5.07
	446783	AW138343	Hs.141867	ESTs	2.82	9.47
	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	110.28	28.00
	446849	AU076617	Hs.16251	cleavage and polyadenylation specific fa	3.26	2.94
25	446856	AI814373	Hs.164175	ESTs	6.38	11.30
	446872	X97058	Hs.16362	pyrimidinergic receptor P2Y, G-protein c	1.98	2.03
	446880	AI811807	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	94.90	113.00
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	1.67	3.90
	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	2.82	3.12
30	447022	AW291223	Hs.157573	ESTs	1.00	170.00
	447033	AI357412	Hs.157601	ESTs	7.15	107.00
	447078	AW885727	Hs.9914	ESTs	47.24	24.00
	447081	Y13896	Hs.17287	potassium inwardly-rectifying channel, s	0.12	17.88
35	447131	NM_004585	Hs.17466	retinoic acid receptor responder (tazaro	0.97	1.48
	447149	BE299857	Hs.326	TAR (HIV) RNA-binding protein 2	1.24	1.26
	447153	AA805202	Hs.315552	ESTs	1.00	54.00
	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	1.00	67.00
	447178	AW594641	Hs.192417	ESTs	3.42	50.00
40	447250	AI878909	Hs.17883	protein phosphatase 1G (formerly 2C), ma	1.60	1.52
	447289	AW247017	Hs.36978	melanoma antigen, family A, 3	1.00	1.00
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	28.63	1.00
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	146.62	51.00
	447350	AI375572	Hs.172634	ESTs	1.00	12.00
45	447377	N27687	Hs.334334	transcription factor AP-2 alpha (activat	2.55	63.00
	447415	AW937335	Hs.28149	ESTs, Weakly similar to KF3B_HUMAN KINES	0.91	1.13
	447425	AI963747	Hs.18573	acylphosphatase 1, erythrocyte (common)	1.00	35.00
	447519	U46258	Hs.339665	ESTs	59.89	49.00
	447532	AK000614	Hs.18791	hypothetical protein FLJ20607	1.23	1.63
50	447534	AA401369	Hs.190721	ESTs	1.00	17.00
	447636	Y10043		high-mobility group (nonhistone chromoso	1.41	1.11
	447688	N87079	Hs.19236	Target CAT	1.00	39.00
	447733	AF157482	Hs.19400	MAD2 (mitotic arrest deficient, yeast, h	1.17	1.12
	447769	AW873704	Hs.320831	Homo sapiens cDNA FLJ14597 fis, clone NT	6.47	5.95
55	447802	AW593432	Hs.161455	ESTs	0.73	2.34
	447850	AB018298	Hs.19822	SEC24 (S. cerevisiae) related gene famil	86.45	116.00
	447924	AI817226	Hs.313413	ESTs, Weakly similar to T23110 hypotheti	1.00	1.00
	447973	AB011169	Hs.20141	similar to S. cerevisiae SSM4	3.50	4.27
	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	4.13	142.00
60	448105	AI538613	Hs.298241	Transmembrane protease, serine 3	1.15	2.24
	448243	AW369771	Hs.52620	integrin, beta 8	15.84	1.00
	448278	W07369	Hs.11782	ESTs	0.97	1.90
	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	1.00	1.00
	448296	BE622756	Hs.10949	Homo sapiens cDNA FLJ14162 fis, clone NT	2.42	2.17
65	448357	BE274396	Hs.108923	RAB38, member RAS oncogene family	1.44	1.08
	448390	AL035414	Hs.21068	hypothetical protein	1.00	43.00
	448469	AW504732	Hs.21275	hypothetical protein FLJ11011	2.63	2.49
	448569	BE382657	Hs.21486	signal transducer and activator of trans	1.84	2.53
	448663	BE614599	Hs.106823	hypothetical protein MGC14797	3.29	46.00
70	448672	AI955511	Hs.225106	ESTs	1.00	21.00
	448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte	1.82	1.08
	448741	BE614567	Hs.19574	hypothetical protein MGC5469	2.48	1.92
	448757	AI366784	Hs.48820	TATA box binding protein (TBP)-associate	23.53	20.00
	448775	AB025237	Hs.388	nudix (nucleoside diphosphate linked moi	2.34	1.97
75	448826	AI580252	Hs.293246	ESTs, Weakly similar to putative p150 [H	74.07	62.67
	448830	AL031658	Hs.22181	hypothetical protein dJ310013.3	1.37	1.31
	448844	AI581519	Hs.177164	ESTs	1.00	31.00
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	1.84	1.95
	448993	AI471630		KIAA0144 gene product	1.63	1.49
80	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o	1.00	1.00
	449029	N28989	Hs.22891	solute carrier family 7 (cationic amino	1.97	2.26
	449040	AF040704	Hs.149443	putative tumor suppressor	0.97	1.56
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	27.13	90.00
	449053	AI625777	Hs.344766	ESTs	8.33	44.00
	449054	AF148848	Hs.22934	myoneurin	72.85	104.00
85	449101	AA205847	Hs.23016	G protein-coupled receptor	2.58	27.00

	449167	T05095	Hs.19597	KIAA1694 protein	1.61	2.36
	449207	AL044222	Hs.23255	nucleoporin 155kD	2.36	1.56
	449228	AJ403107	Hs.148590	protein related with psoriasis	1.15	1.15
5	449230	BE613348	Hs.211579	melanoma cell adhesion molecule	206.65	151.00
	449305	AI638293		gb:tt09b07.x1 NCL_CGAP_GC6 Homo sapiens	17.28	45.00
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	26.39	35.00
	449448	D60730	Hs.57471	ESTs	1.00	1.00
	449467	AW205006	Hs.197042	ESTs	1.00	1.00
10	449523	NM_000579	Hs.64443	chemokine (C-C motif) receptor 5	56.80	218.66
	449722	BE280074	Hs.23960	cyclin B1	150.03	1.00
	449976	H06350	Hs.135056	Human DNA sequence from clone RP5-850E9	2.16	2.85
	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitter)	1.17	1.45
	450098	W27249	Hs.8109	hypothetical protein FLJ21080	1.79	2.38
15	450101	AV649989	Hs.24385	Human hbc647 mRNA sequence	1.00	69.00
	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophila)	1.00	1.00
	450193	AI916071	Hs.15607	Homo sapiens Fanconi anemia complementat	29.85	34.00
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	1.00	1.00
	450372	BE218107	Hs.202436	ESTs	1.00	1.00
20	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	51.26	93.00
	450447	AF212223	Hs.25010	hypothetical protein P15-2	123.20	181.00
	450588	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT	1.00	19.00
	450589	AI701505	Hs.202526	ESTs	1.00	23.00
	450684	AA872605	Hs.25333	interleukin 1 receptor, type II	1.00	100.00
25	450701	H39960	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MA	1.89	1.55
	450705	U90304	Hs.25351	iroquois homeobox protein 2A (IRX-2A) (1.00	45.00
	450832	AA401369	Hs.190721	ESTs	25.17	17.00
	450937	R49131	Hs.26267	ATP-dependant interferon response protei	90.92	90.00
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	3.33	1.70
30	451105	AI761324		gb:wi60b11.x1 NCL_CGAP_Co16 Homo sapiens	15.02	124.00
	451110	AI955040	Hs.265398	ESTs, Weakly similar to transformation-r	1.00	143.00
	451253	H48299	Hs.26126	claudin 10	3.02	2.29
	451291	R39288	Hs.6702	ESTs	1.00	1.00
	451320	AW498974		diacylglycerol kinase, zeta (104kD)	2.92	18.00
35	451380	H09280	Hs.13234	ESTs	6.90	6.67
	451386	AB029006	Hs.26334	spastic paraplegia 4 (autosomal dominant	35.75	72.00
	451437	H24143	Hs.31945	hypothetical protein FLJ11071	1.00	69.00
	451462	AK000367	Hs.26434	hypothetical protein FLJ20360	1.83	2.10
	451524	AK001466	Hs.26516	hypothetical protein FLJ10604	1.13	1.07
40	451541	BE279383	Hs.26557	plakophilin 3	1.88	1.33
	451592	AI805416	Hs.213897	ESTs	1.00	1.00
	451635	AA018899	Hs.127179	cryptic gene	1.52	1.92
	451743	AA401369	Hs.190721	ESTs	4.95	17.00
	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	13.55	31.00
45	451807	W52854		hypothetical protein FLJ23293 similar to	1.55	35.00
	451871	AI821005	Hs.118599	ESTs	1.81	2.53
	451952	AL120173	Hs.301663	ESTs	1.00	22.00
	452012	AA307703	Hs.279766	kinesin family member 4A	3.43	2.26
	452046	AB018345	Hs.27657	KIAA0802 protein	55.59	19.00
50	452194	AI694413	Hs.332649	olfactory receptor, family 2, subfamily	1.67	4.09
	452206	AW340281	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	9.31	53.00
	452240	AA401369	Hs.190721	ESTs	13.42	17.00
	452256	AK000933	Hs.28661	Homo sapiens cDNA FLJ10071 fis, clone HE	39.03	94.00
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	153.01	340.00
55	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	1.95	23.00
	452295	BE379936	Hs.28866	programmed cell death 10	42.33	61.00
	452304	AA025386	Hs.61311	ESTs, Weakly similar to S10590 cysteine	1.17	2.14
	452340	NM_002202	Hs.605	ISL1 transcription factor, LIM/homeodoma	1.00	13.00
	452349	AB028944	Hs.29189	ATPase, Class VI, type 11A	1.09	1.42
60	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	54.49	53.00
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	1.00	32.00
	452410	AL133619		Homo sapiens mRNA; cDNA DKFZp434E2321 (f	1.26	1.99
	452461	N78223	Hs.108106	transcription factor	24.47	35.00
	452571	W31518	Hs.34665	ESTs	54.61	102.00
65	452613	AA461599	Hs.23459	ESTs	1.39	1.32
	452699	AW295390	Hs.213062	ESTs	1.00	26.00
	452705	H49805	Hs.245005	ESTs	1.00	1.00
	452747	AF160477	Hs.61460	Ig superfamily receptor LNIR	112.87	1.29
70	452787	AW294022	Hs.222707	KIAA1718 protein	1.00	1.00
	452795	AW392555	Hs.18878	hypothetical protein FLJ21620	1.00	1.00
	452823	AB012124	Hs.30696	transcription factor-like 5 (basic helix	7.91	75.00
	452833	BE559681	Hs.30736	KIAA0124 protein	3.16	1.92
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	174.35	1.00
	452862	AA401369	Hs.190721	ESTs	98.26	17.00
75	452865	AW173720	Hs.345805	ESTs, Weakly similar to A47582 B-cell gr	1.55	1.00
	452934	AA581322	Hs.4213	hypothetical protein MGC16207	1.73	1.19
	452946	X95425	Hs.31092	EphA5	1.00	1.00
	452976	R44214	Hs.101189	ESTs	1.58	1.98
	453028	AB006532	Hs.31442	RecQ protein-like 4	1.80	1.60
80	453095	AW295660	Hs.252756	ESTs	0.77	1.50
	453102	NM_007197	Hs.31664	frizzled (Drosophila) homolog 10	1.00	1.00
	453103	AI301052	Hs.153444	ESTs	1.00	1.00
	453120	AA292891	Hs.31773	pregnancy-induced growth inhibitor	1.23	1.20
	453153	N53893	Hs.24360	ESTs	1.00	83.00
85	453160	AI263307	Hs.239884	H2B histone family, member L	1.00	30.00
	453197	AI916269	Hs.109057	ESTs, Weakly similar to ALU5_HUMAN ALU S	1.00	134.00

5	453210	AL133161	Hs.32360	hypothetical protein FLJ10867	1.69	1.93		
	453240	AI969564	Hs.166254	hypothetical protein DKFZp566i133	1.00	1.00		
	453317	NM_002277	Hs.41696	keratin, hair, acidic, 1	1.19	1.27		
	453323	AF034102	Hs.32951	solute carrier family 29 (nucleoside tra	4.90	4.11		
	453331	AI240665	Hs.3880	ESTs	199.42	340.00		
	453392	U23752	Hs.32964	SRX (sex determining region Y)-box 11	1.00	16.00		
	453431	AF094754	Hs.32973	glycine receptor, beta	1.00	1.00		
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	3.44	5.17		
	453459	BE047032	Hs.257789	ESTs	2.84	5.58		
10	453563	AW608906.comp		Hs.181163	hypothetical protein MGC5629	4.58	90.00	
	453633	AA357001	Hs.34045	hypothetical protein FLJ20764	1.74	1.60		
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	19.49	1.00		
	453830	AA534296	Hs.20953	ESTs	24.92	25.00		
15	453857	AL080235	Hs.35861	DKFZP586E1621 protein	167.59	66.00		
	453867	AI929383	Hs.33032	hypothetical protein DKFZp434N185	1.00	39.00		
	453883	AI638516	Hs.347524	cofactor required for Sp1 transcriptiona	1.97	1.58		
	453884	AA355925	Hs.36232	KIAA0186 gene product	63.89	20.00		
	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU S	20.41	16.00		
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	7.09	22.00		
20	453941	U39817	Hs.36820	Bloom syndrome	29.75	19.00		
	453964	AI961486	Hs.12744	ESTs	1.00	1.00		
	453968	AA847843	Hs.62711	Homo sapiens, clone IMAGE:3351295, mRNA	2.06	1.81		
	453976	BE463830	Hs.163714	ESTs	3.02	131.00		
	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	1.00	131.00		
25	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	1.23	1.02		
	454042	T19228	Hs.172572	hypothetical protein FLJ20093	30.63	171.00		
	454059	NM_003154	Hs.37048	statheirin	1.00	1.00		
	454066	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid	1.01	1.45		
30	454098	W27953	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	1.26	1.11		
	454241	BE144666		gb:CM2-HT0176-041099-017-c02 HT0176 Homo	6.33	5.04		
	454417	AI244459	Hs.110826	trinucleotide repeat containing 9	4.30	7.82		
	454439	AW819152	Hs.154320	DKFZP566O1646 protein	1.00	1.00		
	455175	AW993247		gb:RC2-BN0033-180200-014-h09 BN0033 Homo	13.75	103.00		
35	455601	AI368680	Hs.816	SRX (sex determining region Y)-box 2	206.11	1.00		
	456237	AA203682		gb:zx52e07.r1 Soares_fetal_liver_spleen_	1.00	1.00		
	456321	NM_001327	Hs.87225	cancer/testis antigen	1.14	1.10		
	456475	NM_000144	Hs.95998	Friedreich ataxia	1.00	48.00		
40	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	162.25	189.00		
	456534	X91195	Hs.100623	phospholipase C, beta 3, neighbor pseudo	2.12	1.80		
	456736	AW248217	Hs.1619	achaete-scute complex (Drosophila) homol	1.15	1.94		
	456759	BE259150	Hs.127792	delta (Drosophila)-like 3	1.00	1.00		
	456990	NM_004504	Hs.171545	HIV-1 Rev binding protein	16.42	84.00		
	457200	U33749	Hs.197764	thyroid transcription factor 1	0.57	1.76		
45	457234	AW968360	Hs.14355	Homo sapiens cDNA FLJ13207 fis, clone NT	2.71	4.15		
	457465	AW301344	Hs.122908	DNA replication factor	46.37	47.00		
	457489	AI693815	Hs.127179	cryptic gene	1.12	1.35		
	457646	AA725650	Hs.112948	ESTs	1.55	2.51		
	457733	AW974812	Hs.291971	ESTs	1.00	55.00		
50	457819	AA057484	Hs.35406	ESTs, Highly similar to unnamed protein	4.36	3.18		
	458092	BE545684	Hs.343566	KIAA0251 protein	1.00	1.32		
	458098	BE550224		metallothionein 1E (functional)	1.00	22.00		
	458207	T28472	Hs.7655	U2 small nuclear ribonucleoprotein auxil	2.06	1.88		
55	458242	BE299588	Hs.28465	Homo sapiens cDNA: FLJ21869 fis, clone H	1.00	1.00		
	458247	R14439	Hs.209194	ESTs	7.00	9.85		
	458679	AW975460	Hs.142913	ESTs	1.00	3.00		
	458778	AW451034	Hs.326525	arylsulfatase D	1.31	2.01		
	458933	AI638429	Hs.24763	RAN binding protein 1	1.98	1.71		
	459352	AW810383	Hs.206828	ESTs	12.60	63.00		
60	459670	F01020	Hs.172004	titin	1.00	1.00		
	459702	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	1.00	237.00		

TABLE 9B

65	Pkey:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
70	Pkey	CAT Number	Accession
	407746	10125_1	AK001962 R69415 BE464605 AA418699 AA053293 AA149075 AA058396 AW338226 AW272659 AA454607 AI139535 AW469852 AI275461
			AW271982 AA730033 AA576507 AA991217 AA782067 AI985851 AA805864 AA505598 AW469857 R69546 AA988279 AW001647 N63320
			D82661 T27343 AA306950 AA360989 R58778
	408070	1036688_1	AW148852 BE350895
75	408660	107294_1	AA525775 AA056342 AI538978 AW975281 AA664986
	409522	113735_1	AA075382 AA075431
	409866	1156522_1	AW502152 H41202 H29772
	410032	1170435_1	BE065985 BE065944 BE066008 BE066083 BE066093
	411089	123172_1	AA456454 AA713730 AA091294 AA584921 N86077 AW836781 AA601031 AA579876 AA551106 AA633188 AW905577 AI955808 AI679386
80	411152	1234028_1	AI679895 AA514764 AA454562 AI082382 AA595822 AA551351 AA586369 AA666384 AA188934 AA666398 AA551297 AA565188
	412537	1304_1	BE069199 AW936012 AW877466 AW819782 AW935798 AW835546 AW936042 BE069121 AW835625 AW877536 AW935885 BE069202
			AW820019 AW935937 BE160180 AW935946 BE069101 BE069125 AW877527 BE160316 BE160398 AW935794 AW835701 AW935784
			AL031778 X59711 NM_002505 M59079 AI870439 AI494259 AW664010 AA405063 AA436132 BE174516 AA412691 AI400314 AA436024
			T29403 BE079412 BE079428 N90322 AI631202 AI141758 AI016793 AI167566 AI862075 AI375230 AI208445 AW235763 AL044113 AA382556
			AW953918 AA927051 AA889823 BE003094 AW390155 AW360805 AW360823 AW360810 AA425472 AI694282 AL044114 AI684577 AI809865

			AI478773 AI160445 AI674630 N69088 AW665529 N49278 AI129239 AI457890 AI621264 AW297152 AI268215 AA907787 AI286170 AI017982 AI963541 AI469807 AI969353 BE552356 N66509 AA736741 AA382555 AW075811 AW292026 H06382 AW957730 AA352014 R13591 AA121201 D60420 BE263253 BE047862 Z41952 AI424991 AI693507 AI863108 AA599060 AI091148 AA598689 R39887 AA813482 AW016452 H06383 R41807 AI364268 AA620528 AI241940 AW089149 AW090733 AW088875 Z38240 AA121202 R17734 BE157489 BE157560 AA926960 AA926959 W76521 W24270 W21526 AA037172 BE267636 H83186 AA469909 N86396 AA001348 BE535736 AA081745 BE566245 AA082436 H72525 H77575 N49786 W80565 H78746 BE569085 W04339 R98127 T55938 BE279271 AW960304 T29812 AA476873 BE297387 AA292753 AA177048 NM_001826 X54941 BE314366 AA908783 AI719075 BE270172 BE269819 AA899955 AI204630 W25243 AI935150 AA872039 W72395 T99630 AI422691 H98460 N31428 BE255916 H03265 AI857576 AA776920 AA910644 AA459522 AA293140 AW514667 R75953 AW662396 AA662522 AI865147 AI423153 AW262230 AA584410 AA583187 AW024595 AW069734 AI828996 AA282997 AA876046 AW613002 AA527373 AW972459 AI831360 AA621337 AA100926 AA772418 AA594628 AI033892 W95096 AI034317 AA398727 AI085031 N95210 AI459432 AI041437 AA932124 AA627684 AA935829 AI004827 AI423513 AI094597 H42079 R54703 AI630359 AA617681 AA978045 AA643280 W44561 AI991988 AI537692 AI090262 AA740817 AI312104 AI911822 AA416871 AI185409 AA129784 AA701623 AI075239 AI139549 AA633648 AI339996 AI336880 AA399239 AI078708 AI085351 AI362835 AI346618 AI146955 AI989380 AI348243 N92892 AA765850 AI494230 AI278887 AA962596 AI492600 W80435 AA001979 R97424 AI129015 N24127 AA157451 AA235549 AA459292 AA037114 AA129785 AI494211 AW059601 AW886710 R92790 N59755 AI361128 AW589407 H47725 H97534 H48076 H48450 T99631 AW300758 H03431 R76789 AA954344 H75776 R96823 AI457100 N92845 NA9682 H42038 BE220698 BE220715 H99552 AA701624 N74173 R54704 H79520 H72923 H03266 BE261919 AW769633 AA480310 AA507454 AA910586 AI203723 AW104725 W25611 W25071 T88980 H03513 T77589 R99156 W95095 R97470 AA702275 T77551 AA911952 H82956 N83673 AA283672 AI267700 AI720344 AA191424 AI023543 AI469633 AA172056 AW958465 AA172236 AW953397 AA355086 AW265494 AA455904 AA195677 AW265432 AW991605 AA456370 N28754 N28747 AI568146 AI979339 AA322671 AA322672 AW955043 AI990326 AA776406 AI016250 AA843678 AW451882 N23137 N23129 W70051 AI038748 AA831327 AI925845 AW945895 Z42183 T31621 T97478 D62703 AA242966 D79798 AU076704 T74854 T74860 T72098 T73265 T73873 T69180 T74658 T58786 T60385 T73410 T68781 T67845 T67593 T73952 T67864 T60630 T68367 T68401 T53959 T72360 T72099 T60377 T58961 T71712 T72821 T64738 T74645 T72037 T68688 T72063 T73258 T72826 T64242 T68220 T74673 T71800 T68355 T61227 T62738 T69317 T53850 T64692 T73768 T73962 T73382 T68914 T70975 T73400 T60631 T73277 T73203 T70498 T61409 T58925 NM_000508 M64982 T68301 T73729 T69445 T60424 T67922 T67736 T68716 T67755 T74765 T73819 T58719 T74756 T60477 T74863 T61109 T68329 T58850 T71857 T73425 T53736 T68607 T58898 T64309 T72031 T72079 T64305 T71908 T68107 T71916 T73787 T56035 T64425 T71870 T60476 T61376 T67820 T71895 T41006 T69441 T68170 T74617 T71958 T69440 T61875 R06796 H48353 T71914 T53939 T64121 AA693996 T72525 T67779 T68078 AA011465 AA345378 AV654847 AV656501 AI064740 T82897 N33594 AA344542 AW805054 AI207457 T61743 AA026737 H94389 AA382695 AA918409 T68044 S82092 T39959 AI017721 AA312395 AA312919 T40156 H66239 AV652989 H38728 R98521 AV655200 R95790 W03250 W00913 AA344136 AV660126 R97923 AA343586 AW470774 AV651256 N54417 AA812862 AW182929 AI111912 H61463 H72060 AA344503 H38639 AI277511 AV661108 AI207625 T47810 AA235252 T27853 T47778 R95746 H70620 AA701463 AW827166 R98475 C20925 AV657287 T71959 T71313 T73920 T73333 T61618 T69293 T72517 R02292 T60599 T69206 T70452 T74677 R29366 T61277 T74914 T60352 R29675 T74843 AV645792 AA344408 T69197 T72057 T69368 T69358 T68258 AV650429 T73341 T61702 T74598 T40095 K02272 T40106 AA343045 AA341908 AA341907 AA342807 AA341964 T53747 T72042 T62764 AI064899 AA343060 T67832 T72440 T71770 T68091 T69108 T72449 T69167 T71289 T68251 AV654844 T64375 AA345234 T67598 AA011414 T68036 H48262 AI207557 T68219 W86031 T69081 T64232 R93196 T62136 AV650539 H67459 T72978 AA344583 T60362 H58121 T95711 T72803 T68055 T71715 R29036 T72793 T69122 T64595 T62888 T69139 T68291 T64652 T67971 T46862 AA693592 AI248502 R29454 T64764 T57001 T73052 T71429 T51176 T58866 AV655414 H90426 AA342489 T73666 T67848 T72512 T53835 T67837 T73317 T74273 T69420 T68245 T74380 T67862 T74474 T56068 AI792788 BE142230 AA252019 AI910275 X00474 X52003 X05030 NM_003225 AA314326 AA308400 AA506787 AA314825 AI571948 AA507595 AA614579 AA587613 R83818 AA568312 AA614409 AA307578 AI925552 AW950155 AI910083 M12075 BE074052 AW004668 AA578674 AA582084 BE074053 BE074126 BE074140 AA514776 AA588034 BE074051 BE074068 AW009769 AW050690 AA858276 R55389 AI001051 AW050700 AW750216 AA614539 BE074045 AI307407 AW602303 BE073575 AI202532 AA524242 AI970839 AI909751 BE076078 AI909749 R55292 AW881145 AA490718 M85637 AA304575 T06067 AA331991 AL119930 AA320696 AW752565 AL031985 AI137241 AI792386 AI733664 AI857654 AI049911 AA337221 AA336756 AW966196 AW953120 R56325 AA349562 AI493134 AI498691 AW771508 AI498457 AI768408 AI783624 AI383985 AI580267 D79813 AA393768 AK001536 AA191092 AW510354 AI554256 AL353968 AA134266 AA663848 AA400100 AA401424 AL038843 AA161338 BE268213 AA425597 N87306 AA092969 BE566038 AA247451 N47392 AI928802 AW182584 AW027872 AI819831 AI936994 W56258 AI653448 AI278611 AI283557 AI824306 AW338658 AW150899 AA687514 N47393 N29885 AA973469 AI038904 AI292064 AI034339 AW574593 N72156 AI079733 AI038683 AI291616 AA491599 AA993675 AA837380 BE006554 BE006473 AI087090 T33044 AA652043 AI203503 AA583959 W35283 AI129926 Z41844 AW020925 AW575848 AI684603 AA493297 AI140689 AI277175 AA425444 AI932767 W02632 BE396786 R37261 AW207206 AW341473 AA448195 AI951341 AA249027 AI038984 AK001993 AL080066 AV652725 BE566226 AA345557 AA315222 AA090585 AA375688 AA301092 AA298454 W05762 AW607939 H51658 D83880 N84323 BE296821 AW947007 D61461 AW079261 AA329482 AW901780 AI354442 AA772275 R31663 AI354441 AI767525 H92431 AI916735 H93575 AI394255 AW014741 AI573090 C06195 AW612857 AW265195 AI339558 AI377532 AI308821 AI919424 AI589705 AW065215 AI336532 AI338051 AA806547 C75509 C00618 AW071172 AW769904 AA630381 AI678018 AI863985 D79662 BE221049 AW265018 AI589700 AW196655 N76573 AI370908 BE042393 N75017 AI698870 AW960115 AL133561 AL041090 AL117481 AL122069 AW439292 AI968826 AW072916 AI184913 AA489195 AW466994 AW469044 N59350 AI819642 AI280239 AI220572 AA789302 AI473611 AW841126 D60937 BE041395 AA491826 AA621946 AA715980 AA666102 AW970622 AA503009 AA502998 AA502989 AA502805 T92188 AA221036 R87170 BE537068 BE544757 C18935 AW812058 T92565 AA227415 AA233942 AA223237 AA668403 AA601627 AW869639 BE061833 BE000620 AW961170 AW847519 AA308542 AW821833 AW945688 C04699 AA205504 AA377241 AW821667 AA055720 AW817981 AW856468 AA155719 AA179928 T03007 AW754298 AA227407 AA113928 AA307904 C16859 AI798376 S46400 AW811617 AW811616 W00557 BE142245 AW858232 AW861851 AW858362 AA232351 AA218567 AA055556 AW858231 AW857541 AW814172 H66214 AW814398 AF134164 AA243093 AA173345 AA199942 AA223384 AA227092 AA227080 T12379 AA092174 T61139 AA149776 AA699829 AW879188 AW813567 AW813538 AI267168 AA157718 AA157719 AA100472 AA100774 AA130756 AA157705 AA157730 AA157715 AA053524 AW849581 AW854566 C05254 AW882836 T92637 AW812621 AA206563 AA209204 BE1556909 AA226824 AI829309 AW991957 N66951 AA527374 H66215 AA045564 AI694265 H60808 AA149726 AW195620 BE081333 BE073424 AW817662 AW817705 AW817703 AW817659 BE081531 H59570 AA628980 AI126603 BE504035
5	412811	132943_1	
	413690	1383256_1	
	414883	15024_1	
10			
15			
20	415989	156454_1	
	417324	166714_1	
	418574	17690_1	
25	418712	1784125_1	
	419443	184788_1	
	419502	18535_1	
30			
35			
40			
45			
50	419936	189181_1	
	421582	2041_1	
	422128	211994_1	
	423034	224122_1	
	423816	23234_1	
	424200	236595_1	
	424999	245835_1	
	426966	273896_1	
	426991	27415_1	
60	427260	276598_1	
	428023	28589_2	
65	429220	301384_1	
	429978	31150_1	
70			
	430439	31808_1	
	430935	325772_1	
	431089	327825_1	
	431322	331543_1	
	432407	34624_1	
80	434414	38585_1	
85	436608	42361_3	

438091	44964_1	AW373062 T55662 AI299190 BE174210 AW579001 H01811 W40186 R67100 AI923886 AW952164 AA628440 AW898607 AW898616 AA709126 AW898628 AW898544 AA947932 AW898625 AW898622 AI276125 AI185720 AW510698 AA987230 T52522 BE467708 AW243400 AW043642 AI288245 AI186932 D52654 D55017 D52715 D52477 D53933 D54679 AI298739 AI146984 AI922204 N98343 BE174213 AA845571 AI813854 AI214518 AI635262 AI139455 AI707807 AI898085 AW884528 AI024768 AI004723 AW087420 AI565133 N94964 AI268939 AW513280 AI061126 AI435818 AI859106 AI360506 AI024767 AA513019 AA757598 X56196 AA902959 AI334784 AI860794 AA010207 AW890091 AW513771 AI951391 AI337671 T52499 AA890205 AI640908 H75966 AA463487 AA358688 AI961767 AI866295 AA780994 AI985913 BE174196 AA029094 AW592159 T55581 N79072 AI611201 AA910812 AI220713 AW149306 AI758412 AA045713 R79750 N76096 AW979121 AA847986 AA829098
439000	467716_1	AL133916 N79113 AF086101 N76721 AW950828 AA364013 AW955684 AI346341 AI867454 N54784 AI655270 AI421279 AW014882
439285	47065_1	AA775552 N62351 N59253 AA626243 AI341407 BE175639 AA456968 AI358918 AA457077
439780	47673_1	AL109688 R23665 R26578
441128	51021_2	AA570256 AW014761 AA573721 AI473237 AI022165 AA554071 AA127551 N90525 AW973623 AA447991 AA243852 BE328850 AI148171 AI359627 AI005068 AI356567 AA232991 AW016855 AA906902 AA233101 AA127550 BE512923
443068	558874_1	AI188710 AI032142 AW078833 N30308 AW675632 AI219028 AI341201 N22181 H95390
443947	586180_1	W24187 W24194 R17789
447636	7301_1	Y10043 NM_005342 L05085 AL034450 BE614226 AW749053 AA379173 AA248230 BE514634 AA334622 R70656 AA367593 AA214649 AA369318 AW957081 R05760 AA039903 AI886597 AW630122 AA906264 AA041527 R01145 AI088688 BE463637 AA398795 AI354883 AI768938 AI569996 AI452952 AI168582 AI189869 AI086670 AW262560 AW613854 AA862839 AA435840 AA670197 AI024032 AI990659 AI990089 N81095 AA847919 AW960150 AA211075 AA044704 AA367594 AW582587 AW858854 AW818630 AW818281 AW818433 AW582595 AA096002 N83992
448993	79225_1	AI471630 BE540637 BE265481 AW407710 BE513882 BE546739 AA053597 BE140503 BE218514 AW956702 AI656234 AI636283 AI567265 AW340858 BE207794 AA053085 R69173 AA292343 AA454908 AA293504 AI659741 AI927478 AA399460 AI760441 AA346416 BE047245 AA730380 AA394063 AA454833 AI982791 AI567270 AI813332 AI767858 AA427705 D20284 AI221458 BE048537 AI263048 AA346417 AA911497 BE537702
449305	804424_1	AI638293 AW813561
451105	859083_1	AI761324 AW880941 AW880937
451320	86576_1	AW118072 AI631982 T15734 AA224195 AI701458 W20198 F26326 AA890570 N90552 AW071907 AI671352 AI375892 T03517 R88265 AI124088 AA224388 AI084316 AI354686 T33652 AI140719 AI720211 T03490 AI372637 T15415 AW205836 AA630384 T03515 T33230 AA017131 AA443303 T33623 AI222556 T33511 T33785 AI419606 D55612
451807	8865_1	W52854 AI117600 BE208116 BE208432 BE206239 BE082291 AW953423 AA351619 BE180648 BE140560 W60080 AA865478 N90291 AW450652 AW449519 AA993634 AI806539 AA351618 AW449522 AI827626 AA904788 AA380381 AA886045 AA774409 BE003229 Z41756 AL133619 AA468118 AA383064 AI476447 T09430 AI673758 AA524895 AI581345 AI300820 AW498812 AA256162 AI559724 AI685732
452410	9163_1	AA602400 AA905453 AI204595 AW166541 AA157456 AA156269 AA383652 AA431072 AW592707 AI435410 AW272464 AI215594 AA622747 R74039 N35031 AI804128 AW513621 AA868351 AI026826 AI493388 AA614641 W81604 AI567080 AI214351 AA730140 AI125754 AI200813 AI269603 AI565082 AI807095 AI476629 AA505909 AI368449 AI686077 AI582930 AW085038 AA757863 AA730154 AI767072 AA468316 AI734130 AI734138 AA426284 AA433997 AI741241 AW043563 AI732741 AI732734 AA437369 AA425820 AA664048 R74130
454241	1067807_1	BE144666 BE184942 AW238414 BE184946
455175	1257335_1	AW993247 AW861464
456237	168730_1	AA203682 R11958
458098	47395_1	BE550224 AA832519 N45402 AW885857 N29245 BE465409 W07677 AW970089 AI299731 AA482971 BE503548 H18151 W79223 AF086393 AA461301 W74510 R34182 AI090689 N46003 BE071550 R28075 AW134982 AI240204 AI138906 AW026179 AI572316 BE466182 AI206395 AI276154 AI273269 AI422817 AI371014 AI421274 AI188525 AA939164 BE549810 AW137865 AI694996 BE503841 AA459718 BE327407 BE467534 BE218421 BE467767 AA989054 BE467063 AI797130 BE327781

TABLE 9C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400512	9796593	Minus	1439-1615
400517	9796686	Minus	49996-50346
400560	9843598	Plus	94182-94323,97056-97243,101095-101236,102824-103005
400664	8118496	Plus	13558-13721,13942-14090,14554-14679
400665	8118496	Plus	16879-17023
400666	8118496	Plus	17982-18115,20297-20456
400749	7331445	Minus	9162-9293
400763	8131616	Minus	35537-35784
401027	7230983	Minus	70407-70554,71060-71160
401093	8516137	Minus	22335-23166
401203	9743387	Minus	172961-173056,173868-173928
401212	9858408	Plus	87839-88028
401411	7799787	Minus	144144-144329
401435	8217934	Minus	54508-55233
401464	6682291	Minus	170688-170834
401714	6715702	Plus	96484-96681
401747	9789672	Minus	118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011
401760	9929699	Plus	83126-83250,85320-85540,94719-95287
401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814
401785	7249190	Minus	165776-165996,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942
401797	6730720	Plus	6973-7118
401961	4581193	Minus	124054-124209
401985	2580474	Plus	61542-61750
401994	4153858	Minus	42904-43124,43211-43336,44607-44763,45199-45281,46337-46732
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
402260	3399665	Minus	113765-113910,115653-115765,116808-116940
402265	3287673	Plus	21059-21168
402297	6598824	Plus	35279-35405,35573-35659
402408	9796239	Minus	110326-110491

	402420	9796339	Plus	129750-129919
	402674	8077108	Minus	39290-39502
	402802	3287156	Minus	53242-53432
5	402994	2996643	Minus	4727-4969
	403137	9211494	Minus	92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337
	403306	8099945	Plus	127100-127251
	403329	8516120	Plus	96450-96598
	403381	9438267	Minus	26009-26178
10	403478	9958258	Plus	116458-116564
	403485	9966528	Plus	2888-3001,3198-3532,3655-4117
	403627	8569879	Minus	23868-24342
	403715	7239669	Plus	85128-85292
	404044	9558573	Minus	225757-225939
15	404076	9931752	Minus	3848-3967
	404101	8076925	Minus	125742-125997
	404140	9843520	Plus	37761-38147
	404165	9926489	Minus	69025-69128
	404185	4572584	Minus	129171-129327
20	404210	5006246	Plus	169926-170121
	404253	9367202	Minus	55675-56055
	404287	2326514	Plus	53134-53281
	404298	9944263	Minus	73591-73723
	404347	9838195	Plus	74493-74829
25	404440	7528051	Plus	80430-81581
	404721	9856648	Minus	173763-174294
	404794	4826439	Plus	101619-101898
	404854	7143420	Plus	14260-14537
	404877	1519284	Plus	1095-2107
30	404927	7342002	Plus	68690-69563
	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
	405449	7622497	Plus	42236-42570
	405568	6006906	Plus	35912-36065
	405572	3800891	Plus	85230-85938
35	405646	4914350	Plus	741-969
	405676	4557087	Plus	73195-73917
	405770	2735037	Plus	61057-62075
	405932	7767812	Minus	123525-123713
	406137	9166422	Minus	30487-31058
40	406360	9256107	Minus	7513-7673
	406399	9256288	Minus	63448-63554
	406467	9795551	Plus	182212-182958

TABLE 10A: Potential Therapeutic, Diagnostic and Prognostic targets for Therapy of Lung Cancer and Non-malignant Lung Disease
 Table 2A shows about 307 genes up-regulated in non-malignant lung disease relative to lung tumors and normal body tissues and/or down-regulated in lung tumors relative to normal lung and non-malignant lung disease. These genes were selected from about 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

Table 10B show the accession numbers for those Pkey's lacking UnigenelD's for table 10A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 10C show the genomic positioning for those Pkey's lacking UnigenelD's and accession numbers in table 10A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigenelD:	Unigene number			
60	Unigene Title:	Unigene gene title			
	R1:	Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the average of normal lung samples			
	R2:	Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples			
65	Pkey	ExAccn	UnigenelD	Unigene Title	R1 R2
	404394			ENSP00000241075:TRRAP PROTEIN.	0.79 3.10
	404916			Target Exon	1.00 159.00
	405257			Target Exon	1.00 422.00
70	407228	M25079	Hs.155376	hemoglobin, beta	0.47 2.33
	407568	AA740964	Hs.62699	ESTs	1.00 123.00
	408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	1.00 230.00
	409031	AA376836	Hs.76728	ESTs	1.00 128.00
	410434	AF051152	Hs.63668	toll-like receptor 2	39.65 149.00
75	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	1.00 109.00
	410808	T40326	Hs.167793	ESTs	1.14 13.14
	412351	AL135960	Hs.73828	T-cell acute lymphocytic leukemia 1	0.37 2.27
	412372	R65998	Hs.285243	hypothetical protein FLJ22029	1.00 173.00
	413795	AL040178	Hs.142003	ESTs	0.10 11.90
80	414154	AW205314	Hs.323060	ESTs	0.62 2.09
	414214	D49958	Hs.75819	glycoprotein M6A	0.03 4.55
	414998	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	0.64 2.97
	415122	D60708	Hs.22245	ESTs	0.07 8.97
	415765	NM_005424	Hs.78824	tyrosine kinase with immunoglobulin and	0.67 1.65
85	415775	H00747	Hs.29792	ESTs, Weakly similar to I38022 hypothe	0.29 2.64
	415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	1.00 145.00

5	416319	AI815601	Hs.79197	CD83 antigen (activated B lymphocytes, i	15.32	237.00
	416402	NM_000715	Hs.1012	complement component 4-binding protein,	0.64	4.00
	417355	D13168	Hs.82002	endothelin receptor type B	0.01	3.90
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	36.30	357.00
	417511	AL049176	Hs.82223	chordin-like	1.00	179.00
10	418489	U76421	Hs.85302	adenosine deaminase, RNA-specific, B1 (h	0.02	6.00
	418726	BE241812	Hs.87860	protein tyrosine phosphatase, non-recept	1.00	113.00
	418741	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom	0.44	1.90
	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	0.96	2.04
	419086	NM_000216	Hs.89591	Kallmann syndrome 1 sequence	0.62	2.74
15	419150	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous	0.03	6.90
	419235	AW470411	Hs.288433	neurotrimin	1.48	5.13
	419407	AW410377	Hs.41502	hypothetical protein FLJ21276	37.55	336.00
	420556	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	0.80	3.65
	420656	AA279098	Hs.187636	ESTs	1.65	8.07
20	420729	AW964897	Hs.290825	ESTs	2.99	25.82
	421177	AW070211	Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (f	0.46	1.95
	422060	R20893	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	1.00	166.00
	422426	W79117	Hs.58559	ESTs	0.03	7.44
	422652	AW967969	Hs.118958	syntaxin 11	0.14	3.62
25	423099	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t	0.01	3.16
	424433	H04607	Hs.9218	ESTs	0.75	141.75
	424585	AA464840	Hs.131987	ESTs	1.00	167.00
	424711	NM_005795	Hs.152175	calcitonin receptor-like	0.43	3.01
	424973	X92521	Hs.154057	matrix metalloproteinase 19	0.37	19.45
30	425023	AW956889	Hs.154210	endothelial differentiation, sphingolipi	0.14	3.35
	425664	AJ006276	Hs.159003	transient receptor potential channel 6	1.00	94.00
	425998	AU076629	Hs.165950	fibroblast growth factor receptor 4	0.68	1.42
	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	0.03	3.74
	426753	T89832	Hs.170278	ESTs	1.00	141.00
35	427558	D49493	Hs.2171	growth differentiation factor 10	1.00	117.00
	427983	M17706	Hs.2233	colony stimulating factor 3 (granulocyte	0.75	2.20
	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	0.76	2.25
	428927	AA441837	Hs.90250	ESTs	0.01	3.62
	429496	AA453800	Hs.192793	ESTs	1.00	138.00
40	430468	NM_004673	Hs.241519	angiopoietin-like 1	1.00	132.00
	431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	1.00	157.00
	431728	NM_007351	Hs.268107	multimerin	1.00	157.00
	431848	AI378857	Hs.126758	ESTs, Highly similar to AF175283 1 zinc	0.34	2.24
	432128	AA127221	Hs.117037	ESTs	0.00	1.15
45	432519	AI221311	Hs.130704	ESTs, Weakly similar to BCHUIA S-100 pro	0.01	2.06
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	1.00	267.00
	433803	AI823593	Hs.27688	ESTs	1.00	105.00
	434730	AA644669	Hs.193042	ESTs	1.05	3.15
	435472	AW972330	Hs.283022	triggering receptor expressed on myeloid	0.83	1.94
50	436532	AA721522	gb:mv54h12.r1 NCI_CGAP_Ew1 Homo sapiens	1.00	218.00	
	437119	AI379921	Hs.177043	ESTs	1.00	133.00
	437140	AA312799	Hs.283689	activator of CREM in testis	0.67	122.67
	437211	AA382207	Hs.5509	ecotropic viral integration site 2B	1.00	142.00
	437960	AI669586	Hs.222194	ESTs	1.00	147.00
55	438202	AW169287	Hs.22588	ESTs	1.00	141.00
	438873	AI302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	0.71	3.66
	438875	AA827640	Hs.189059	ESTs	23.32	370.00
	441048	AA913488	Hs.192102	ESTs	0.77	8.50
	441188	AW292830	Hs.255609	ESTs	3.43	16.36
60	441499	AW298235	Hs.101689	ESTs	1.00	167.00
	444513	AL120214	Hs.7117	glutamate receptor, ionotropic, AMPA 1	1.00	151.00
	444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	46.47	153.00
	444561	NM_004469	Hs.11392	c-fos induced growth factor (vascular en	0.01	3.08
	445279	R41900	Hs.22245	ESTs	0.60	141.00
65	446017	N98238	Hs.55185	ESTs	0.18	2.39
	446984	AB020722	Hs.16714	Rho guanine exchange factor (GEF) 15	0.10	2.16
	446998	N99013	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	0.01	2.53
	447357	AI375922	Hs.159367	ESTs	0.46	2.64
	448106	AI800470	Hs.171941	ESTs	18.05	296.00
70	448253	H25899	Hs.201591	ESTs	1.00	141.00
	449275	AW450848	Hs.205457	periaxin	0.56	1.38
	450400	AI694722	Hs.279744	ESTs	0.88	4.33
	450696	AI654223	Hs.16026	hypothetical protein FLJ23191	0.52	2.08
	450726	AW204600	Hs.250505	retinoic acid receptor, alpha	0.79	2.01
75	451497	H83294	Hs.284122	Wnt inhibitory factor-1	0.35	2.03
	451533	NM_004657	Hs.26530	serum deprivation response (phosphatidyl	0.13	2.25
	453636	R67837	Hs.169872	ESTs	1.00	116.00
	458332	AI000341	Hs.220491	ESTs	1.00	192.00
	459580	AA022888	Hs.176065	ESTs	0.20	2.98
80	400269			Eos Control	0.40	2.40
	403421			NM_016369*:Homo sapiens claudin 18 (CLDN	0.53	1.77
	407570	Z19002	Hs.37096	zinc finger protein 145 (Kruppel-like, e	0.01	3.18
	412295	AW088826	Hs.117176	poly(A)-binding protein, nuclear 1	0.56	1.74
	414517	M24461	Hs.76305	surfactant, pulmonary-associated protein	0.64	1.50
85	417204	N81037	Hs.1074	surfactant, pulmonary-associated protein	0.33	1.16
	418307	U70867	Hs.83974	solute carrier family 21 (prostaglandin	0.53	1.55
	418935	T28499	Hs.89485	carbonic anhydrase IV	0.20	1.28
	421502	AF111856	Hs.105039	solute carrier family 34 (sodium phospho	0.78	1.90
	421798	N74880	Hs.29877	N-acylsphingosine amidohydrolase (acid c	0.59	1.54

5	423354	AB011130	Hs.127436	calcium channel, voltage-dependent, alph	0.59	1.55
	423738	AB002134	Hs.132195	airway trypsin-like protease	10.14	51.00
	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	0.35	1.62
	425438	T62216	Hs.270840	ESTs	0.23	9.45
	426828	NM_000020	Hs.172670	activin A receptor type II-like 1	0.03	1.71
10	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	0.01	1.49
	428043	T92248	Hs.2240	uteroglobin	0.42	1.26
	430280	AA361258	Hs.237868	interleukin 7 receptor	0.46	2.43
	431433	X65018	Hs.253495	surfactant, pulmonary-associated protein	0.57	1.59
	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	0.29	1.80
15	432985	T92363	Hs.178703	ESTs	0.32	2.27
	441835	AB036432	Hs.184	advanced glycosylation end product-speci	0.31	1.51
	442275	AW449467	Hs.54795	ESTs	0.55	1.78
	443709	AI082692	Hs.134662	ESTs	0.00	3.02
	444325	AW152618	Hs.16757	ESTs	0.32	2.49
20	450954	AI904740	Hs.25691	receptor (calcitonin) activity modifying	0.46	1.74
	451558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1	0.52	1.87
	453310	X70697	Hs.553	solute carrier family 6 (neurotransmitte	0.00	3.30
	456855	AF036528	Hs.153863	MAD (mothers against decapentaplegic, Dr	0.01	2.31
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	0.66	2.20
25	400754			Target Exon	1.00	297.00
	401045			C11001883:gij6753278 ref NP_033938.1 c	1.00	109.00
	401083			NM_016582*:Homo sapiens peptide transpor	0.89	1.39
	402474			NM_004079:Homo sapiens cathepsin S (CTSS	1.45	4.47
	402808			ENSP00000235229:SEMB.	1.00	1.87
30	403021			C21000030:gij9955960 ref NP_063957.1 AT	1.00	149.00
	403438			NM_031419*:Homo sapiens molecule possess	1.06	2.96
	403687			NM_007037*:Homo sapiens a disintegrin-li	0.04	4.89
	403764			NM_005463:Homo sapiens heterogeneous nuc	1.00	225.00
	404277			NM_019111*:Homo sapiens major histocompa	0.97	1.93
35	404288			NM_002944*:Homo sapiens v-ros avian UR2	1.00	68.00
	404518	AI815601		CD83 antigen (activated B lymphocytes, i	0.02	1.83
	405106			C11001637*:gij5032241 ref NP_005732.1 z	1.00	235.00
	405381			Target Exon	1.00	93.00
	406387			Target Exon	1.37	6.02
40	406646	M33600		major histocompatibility complex, class	0.86	2.46
	406714	AI219304	Hs.266959	hemoglobin, gamma G	0.01	3.19
	406753	AA505665	Hs.217493	annexin A2	1.00	147.00
	406973	M34996	Hs.198253	major histocompatibility complex, class	1.03	2.04
	407248	U82275	Hs.94498	leukocyte immunoglobulin-like receptor,	1.00	64.00
45	407510	U96191		gb:Human trophoblast hypoxia-regulated f	1.00	90.00
	407731	NM_000066	Hs.38069	complement component 8, beta polypeptide	1.00	67.00
	407830	NM_001086	Hs.587	arylacetamide deacetylase (esterase)	1.00	102.00
	408045	AW138959	Hs.245123	ESTs	1.00	70.00
	408074	R20723		ESTs	1.00	112.00
50	408374	AW025430	Hs.155591	forkhead box F1	0.07	10.17
	409064	AA062954	Hs.141883	ESTs	0.39	2.31
	409083	AF050083	Hs.673	interleukin 12A (natural killer cell sti	1.00	95.00
	409153	W03754	Hs.50813	hypothetical protein FLJ20022	0.01	4.55
	409203	AA780473	Hs.687	cytochrome P450, subfamily IVB, polypept	0.01	3.72
55	409238	AL049990	Hs.51515	Homo sapiens mRNA; cDNA DKFZp564G112 (fr	1.00	79.00
	409389	AB007979	Hs.301281	Homo sapiens mRNA, chromosome 1 specific	0.14	27.35
	409718	D86640	Hs.56045	src homology three (SH3) and cysteine ri	1.00	113.00
	410798	BE178622	Hs.16291	gb:PM3-HT0605-270200-001-a02 HT0605 Homo	0.64	2.47
	411020	NM_006770	Hs.67726	macrophage receptor with collagenous str	0.55	2.40
60	411667	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	1.00	111.00
	412000	AW576555	Hs.15780	ATP-binding cassette, sub-family A (ABC1	1.00	95.00
	412358	BE047490	Hs.24172	ESTs	1.00	87.00
	412420	AL035668	Hs.73853	bone morphogenetic protein 2	1.43	8.07
	412564	X83703	Hs.31432	cardiac ankyrin repeat protein	0.02	3.07
65	412869	AA290712	Hs.82407	CXC chemokine ligand 16	0.93	1.72
	412870	N22788	Hs.82407	CXC chemokine ligand 16	0.97	1.51
	413529	U11874	Hs.846	interleukin 8 receptor, beta	0.02	2.42
	413533	BE146973		gb:QV4-HT0222-011199-019-e05 HT0222 Homo	0.65	1.50
	413689	BE157286	Hs.20631	zinc finger protein, subfamily 1A, 5 (Pe	20.87	232.00
70	413724	AA131466	Hs.23767	hypothetical protein FLJ12666	1.00	80.00
	413800	AI129238	Hs.192235	ESTs	1.00	85.00
	413802	AW964490	Hs.32241	ESTs, Weakly similar to S65657 alpha-1C-	1.00	213.00
	413829	NM_001872	Hs.75572	carboxypeptidase B2 (plasma)	0.02	3.93
	414376	BE393856	Hs.66915	ESTs, Weakly similar to 16.7Kd protein [1.00	115.00
75	414577	AI056548	Hs.72116	hypothetical protein FLJ20992 similar to	0.49	1.94
	414700	H63202	Hs.38163	ESTs	0.03	3.75
	415078	AA311223	Hs.283091	found in inflammatory zone 3	0.86	1.95
	415120	N64464	Hs.34950	ESTs	1.00	120.00
	415323	BE269352	Hs.949	neutrophil cytosolic factor 2 (65kD, chr	0.60	2.48
80	415335	AA847758	Hs.111030	ESTs	1.00	95.00
	415582	W92445	Hs.165195	Homo sapiens cDNA FLJ14237 fis, clone NT	1.00	136.00
	416030	H15261	Hs.21948	ESTs	0.02	8.07
	416427	BE244050	Hs.79307	Rac/Cdc42 guanine exchange factor (GEF)	1.00	73.00
	416464	NM_000132	Hs.79345	coagulation factor VIII, procoagulant co	0.70	3.36
85	416585	X54162	Hs.79386	leiomodin 1 (smooth muscle)	0.06	6.56
	416847	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do	0.70	3.66
	417148	AA359896	Hs.293885	hypothetical protein FLJ14902	1.00	114.00
	417370	T28651	Hs.82030	tryptophanyl-tRNA synthetase	0.85	1.30
	417673	T87281	Hs.16355	ESTs	0.15	15.54

	418067	AI127958	Hs.83393	cystatin E/M	0.81	1.74
	418296	C01566	Hs.86671	ESTs	1.00	99.00
	418643	J03798	Hs.86948	small nuclear ribonucleoprotein D1 polyp	1.00	60.00
	418832	X04011	Hs.88974	cytochrome b-245, beta polypeptide (chro	2.40	14.74
5	418945	BE246762	Hs.89499	arachidonate 5-lipoxygenase	0.67	3.16
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	1.00	73.00
	419564	U08989	Hs.91139	solute carrier family 1 (neuronal/epithe	1.00	192.00
	419574	AK001989	Hs.91165	hypothetical protein	1.00	94.00
10	419968	X04430	Hs.93913	interleukin 6 (interferon, beta 2)	61.16	500.00
	420256	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula	0.52	1.70
	420285	AA258124	Hs.293878	ESTs, Moderately similar to ZN91_HUMAN Z	1.00	172.00
	420577	AA278436	Hs.186649	ESTs	1.00	97.00
	421262	AA286746	Hs.9343	Homo sapiens cDNA FLJ14265 fis, clone PL	1.00	64.00
15	421445	AA913059	Hs.104433	Homo sapiens, clone IMAGE:4054868, mRNA	0.88	1.51
	421470	R27496	Hs.1378	annexin A3	0.05	11.26
	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	1.00	73.00
	421563	NM_006433	Hs.105806	granulysin	0.82	2.42
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	5.50	31.57
20	421855	F06504	Hs.27384	ESTs, Moderately similar to ALU4_HUMAN A	1.00	129.00
	421913	AI934365	Hs.109439	osteoglycin (osteoglycin factor, mime	1.00	101.00
	421952	AA300900	Hs.98849	ESTs, Moderately similar to AF161511 1 H	0.60	63.60
	422232	D43945	Hs.113274	transcription factor EC	1.00	148.00
	422386	AF105374	Hs.115830	heparan sulfate (glucosamine) 3-O-sulfot	1.40	3.98
25	423168	R34385	Hs.124940	GTP-binding protein	0.34	3.59
	423196	AK001866	Hs.125139	hypothetical protein FLJ11004	0.55	2.00
	423387	AJ012074		vasoactive intestinal peptide receptor 1	0.09	2.13
	423424	AF150241	Hs.128433	prostaglandin D2 synthase, hematopoietic	1.00	141.00
	423456	AL110151	Hs.128797	DKFZP586D0824 protein	1.00	66.00
30	423696	Z92546		Sushi domain (SCR repeat) containing	0.73	1.27
	424027	AW337575	Hs.201591	ESTs	0.54	2.58
	424212	NM_005814	Hs.143131	glycoprotein A33 (transmembrane)	0.77	2.47
	425087	R62424	Hs.126059	ESTs	1.00	74.00
	425175	AF020202	Hs.155001	UNC13 (C. elegans)-like	0.85	1.96
35	425771	BE561776	Hs.159494	Bruton agammaglobulinemia tyrosine kinas	1.18	2.56
	426486	BE178285	Hs.170056	Homo sapiens mRNA; cDNA DKFZp586B0220 (f	1.00	76.00
	427507	AF240467	Hs.179152	toll-like receptor 7	1.00	63.00
	427618	NM_000760	Hs.2175	colony stimulating factor 3 receptor (gr	0.60	2.19
	427732	NM_002980	Hs.2199	secretin receptor	0.97	1.42
40	427952	AA765368	Hs.293941	ESTs, Moderately similar to A53959 throm	1.00	105.00
	428709	BE268717	Hs.104916	hypothetical protein FLJ21940	1.00	80.00
	428769	AW207175	Hs.106771	ESTs	0.09	2.55
	428780	AI478578	Hs.50636	ESTs	1.00	98.00
	428833	AI928355	Hs.185805	ESTs	1.00	113.00
45	429657	D13626	Hs.2465	KIAA0001 gene product; putative G-protei	1.00	52.00
	430212	AA469153		gb:nc67f04.s1 NCI_CGAP_Pr1 Homo sapiens	1.00	132.00
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	0.11	15.60
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	1.00	103.00
	430414	AW365665	Hs.120388	ESTs	0.50	6.96
50	430656	AA482900	Hs.162080	ESTs	1.00	70.00
	430843	AI734149	Hs.119514	ESTs	1.00	90.00
	430998	AF128847	Hs.204038	indolethylamine N-methyltransferase	0.29	1.84
	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	1.00	79.00
	431921	N46466	Hs.58879	ESTs	0.91	1.67
55	432176	AW090386	Hs.112278	arrestin, beta 1	0.66	2.63
	432203	AA305746	Hs.49	macrophage scavenger receptor 1	1.00	76.00
	432231	AA339977	Hs.274127	CLST 11240 protein	0.46	1.46
	432485	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	0.79	2.25
	432522	D11466	Hs.51	phosphatidylinositol glycan, class A (pa	1.93	4.83
60	432596	AJ224741	Hs.278461	mairilin 3	0.04	5.79
	432850	X87723	Hs.3110	angiotensin receptor 2	1.00	167.00
	433138	AB029496	Hs.59729	semaphorin sem2	0.04	9.16
	433563	AI732637	Hs.277901	ESTs	1.00	91.00
	433588	AI056872	Hs.133386	ESTs	120.16	315.00
65	434445	AI349306	Hs.11782	ESTs	0.60	1.84
	435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-r	1.00	128.00
	435974	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor	1.00	108.00
	436061	AI248584	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone C	1.00	91.00
	437157	BE048860	Hs.120655	ESTs	1.00	87.00
70	437207	T27503	Hs.15929	hypothetical protein FLJ12910	1.00	105.00
	437311	AA370041	Hs.9456	SWI/SNF related, matrix associated, acti	1.00	71.00
	437439	H29796	Hs.269622	ESTs	1.00	115.00
	438199	AW016531	Hs.122147	ESTs	1.00	80.00
	439551	W72062	Hs.11112	ESTs	0.30	3.10
75	440515	AJ131245	Hs.7239	SEC24 (S. cerevisiae) related gene famil	1.00	77.00
	440887	AI799488	Hs.135905	ESTs	1.00	85.00
	441025	AA913880	Hs.176379	ESTs	1.00	82.00
	441384	AA447849	Hs.288660	Homo sapiens cDNA: FLJ22182 fis, clone H	0.79	1.89
	441735	AI738675	Hs.127346	ESTs	1.00	75.00
80	442200	AW590572	Hs.235768	ESTs	0.78	5.83
	442832	AW206560	Hs.253569	ESTs	0.03	10.88
	442957	AI949952	Hs.49397	ESTs	1.00	70.00
	443282	T47764	Hs.132917	ESTs	1.00	197.00
	443547	AW271273	Hs.23767	hypothetical protein FLJ12666	1.00	253.00
	443951	F13272	Hs.111334	ferritin, light polypeptide	0.55	2.09
85	444330	AI597655	Hs.49265	ESTs	1.00	90.00

	444515	AW204908	Hs.169979	ESTs	1.00	84.00
	445769	AI741471	Hs.23666	ESTs	0.02	4.38
	445908	R13580	Hs.13436	Homo sapiens clone 24425 mRNA sequence	1.00	97.00
5	446291	BE397753	Hs.14623	interferon, gamma-inducible protein 30	0.93	1.69
	446917	AI347863	Hs.156672	ESTs	1.00	106.00
	447261	NM_006691	Hs.17917	extracellular link domain-containing 1	0.40	47.20
	447432	AW958473	Hs.301957	nudix (nucleoside diphosphate linked moi	1.00	100.00
	447482	AB033059	Hs.18705	KIAA1233 protein	0.05	8.21
10	447997	H00656	Hs.29792	ESTs, Weakly similar to I38022 hypotheti	0.02	5.42
	448299	AA497044	Hs.20887	hypothetical protein FLJ10392	1.00	79.00
	448782	AL050295	Hs.22039	KIAA0758 protein	0.42	1.56
	450575	NM_005859	Hs.29117	purine-rich element binding protein A	0.17	11.33
	450584	AA040403	Hs.60371	ESTs	1.00	94.00
15	450693	AW450461	Hs.203965	ESTs	1.00	91.00
	450715	AI266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	1.00	152.00
	451103	R52804	Hs.25956	DKFZP564D206 protein	1.00	86.00
	451220	AF124251	Hs.26054	novel SH2-containing protein 3	0.60	1.30
	451668	Z43948	Hs.326444	cartilage acidic protein 1	0.54	1.91
20	452197	AW023595	Hs.232048	ESTs	1.00	67.00
	452331	AA598509	Hs.29117	purine-rich element binding protein A	4.53	11.07
	452353	C18825	Hs.29191	epithelial membrane protein 2	0.72	2.24
	453049	BE537217	Hs.30343	ESTs	1.00	68.00
	453107	NM_016113	Hs.279746	vanilloid receptor-like protein 1	0.83	1.70
25	453355	AW295374	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	1.00	132.00
	453390	AA862496	Hs.28482	ESTs	1.00	72.00
	453531	AA417940		ESTs, Weakly similar to JC5795 CDEP prot	1.00	68.00
	454741	BE154396		gb:CM2-HT0342-091299-050-b05 HT0342 Homo	0.57	2.89
	456579	AA287827	Hs.284205	up-regulated by BCG-CWS	1.00	82.00
30	456672	AK002016	Hs.114727	Homo sapiens, clone MGC:16327, mRNA, com	0.79	1.96
	457400	AF032906	Hs.252549	cathepsin Z	1.03	3.25
	457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	1.00	113.00
	459696	F03027		gb:HSC1KA072 normalized infant brain cDN	1.00	544.00

TABLE 10B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

40	Pkey	CAT Number	Accession
	408074	103684_1	R20723 AA263003 AA333976 AA334725 AA334151 AW965490 AA310513 AI810530 D31302 AW134897 AA830127 AA046953 AI668930 C06094 AW104534
	411667	1253334_1	BE160198 AW935898 T11520 AW935930 AW856073 AW861034
45	413533	1375344_1	BE146973 BE146972 BE147042 BE147018 BE146783 BE147020 BE146781 BE147019 BE146766 BE147021 BE146952 BE146767 BE147044 BE146797 BE146776 BE146985 BE146793 BE146768 BE146771 BE146954 BE146760 BE147048 BE147025 BE147030
	423387	22779_1	AJ012074 U11087 L13288 X75299 L20295 AW630780 H14880 T28037 AI872991 R72136 AW449839 T81622 T79697 T29519 R94105 T83923 R73300 AI797007 R73390 AA961010 H74168 AI689932 BE045543 AI808418 AI608912 AI806573 AW884084 AW872978 AW872985 AA565655 AI022915 R50647 R73210 H45098 R46451 AW166269 T71132 AI264547 R52146 AI304920 R73391 AW884059 AW884085 H73241 T60038 T79612 R73145 R50549 AI094557 AI668793 R72302 AI564366 W01956 AA418962 W32571 R72840 H45409 R72085 R46356 R46758
50	423696	23112_1	AA508805 AA418798 T83751 R94072 T16182 AA928785 AA903896 Z92546 AA330586 AI570568 AW341487 AI827050 AW298668 AI792189 AI015693 AI733599 AI572251 AI672488 AW193262 AI244716 AI864375 AI206100 AA912444 AI269365 AI640254 AW772466 AI867336 AA627604 H16914 AA358477 AA338009
	430212	314437_1	AA469153 AI718503 AA469225
55	436532	421802_1	AA721522 AW975443 T93070
	453531	97026_1	AA417940 AA036735 T07025
	454741	1232559_1	BE154396 AW817959 BE154393

TABLE 10C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	Nt_position
70	400754	7331445	Plus	144559-144684
	401045	8117619	Plus	90044-90184,91111-91345
	401083	3242744	Plus	33192-33360
	402474	7547175	Minus	53526-53628,55755-55920,57530-57757
	402808	6456148	Minus	114964-115136,115461-115585,115931-116047,117666-117771,118004-118102
	403021	7547270	Plus	120799-120966
75	403421	9665041	Minus	126609-126773,139986-140205
	403438	9719679	Plus	90792-90938
	403687	7387384	Plus	9009-9534
	403764	7717105	Minus	118692-118853
	404277	1834458	Minus	91665-91946
80	404288	2769644	Plus	3512-3691
	404394	3135305	Minus	37121-37205,37491-37762,41053-41140,41322-41593,41773-41919
	404518	8151988	Plus	84494-84603
	404916	7341826	Plus	91057-91188
	405106	8079395	Minus	80877-81418
85	405257	7329310	Plus	73121-73273
	405381	6006920	Minus	7636-8054

TABLE 11A: Genes Distinguishing Adenocarcinoma from Other Lung Diseases and Normal Lung

Table 11A shows about 84 genes upregulated in lung adenocarcinomas relative to other lung tumors, non-malignant lung disease, and normal lung. These genes were selected from about 59680 probesets on the Eos/Atfyetrix Hu03 Genechip array.

Table 11B show the accession numbers for those Pkey's lacking UnigeneID's for table 11A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 11C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 11A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the average of normal lung samples
 R2: Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples

Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
403329			Target Exon	1.00	61.00
406399			NM_003122*:Homo sapiens serine protease	1.00	39.00
406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	226.37	350.00
407869	AI827976	Hs.24391	hypothetical protein FLJ13612	0.77	1.18
407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	1.00	10.00
408908	BE296227	Hs.250822	serine/threonine kinase 15	7.76	1.00
409103	AF251237	Hs.112208	XAGE-1 protein	80.44	40.00
409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitoch	1.00	1.00
409269	AA576953	Hs.22972	hypothetical protein FLJ13352	1.00	1.00
410076	T05387	Hs.7991	ESTs	1.12	1.50
410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	9.89	1.00
410399	BE068889		synuclein, gamma (breast cancer-specific	0.92	1.06
411908	L27943	Hs.72924	cytidine deaminase	1.00	1.00
412612	NM_000047	Hs.74131	arylsulfatase E (chondrodysplasia puncta	1.02	1.03
414075	U11862	Hs.75741	amiloride binding protein 1 (amine oxida	0.84	1.07
416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	3.67	1.00
417542	J04129	Hs.82269	progesterone-associated endometrial prole	1.28	1.35
419183	U06669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	1.00	1.00
419502	AU076704		fibrinogen, A alpha polypeptide	13.05	115.00
419631	AW188117	Hs.303154	popeye protein 3	1.00	13.00
420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	1.00	8.00
421155	H87879	Hs.102267	lysyl oxidase	1.00	15.00
421190	U95031	Hs.102482	mucin 5, subtype B, tracheobronchial	1.17	1.55
421474	U76362	Hs.104637	solute carrier family 1 (glutamate trans	1.46	1.76
421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, I	1.00	3.00
421582	AI910275		trefoil factor 1 (breast cancer, estroge	1.23	1.00
422026	U80736	Hs.110826	trinucleotide repeat containing 9	1.00	52.00
422095	AI868872	Hs.282804	hypothetical protein FLJ22704	4.37	2.34
422311	AF073515	Hs.114948	cytokine receptor-like factor 1	1.15	1.78
422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	1.69	3.17
423472	AF041260	Hs.129057	breast carcinoma amplified sequence 1	48.13	72.00
423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	1.00	50.00
424502	AF242388	Hs.149585	lengsin	1.00	1.00
424544	M88700	Hs.150403	dopa decarboxylase (aromatic L-amino aci	1.00	59.00
424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	21.35	1.00
424960	BE245380	Hs.153952	5' nucleotidase (CD73)	1.00	1.00
425523	AB007948	Hs.158244	KIAA0479 protein	1.00	35.00
426230	AA367019	Hs.241395	protease, serine, 1 (trypsin 1)	1.00	83.00
427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	7.41	34.00
428585	AB007863	Hs.185140	KIAA0403 protein	1.00	6.00
428758	AA433988	Hs.98502	hypothetical protein FLJ14303	1.06	1.13
429170	NM_001394	Hs.2359	dual specificity phosphatase 4	16.18	105.00
429263	AA019004	Hs.198396	ATP-binding cassette, sub-family A (ABC1	1.07	1.00
429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	1.59	1.69
430508	AI015435	Hs.104637	ESTs	4.75	7.27
430985	AA490232	Hs.27323	ESTs, Weakly similar to I78885 serine/th	0.94	1.28
431548	AI834273	Hs.9711	novel protein	5.66	15.00
431566	AF176012	Hs.260720	J domain containing protein 1	49.76	37.00
431986	AA536130	Hs.149018	Novel human gene mapping to chromosome 20	1.19	1.47
432375	BE536069	Hs.2962	S100 calcium-binding protein P	1.65	1.06
432677	NM_004482	Hs.278611	UDP-N-acetyl-alpha-D-galactosamine:polyp	1.00	48.00
433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	1.00	19.00
433819	AW511097	Hs.112765	ESTs	3.71	8.00
434001	AW950905	Hs.3697	serine (or cysteine) proteinase inhibito	29.31	72.00
434424	AI811202	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	1.00	64.00
434792	AA649253	Hs.132458	ESTs	8.52	44.00
436217	T53925	Hs.107	fibrinogen-like 1	57.97	31.00
436749	AA584890	Hs.5302	lectin, galactoside-binding, soluble, 4	1.10	1.41
436972	AA284679	Hs.25640	claudin 3	1.59	1.46
437866	AA156781		metallothionein 1E (functional)	3.62	101.00
437935	AW939591	Hs.5940	mucin 13, epithelial transmembrane	1.60	1.39
438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	1.00	1.00
439451	AF086270	Hs.278554	heterochromatin-like protein 1	23.28	52.00

	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	1.00	21.00
	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	1.41	99.00
	441377	BE218239	Hs.202666	ESTs	22.03	1.00
5	443614	AV655386	Hs.7645	fibrinogen, B beta polypeptide	1.00	16.00
	443813	AA876372	Hs.93961	Homo sapiens mRNA; cDNA DKFZp667D095 (fr	1.20	1.99
	443991	NM_002250	Hs.10082	potassium intermediate/small conductance	5.71	6.87
	444670	H58373	Hs.332938	hypothetical protein MGC5370	1.98	38.00
	444931	AV652066	Hs.75113	general transcription factor IIIa	1.00	54.00
10	446102	AW168067	Hs.317694	ESTs	1.00	1.00
	446163	AA026880	Hs.25252	Homo sapiens cDNA FLJ13603 fis, clone PL	1.00	36.00
	446469	BE094848	Hs.15113	homogentisate 1,2-dioxygenase (homogenti	1.00	11.00
	447388	AW630534	Hs.76277	Homo sapiens, clone MGC:9381, mRNA, comp	1.24	1.16
	447532	AK000614	Hs.18791	hypothetical protein FLJ20607	1.23	1.63
	448243	AW369771	Hs.52620	integrin, beta 8	15.84	1.00
15	448844	AI581519	Hs.177164	ESTs	1.00	31.00
	449444	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	1.00	83.00
	451807	W52854		hypothetical protein FLJ23293 similar to	1.55	35.00
	452689	F33868	Hs.284176	transferrin	1.54	1.44
	453392	U23762	Hs.32964	SRY (sex determining region Y)-box 11	1.00	16.00
20	453464	AI884911	Hs.32989	receptor (calcitonin) activity modifying	1.55	2.45
	453735	AI066629	Hs.125073	ESTs	1.01	1.30

TABLE 11B

25	Pkey: Unique Eos probeset identifier number CAT number: Gene cluster number Accession: Genbank accession numbers		
30	Pkey	CAT Number	Accession
	410399	11995_1	BE068889 BE068882 AF044311 AF017256 NM_003087 AF037207 AF010126 AA633976 AA872836 BE298825 BE299899 AI016464 AI684600 AI936527 AA804675 AA394097 AI139933 AA946606 BE171313 AA722407 AA293803 AI688480 AA056035 AA055968 AW796957 AI637713 AA410737 H49348 AA486472 AA411094 AA235594 AA402624 AA443638 AW452137 AA421708 AW265211 AI493266 AA365132 AW966044 AU076704 T74854 T74860 T72098 T73265 T73873 T69180 T74658 T58786 T60385 T73410 T68781 T67845 T67593 T73952 T67864 T60630 T68367 T68401 T53959 T72360 T72099 T60377 T58961 T71712 T72821 T64738 T74645 T72037 T68688 T72063 T73258 T72826 T64242 T68220 T74673 T71800 T68355 T61227 T62738 T69317 T53850 T64692 T73768 T73962 T73382 T68914 T70975 T73400 T60631 T73277 T73203 T70498 T61409 T58925 NM_000508 M64982 T68301 T73729 T69445 T60424 T67922 T67736 T68716 T67755 T74765 T73819 T58719 T74756 T60477 T74863 T61109 T68329 T58850 T71857 T73425 T53736 T68607 T58898 T64309 T72031 T72079 T64305 T71908 T68107 T71916 T73787 T56035 T64425 T71870 T60476 T61376 T67820 T71895 T41006 T69441 T68170 T74617 T71958 T69440 T61875 R06796 H48353 T71914 T53939 T64121 AA693996 T72525 T67779 T68078 AA011465 AA345378 AV654847 AV654272 AV656001 AI064740 T82897 N33594 AA344542 AW805054 AI207457 T61743 AA026737 H94389 AA382695 AA918409 T68044 S82092 T39959 AI017721 AA312395 AA312919 T40156 H66239 AV652989 H38728 R98521 AV655200 R95790 W03250 W00913 AA344136 AV660126 R97923 AA343596 AW470774 AV651256 N54417 AA812862 AW182929 AI111192 H61463 H72060 AA344503 H38639 AI277511 AV661108 AI207625 T47810 AA235252 T27853 T47778 R95746 H70620 AA701463 AW827166 R98475 C20925 AV657287 T71959 T71313 T73920 T73333 T61618 T69293 T69283 T73931 T72178 T72456 AV645639 AV653476 T72957 T72300 T58906 T71457 T70494 T72956 T70495 T68267 T74407 T85778 AA344726 T27854 T74485 T74101 T73868 T71518 T72304 AA343853 T73909 T68070 T72065 H72149 T73493 T73495 AV645993 R02293 T70475 T64751 AA344441 AA343657 AA345732 AA344328 AI110639 AA344603 AF063513 T64696 T68516 T72223 T60507 T67633 R29500 T72517 R02292 T60599 T69206 T70452 T74677 R29366 T61277 T74914 T60352 R29675 T74843 AV645792 AA344408 T69197 T72057 T69368 T69358 T68258 AV650429 T73341 T61702 T74598 T40095 K02272 T40106 AA343045 AA341908 AA341907 AA342807 AA341964 T53747 T72042 T62764 AI064899 AA343080 T67832 T72440 T71770 T68091 T69108 T72449 T69167 T71289 T68251 AV654844 T64375 AA345234 T67598 AA011414 T68036 H48262 AI207557 T68219 W86031 T69081 T64232 R93196 T62136 AV650539 H67459 T72978 AA344583 T60362 H58121 T95711 T72803 T68055 T71715 R29036 T72793 T69122 T64595 T62888 T69139 T68291 T64652 T67971 T46862 AA693592 AI248502 R29454 T64764 T57001 T73052 T71429 T51176 T58866 AV655414 H90426 AA342489 T73666 T67848 T72512 T53835 T67837 T73317 T74273 T69420 T68245 T74380 T67862 T74474 T56068 AI910275 X00474 X52003 X05030 NM_003225 AA314326 AA308400 AA506787 AA314825 AI571948 AA507595 AA614579 AA587613 R83818 AA568312 AA614409 AA307578 AI925552 AW950155 AI910083 M12075 BE074052 AW004668 AA578674 AA582084 BE074053 BE074126 BE074140 AA514776 AA588034 BE074051 BE074068 AW009769 AW050690 AA858276 R55389 AI001051 AW050700 AW750216 AA614539 BE074045 AI307407 AW602303 BE073575 AI202532 AA524242 AI970839 AI909751 BE076078 AI909749 R55292 AA156781 AW293839 U52054 AA024963 AA778446 BE073977 AW444904 AW602574 BE164040 BE164012 BE163972 BE163974 BE163992 AA837481 AW468444 BE185091 AW468002 AA687333 AA811830 AA581806 AI866686 AI572124 AA043777 AA040926 D20160 AI536733 AA812489 AW874142 AI471883 W84421 AA156850 W52854 AL117600 BE208116 BE208432 BE206239 BE082291 AW953423 AA351619 BE180648 BE140560 W60080 AA865478 N90291 AW450652 AW449519 AA993634 AI806539 AA351618 AW449522 AI827628 AA904788 AA380381 AA886045 AA774409 BE003229 Z41756

TABLE 11C

70	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
	Nt_position:	Indicates nucleotide positions of predicted exons.		
75	Pkey	Ref	Strand	Nt_position
	403329	8516120	Plus	96450-96598
	406399	9256288	Minus	63448-63554

TABLE 12A: Genes Distinguishing Squamous Cell Carcinoma from Other Lung Diseases and Normal Lung

Table 12A shows about 72 genes upregulated in squamous cell carcinomas of the lung relative to other lung tumors, non-malignant lung disease, and normal lung. These genes were selected from about 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

Table 12B show the accession numbers for those Pkey's lacking UnigenelD's for table 12A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 12C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 12A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the average of normal lung samples
 R2: Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples

Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	132.45	4.00
400666			NM_002425:Homo sapiens matrix metallopro	3.26	3.22
401780			NM_005557*:Homo sapiens keratin 16 (foca	26.47	10.50
401781			Target Exon	10.33	4.61
401785			NM_002275*:Homo sapiens keratin 15 (KRT1	4.13	2.70
401994			Target Exon	61.84	47.00
402075			ENSP00000251056*:Plasma membrane calcium	1.00	1.00
404996			Target Exon	1.00	1.00
407839	AA045144	Hs.161566	ESTs	173.91	108.00
408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	151.17	8.00
408522	AI541214	Hs.46320	Small proline-rich protein SPRK [human,	1.98	1.24
410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	10.04	1.00
415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	1.00	30.00
415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	24.30	1.00
416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	53.29	51.00
417034	NM_006183	Hs.80962	neurotensin	1.00	1.00
417366	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)	8.97	3.27
418663	AK001100	Hs.41690	desmocollin 3	112.17	19.00
418678	NM_001327	Hs.87225	cancer/testis antigen	1.18	1.10
419121	AA374372	Hs.89626	parathyroid hormone-like hormone	1.00	1.00
420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	3.04	1.25
421773	W69233	Hs.112457	ESTs	1.12	1.14
421948	L42583	Hs.334309	keratin 6A	51.83	20.25
421978	AJ243662	Hs.110196	NICE-1 protein	1.01	0.91
422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	2.37	1.10
422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	47.53	32.00
423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	76.02	1.00
423725	AJ403108	Hs.132127	hypothetical protein LOC57822	4.20	1.00
423738	AB002134	Hs.132195	airway trypsin-like protease	10.14	51.00
424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	233.42	68.00
424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	1.00	1.00
424098	AF077374	Hs.139322	small proline-rich protein 3	137.82	54.00
424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	56.19	12.00
425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	33.45	1.00
427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	4.24	17.00
427335	AA448542	Hs.251677	G antigen 7B	51.83	4.00
428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT	1.00	1.00
428645	AA431400	Hs.98729	ESTs, Weakly similar to 2017205A dihydro	1.00	16.00
428748	AW593206	Hs.98785	Ksp37 protein	1.00	87.00
429259	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	2.01	1.18
429538	BE182592	Hs.11261	small proline-rich protein 2A	4.43	2.90
429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	11.80	1.00
430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	12.28	41.00
430890	X54232	Hs.2699	glypican 1	1.58	1.40
431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	60.25	28.00
431846	BE019924	Hs.271580	uroplakin 1B	4.49	2.51
433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	1.20	1.09
434360	AW015415	Hs.127780	ESTs	40.98	27.00
434880	U02388	Hs.101	cytochrome P450, subfamily IVF, polypept	1.00	1.00
435505	AF200492	Hs.211238	interleukin-1 homolog 1	1.00	38.00
435793	AB037734	Hs.4993	KIAA1313 protein	23.68	42.00
436511	AA721252	Hs.291502	ESTs	16.76	14.00
438403	AA806607	Hs.292206	ESTs	1.00	1.00
439285	AL133916		hypothetical protein FLJ20093	46.23	139.00
439605	W79123	Hs.58561	G protein-coupled receptor 87	33.61	1.00
439670	AF088076	Hs.59507	ESTs, Weakly similar to AC004858 3 U1 sm	1.00	1.00
439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	86.55	11.00
440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma	62.88	147.00
441525	AW241867	Hs.127728	ESTs	1.53	1.42
443162	T49951	Hs.9029	DKFZP434G032 protein	31.11	38.00
444378	R41339	Hs.12569	ESTs	1.00	1.00

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446292	AF081497	Hs.279682	Rh type C glycoprotein	1.55	1.26
447078	AW885727	Hs.9914	ESTs	47.24	24.00
447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	28.63	1.00
449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o	1.00	1.00
449101	AA205847	Hs.23016	G protein-coupled receptor	2.58	27.00
450832	AW970602	Hs.105421	ESTs	25.17	36.00
452240	AI591147	Hs.61232	ESTs	13.42	1.00
453317	NM_002277	Hs.41696	keratin, hair, acidic,1	1.19	1.27
453830	AA534296	Hs.20953	ESTs	24.92	25.00
454098	W27953	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	1.26	1.11
455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	206.11	1.00

TABLE 12B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
439285	47065_1	AL133916 N79113 AF086101 N76721 AW950828 AA364013 AW955684 AI346341 AI867454 N54784 AI655270 AI421279 AW014882 AA775552 N62351 N59253 AA626243 AI341407 BE175639 AA456968 AI358918 AA457077

TABLE 12C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400666	8118496	Plus	17982-18115,20297-20456
401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814
401785	7249190	Minus	165776-165996,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942
401994	4153858	Minus	42904-43124,43211-43336,44607-44763,45199-45281,46337-46732
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450

TABLE 13A: Genes Distinguishing Non-Malignant Lung Disease from Lung Tumors and Normal lung

Table 13A shows about 23 genes upregulated in non-malignant lung disease relative to lung tumors and normal lung. These genes were selected from about 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

Table 13B show the accession numbers for those Pkey's lacking UnigenelD's for table 13A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 13C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 13A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the average of normal lung samples
 R2: Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples

Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	1.00	230.00
409031	AA376836	Hs.76728	ESTs	1.00	128.00
412372	R65998	Hs.285243	hypothetical protein FLJ22029	1.00	173.00
415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	1.00	145.00
417511	AL049176	Hs.82223	chordin-like	1.00	179.00
418819	AA228776	Hs.191721	ESTs	1.00	140.00
422060	R20893	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	1.00	156.00
424585	AA464840	Hs.131987	ESTs	1.00	167.00
426753	T89832	Hs.170278	ESTs	1.00	141.00
429496	AA453800	Hs.192793	ESTs	1.00	138.00
430719	AA488988	Hs.293796	ESTs	1.00	133.00
431089	BE041395		ESTs, Weakly similar to unknown protein	23.32	941.00
431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	1.00	157.00
431728	NM_007351	Hs.268107	multimerin	1.00	157.00
436532	AA721522		gb:nv54h12.r1 NCL_CGAP_Ew1 Homo sapiens	1.00	218.00
437960	AI669586	Hs.222194	ESTs	1.00	147.00
438202	AW169287	Hs.22588	ESTs	1.00	141.00
441499	AW298235	Hs.101689	ESTs	1.00	167.00
444513	AL120214	Hs.7117	glutamate receptor, ionotropic, AMPA 1	1.00	151.00
448253	H25899	Hs.201591	ESTs	1.00	141.00
453636	R67837	Hs.169872	ESTs	1.00	116.00
458332	AI000341	Hs.220491	ESTs	1.00	192.00
459587	AA031956		gb:zk15e04.s1 Soares_pregnant_uterus_NbH	1.00	154.00

TABLE 13B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
431089	327825_1	BE041395 AA491826 AA621946 AA715980 AA666102
436532	421802_1	AA721522 AW975443 T93070

TABLE 13C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076

TABLE 14A: Preferred Utility and Subcellular Localization for Potential Lung Disease Targets

Table 14A shows the subcellular localization and preferred utility for the genes appearing in Tables 9A and 10A. mAb symbolizes monoclonal antibody, diag symbolizes diagnostic, s.m. symbolizes small molecule, and CTL symbolizes cytotoxic lymphocytic ligand. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

Table 14B show the accession numbers for those Pkey's lacking UnigenelD's for table 14A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 14C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 14A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique Eos probeset identifier number

ExAccn: Exemplar Accession number, Genbank accession number

UnigenelD: Unigene number

Unigene Title: Unigene gene title

Pref.Utility: Preferred Utility

Pred.Loc: Predicted subcellular localization

Pkey	ExAccn	UnigenelD	Unigene Title	Pref Utility	Pred. Loc
400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	mAb & diag & s.m.	extracellular
400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	mAb	plasma membrane
402075			ENSP00000251056*:Plasma membrane calcium	mAb & diag	secreted
407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagonist	diag	secreted
408243	Y00787	Hs.624	interleukin 8	diag	secreted
408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	mAb & s.m.	plasma membrane
408908	BE296227	Hs.250822	serine/threonine kinase 15	s.m.	cytoplasm
409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	CTL & diag	secreted
409103	AF251237	Hs.112208	XAGE-1 protein	CTL	nuclear
409420	Z15008	Hs.54451	laminin, gamma 2 (niclin (100kD), kalini	diag	secreted
409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibitor	diag	secreted
409757	NM_001898	Hs.123114	cystatin SN	diag	extracellular
409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	CTL	nuclear
409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	diag	extracellular
410001	AB041036	Hs.57771	kallikrein 11	diag	extracellular
410407	X66839	Hs.63287	carbonic anhydrase IX	mAb & s.m.	plasma membrane
410418	D31382	Hs.63325	transmembrane protease, serine 4	mAb & diag & s.m.	plasma membrane
412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	s.m.	
412719	AW016610	Hs.816	ESTs	s.m.	nuclear
414774	X02419	Hs.77274	plasminogen activator, urokinase	diag	extracellular
414883	AA926960		CDC28 protein kinase 1	s.m.	
415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	CTL & diag	extracellular
415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibitor	mAb & diag & s.m.	secreted
415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	mAb & s.m.	plasma membrane
416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	diag	extracellular
417034	NM_006183	Hs.80962	neurotensin	diag	extracellular
417079	U65590	Hs.81134	interleukin 1 receptor antagonist	diag	extracellular
417308	H60720	Hs.81892	KIAA0101 gene product	s.m.	mitochondrial
417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	mAb & diag	secreted
417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	mAb	plasma membrane
417933	X02308	Hs.82962	thymidylate synthetase	s.m.	endoplasmic reticulum
418478	U88945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	s.m.	cytoplasm
418506	AA084248	Hs.85339	G protein-coupled receptor 39	mAb & s.m.	plasma membrane
418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)	CTL	cytoplasmic
419121	AA374372	Hs.89626	parathyroid hormone-like hormone	diag	secreted
419171	NM_002846	Hs.89655	protein tyrosine phosphatase, receptor t	mAb & s.m.	plasma membrane
419183	U06659	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	CTL & s.m.	mitochondrial
419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	diag	secreted
419235	AW470411	Hs.288433	neurotrophin	mAb & diag	plasma membrane
419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	mAb & s.m.	plasma membrane
419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	mAb & diag	extracellular*
420610	AI683183	Hs.99348	distal-less homeo box 5	CTL	nuclear
421110	AJ250717	Hs.1355	cathepsin E	sm & diag	extracellular
421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	diag	secreted
421474	U76362	Hs.104637	solute carrier family 1 (glutamate trans	mAb & s.m.	plasma membrane
421552	AF026692	Hs.105700	secreted frizzled-related protein 4	diag	secreted
421753	BE314828	Hs.107911	ATP-binding cassette, sub-family B (MDR/	mAb & s.m.	plasma membrane
421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	mAb & s.m.	plasma membrane
422109	S73265	Hs.1473	gastrin-releasing peptide	diag	secreted
422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	diag	secreted
422282	AF019225	Hs.114309	apolipoprotein L	diag	secreted
422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	s.m.	nuclear
422424	AI186431	Hs.296638	prostate differentiation factor	diag	extracellular
422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	s.m.	cytoplasm
422809	AK001379	Hs.121028	hypothetical protein FLJ10549	s.m.	nuclear
422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	diag	extracellular
422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	CTL & s.m.	
423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	diag	
423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	mAb & diag & s.m.	secreted
423961	D13666	Hs.136348	perostin (OSF-2os)	mAb & diag	extracellular
424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibitor	diag	secreted
424381	AA285249	Hs.146329	protein kinase Chk2	s.m.	nuclear

	424502	AF242388	Hs.149585	lengsin	s.m.	cytoplasmic
	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	mAb & s.m.	plasma membrane
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	diag	extracellular
5	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	mAb & diag & s.m.	secreted
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	s.m.	cytoplasmic
	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	mAb	plasma membrane
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	s.m.	
	425776	U25128	Hs.159499	parathyroid hormone receptor 2	mAb & diag	plasma membrane
10	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member	mAb & s.m.	plasma membrane
	426215	AW963419	Hs.155223	stanniocalcin 2	mAb & diag	secreted
	426427	M86699	Hs.169840	TTK protein kinase	CTL & s.m.	nuclear
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	mAb & diag	secreted
	427335	AA448542	Hs.251677	G antigen 7B	CTL	cytoplasmic
15	427747	AW411425	Hs.180655	serine/threonine kinase 12	s.m.	cytoplasmic
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	diag	
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	mAb & diag & s.m.	extracellular
	428450	NM_014791	Hs.184339	KIAA0175 gene product	s.m.	nuclear
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	s.m.	nuclear
20	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	mAb & s.m.	plasma membrane
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	CTL & s.m.	nuclear
	428698	AA852773	Hs.334838	KIAA1866 protein	mAb	
	428748	AW593206	Hs.98785	Ksp37 protein	diag	extracellular
	428758	AA433988	Hs.98502	CA125 antigen; mucin 16	diag	mitochondria*
25	428969	AF120274	Hs.194689	artemin	diag	extracellular
	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	mAb & s.m.	plasma membrane
	429263	AA019004	Hs.198396	ATP-binding cassette, sub-family A (ABC1	mAb & s.m.	plasma membrane
	429547	AW009166	Hs.99376	ESTs	diag	secreted
	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	mAb & diag	secreted
30	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	s.m.	
	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	mAb & s.m.	plasma membrane
	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	diag	extracellular
	431515	NM_012152	Hs.258583	endothelial differentiation, lysophospha	mAb & s.m.	plasma membrane
	431846	BE019924	Hs.271580	uroplakin 1B	mAb & diag	plasma membrane
35	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	mAb & diag	plasma membrane
	432201	AI538613	Hs.298241	Transmembrane protease, serine 3	mAb & diag & s.m.	plasma membrane
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	s.m.	nuclear
	435505	AF200492	Hs.211238	interleukin-1 homolog 1	diag	secreted
40	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	s.m.	
	437016	AU076916	Hs.5398	guanine monophosphate synthetase	s.m.	cytoplasm
	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an	CTL	ER
	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	CTL	nuclear
	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365012.1 [H.sa	mAb & s.m.	plasma membrane
	439223	AW238299	Hs.250618	UL16 binding protein 2	mAb	plasma membrane
45	439477	W69813	Hs.58042	ESTs, Moderately similar to GFR3_HUMAN G	mAb & s.m.	
	439606	W79123	Hs.58561	G protein-coupled receptor 87	mAb & s.m.	plasma membrane
	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	mAb & s.m.	plasma membrane
	440006	AK000517	Hs.6844	NALP2 protein; PYRIN-Containing APAF1-li	s.m.	nuclear
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	s.m.	
50	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	mAb & s.m.	plasma membrane
	443247	BE614387	Hs.333893	c-Myc target JPO1	CTL	extracellular*
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	CTL	
	443859	NM_013409	Hs.9914	folliculin	diag	extracellular
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	mAb	plasma membrane
55	444371	BE540274	Hs.239	forkhead box M1	s.m.	nuclear
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	diag	secreted
	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	mAb & diag	plasma membrane
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	mAb & diag	secreted
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	diag	secreted
60	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	diag	extracellular
	447033	AI357412	Hs.157601	ESTs	CTL & diag	secreted
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	CTL	
	448243	AW369771	Hs.52620	integrin, beta 8	mAb & s.m.	plasma membrane
	448844	AI581519	Hs.177164	ESTs	mAb & s.m.	
65	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	mAb	plasma membrane
	449722	BE280074	Hs.23960	cyclin B1	s.m.	cytoplasm
	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitte	mAb & s.m.	plasma membrane
	450375	AA009647		a disintegrin and metalloproteinase doma	mAb & diag & s.m.	plasma membrane
70	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-	mAb & diag	plasma membrane
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	diag	secreted
	451668	Z43948	Hs.326444	cartilage acidic protein 1	mAb & diag	plasma membrane
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	diag	
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	diag	
	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	mAb	extracellular
75	452838	U65011	Hs.30743	preferentially expressed antigen in mela	CTL	plasma membrane
	453968	AA847843	Hs.62711	High mobility group (nonhistone chromoso	CTL & s.m.	nuclear
	457489	AI693815	Hs.127179	cryptic gene	diag	secreted

TABLE 14B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
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414883 15024_1 AA926960 AA926959 W76521 W24270 W21526 AA037172 BE267636 H83186 AA469909 N86396 AA001348 BE535736 AA081745 BE566245
 AA082436 H72525 H77575 N49786 W80565 H78746 BE569085 W04339 R98127 T55938 BE279271 AW960304 T29812 AA476873 BE297387
 AA292753 AA177048 NM_001826 X54941 BE314366 AA908783 AI719075 BE270172 BE269819 AA889955 AI204630 W25243 AI935150
 AA872039 W72395 T99630 AI422691 H98460 N31428 BE255916 H03265 AI857576 AA776920 AA910644 AA459522 AA293140 AW514667
 R75953 AW662396 AA662522 AI865147 AI423153 AW262230 AA584410 AA583187 AW024595 AW069734 AI828996 AA282997 AA876046
 AW613002 AA527373 AW972459 AI831360 AA621337 AA100926 AA772418 AA594628 AI033892 W95096 AI034317 AA398727 AI085031
 N95210 AI459432 AI041437 AA932124 AA627684 AA935829 AI004827 AI423513 AI094597 H42079 R54703 AI630359 AA617681 AA978045
 AA643280 W44561 AI991988 AI537692 AI090262 AA740817 AI312104 AI911822 AA416871 AI185409 AA129784 AA701623 AI075239
 AI139549 AA633648 AI339996 AI336880 AA399239 AI078708 AI085351 AI362835 AI346618 AI146955 AI989380 AI348243 N92892 AA765850
 AI494230 AI278887 AA962596 AI492600 W80435 AA001979 R97424 AI129015 N24127 AA157451 AA235549 AA459292 AA037114 AA129785
 AI494211 AW059601 AW886710 R92790 N59755 AI361128 AW589407 H47725 H97534 H48076 H48450 T99631 AW300758 H03431 R76789
 AA954344 H77576 R96823 AI457100 N92845 N49682 H42038 BE220698 BE220715 H99552 AA701624 N74173 R54704 H79520 H72923
 H03266 BE261919 AA769633 AA480310 AA507454 AA910586 AI203723 AW104725 W25611 W25071 T88980 H03513 T77589 R99156
 W95095 R97470 AA702275 T77551 AA911952 H82956 N83673 AA283672
 450375 83327_1 AA009647 AA131254 AA374293 AW954405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532
 AA190993 H03231 H59605 H01642 AA852876 AA113758 AA626915 AA746952 AI161014 AA099554 R69067

TABLE 14C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA
 sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
402075	8117407	Plus	121907-122035, 122804-122921, 124019-124161, 124455-124610, 125672-126076

TABLE 15A: Information for all sequences in Table 16

Table 15A shows the Seq ID No, Pkey, ExAccn, UnigenelD, and Unigene Title for all of the sequences in Table 16.

Table 15B show the accession numbers for those Pkey's lacking UnigenelD's for table 15A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 15C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 15A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Seq ID No: Sequence ID number
 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title

Seq ID No:	Pkey	ExAccn	UnigenelD	Unigene Title
Seq ID No: 1 & 2	410407	X66839	Hs.63287	carbonic anhydrase IX
Seq ID No: 3 & 4	412719	AW016610	Hs.816	ESTs
Seq ID No: 5 & 6	417034	NM_006183	Hs.80962	neurotensin
Seq ID No: 7 & 8	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam
Seq ID No: 9 & 10	407788	BE514982	Hs.38991	S100 calcium-binding protein A2
Seq ID No: 11 & 12	407788	BE514982	Hs.38991	S100 calcium-binding protein A2
Seq ID No: 13 & 14	407788	BE514982	Hs.38991	S100 calcium-binding protein A2
Seq ID No: 15 & 16	407788	BE514982	Hs.38991	S100 calcium-binding protein A2
Seq ID No: 17 & 18	439285	AL133916		hypothetical protein FLJ20093
Seq ID No: 19 & 20	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin
Seq ID No: 21 & 22	120486	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog
Seq ID No: 23 & 24	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen
Seq ID No: 25 & 26	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines
Seq ID No: 27 & 28	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage
Seq ID No: 29 & 30	452838	U65011	Hs.30743	preferentially expressed antigen in mela
Seq ID No: 31 & 32	418663	AK001100	Hs.41690	desmocollin 3
Seq ID No: 33 & 34	418663	AK001100	Hs.41690	desmocollin 3
Seq ID No: 35 & 36	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito
Seq ID No: 37 & 38	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas
Seq ID No: 39 & 40	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad
Seq ID No: 41 & 42	431846	BE019924	Hs.271580	uroplakin 1B
Seq ID No: 43 & 44	418830	BE513731	Hs.88959	hypothetical protein MGC4816
Seq ID No: 45 & 46	424098	AF077374	Hs.139322	small proline-rich protein 3
Seq ID No: 47 & 48	443648	AI085377	Hs.143610	ESTs
Seq ID No: 49	311034	BE567130	Hs.311389	ESTs, Highly similar to NKGD_HUMAN NKG2-
Seq ID No: 50 & 51	408522	AI541214	Hs.46320	Small proline-rich protein SPRK [human,
Seq ID No: 52 & 53	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL
Seq ID No: 54 & 55	435505	AF200492	Hs.211238	interleukin-1 homolog 1
Seq ID No: 56 & 57	417366	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)
Seq ID No: 58 & 59	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta
Seq ID No: 60 & 61	441020	W79283	Hs.35962	ESTs
Seq ID No: 62 & 63	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys
Seq ID No: 64 & 65	429538	BE182592	Hs.11261	small proline-rich protein 2A
Seq ID No: 66 & 67	448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte
Seq ID No: 68 & 69	444371	BE540274	Hs.239	forkhead box M1
Seq ID No: 70 & 71	444371	BE540274	Hs.239	forkhead box M1
Seq ID No: 72 & 73	444371	BE540274	Hs.239	forkhead box M1
Seq ID No: 74 & 75	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias
Seq ID No: 76 & 77	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias
Seq ID No: 78 & 79	429259	AA420450	Hs.292911	Plakophilin
Seq ID No: 80 & 81	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu
Seq ID No: 82 & 83	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an
Seq ID No: 84 & 85	423662	AK001035	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro
Seq ID No: 86 & 87	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino
Seq ID No: 88 & 89	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3
Seq ID No: 90 & 91	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor
Seq ID No: 92 & 93	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr
Seq ID No: 94 & 95	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated
Seq ID No: 96 & 97	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re
Seq ID No: 98 & 99	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic
Seq ID No: 100 & 101	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o
Seq ID No: 102 & 103	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3
Seq ID No: 104 & 105	409103	AF251237	Hs.112208	XAGE-1 protein
Seq ID No: 106 & 107	417542	J04129	Hs.82269	progesterone-associated endometrial prote
Seq ID No: 108 & 109	428471	X57348	Hs.184510	stratiferin
Seq ID No: 110 & 111	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member
Seq ID No: 112 & 113	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2
Seq ID No: 114 & 115	418203	X54942	Hs.83758	CDC28 protein kinase 2
Seq ID No: 116	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m
Seq ID No: 117 & 118	437016	AU076916	Hs.5398	guanine monophosphate synthetase
Seq ID No: 119 & 120	449230	BE613348	Hs.211579	melanoma cell adhesion molecule
Seq ID No: 121 & 122	446989	AK001898	Hs.16740	hypothetical protein FLJ11036
Seq ID No: 123 & 124	457819	AA057484	Hs.35406	ESTs, Highly similar to unnamed protein
Seq ID No: 125 & 126	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B

	Seq ID No: 127 & 128	414430	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1
	Seq ID No: 129 & 130	418462	BE001596	Hs.85266	integrin, beta 4
	Seq ID No: 131 & 132	100668	L05424	Hs.169610	CD44 antigen (homing function and Indian
5	Seq ID No: 133 & 134	458933	AI638429	Hs.24763	RAN binding protein 1
	Seq ID No: 135 & 136	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me
	Seq ID No: 137 & 138	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me
	Seq ID No: 139 & 140	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me
	Seq ID No: 141 & 142	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me
10	Seq ID No: 143 & 144	446269	AW263155	Hs.14559	hypothetical protein FLJ10540
	Seq ID No: 145 & 146	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur
	Seq ID No: 147 & 148	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con
	Seq ID No: 149 & 150	440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma
	Seq ID No: 151 & 152	439606	W79123	Hs.58561	G protein-coupled receptor 87
15	Seq ID No: 153 & 154	453884	AA355925	Hs.36232	KIAA0186 gene product
	Seq ID No: 155 & 156	453884	AA355925	Hs.36232	KIAA0186 gene product
	Seq ID No: 157 & 158	453884	AA355925	Hs.36232	KIAA0186 gene product
	Seq ID No: 159 & 160	453884	AA355925	Hs.36232	KIAA0186 gene product
	Seq ID No: 161 & 162	404877			NM_005365:Homo sapiens melanoma antigen,
20	Seq ID No: 163 & 164	413129	AF292100	Hs.104613	RP42 homolog
	Seq ID No: 165 & 166	413281	AA861271	Hs.222024	transcription factor BMAL2
	Seq ID No: 167 & 168	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote
	Seq ID No: 169 & 170	416819	U77735	Hs.80205	p1m-2 oncogene
	Seq ID No: 171 & 172	451320	AW118072		diacylglycerol kinase, zeta (104kD)
25	Seq ID No: 173 & 174	418543	NM_005329	Hs.85962	hyaluronan synthase 3
	Seq ID No: 175 & 176	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member
	Seq ID No: 177 & 178	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)
	Seq ID No: 179 & 180	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 181 & 182	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
30	Seq ID No: 183 & 184	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 185 & 186	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 187 & 188	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 189 & 190	419121	AA374372	Hs.89626	parathyroid hormone-like hormone
	Seq ID No: 191 & 192	448993	AI471630	Hs.8127	KIAA0144 gene product
35	Seq ID No: 193 & 194	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR
	Seq ID No: 195 & 196	430393	BE185030	Hs.241305	estrogen-responsive B box protein
	Seq ID No: 197 & 198	425057	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol
	Seq ID No: 199 & 200	420462	AF050147	Hs.97932	chondromodulin I precursor
40	Seq ID No: 201 & 202	102963	X02404	Hs.274534	calcitonin-related polypeptide, beta
	Seq ID No: 203 & 204	100576	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid
	Seq ID No: 205 & 206	101175	U82671	Hs.36980	melanoma antigen, family A, 2
	Seq ID No: 207 & 208	429038	AL023513	Hs.194766	seizure related gene 6 (mouse)-like
	Seq ID No: 209 & 210	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)
	Seq ID No: 211 & 212	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)
45	Seq ID No: 213 & 214	131927	AJ003112	Hs.34780	doublecortin; lissencephaly, X-linked (d
	Seq ID No: 215 & 216	428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT
	Seq ID No: 217 & 218	427335	AA448542	Hs.251677	G antigen 7B
	Seq ID No: 219 & 220	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini
	Seq ID No: 221 & 222	114346	AL137256	Hs.130489	ATPase, aminophospholipid transporter-II
50	Seq ID No: 223 & 224	438956	W00847	Hs.135056	Human DNA sequence from clone RP5-850E9
	Seq ID No: 225 & 226	404440			NM_021048:Homo sapiens melanoma antigen,
	Seq ID No: 227 & 228	415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito
	Seq ID No: 229 & 230	103312	Y12642	Hs.3185	lysosomal
55	Seq ID No: 231 & 232	320843	BE069288	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr
	Seq ID No: 233	429065	AI753247	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT
	Seq ID No: 234 & 235	446102	AW168067	Hs.317694	ESTs
	Seq ID No: 236 & 237	330495	U47924	Hs.71642	guanine nucleotide binding protein (G pr
60	Seq ID No: 238	413573	AI733859	Hs.149089	ESTs
	Seq ID No: 239 & 240	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to
	Seq ID No: 241 & 242	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to
	Seq ID No: 243 & 244	332180	AF134160	Hs.7327	claudin 1
	Seq ID No: 245	437915	AI637993	Hs.202312	Homo sapiens clone N11 Ntera2D1 teratoca
	Seq ID No: 246 & 247	441553	AA281219	Hs.121296	ESTs
	Seq ID No: 248 & 249	331692	AI683487	Hs.152213	wingless-type MMTV integration site fami
65	Seq ID No: 250 & 251	429413	NM_014058	Hs.201877	DESC1 protein
	Seq ID No: 252 & 253	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis
	Seq ID No: 254 & 255	448357	N20169	Hs.108923	RAB38, member RAS oncogene family
	Seq ID No: 256 & 257	446292	AF081497	Hs.279682	Rh type C glycoprotein
70	Seq ID No: 258 & 259	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h
	Seq ID No: 260 & 261	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1
	Seq ID No: 262 & 263	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito
	Seq ID No: 264 & 265	439223	AW238299	Hs.250618	UL16 binding protein 2
	Seq ID No: 266 & 267	429228	AI553633	Hs.326447	ESTs
	Seq ID No: 268 & 269	409757	NM_001898	Hs.123114	cystatin SN
75	Seq ID No: 270 & 271	411089	AA456454	Hs.214291	cell division cycle 2-like 1 (PITSLRE pr
	Seq ID No: 272 & 273	436511	AA721252	Hs.291502	ESTs
	Seq ID No: 274 & 275	428969	AF120274	Hs.194689	artemin
	Seq ID No: 276 & 277	428969	AF120274	Hs.194689	artemin
	Seq ID No: 278 & 279	428969	AF120274	Hs.194689	artemin
80	Seq ID No: 280 & 281	428969	AF120274	Hs.194689	artemin
	Seq ID No: 282	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen
	Seq ID No: 283 & 284	412723	AA648459	Hs.335951	hypothetical protein AF301222
	Seq ID No: 285 & 286	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-
	Seq ID No: 287 & 288	405770			NM_002362:Homo sapiens melanoma antigen,
85	Seq ID No: 289 & 290	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13
	Seq ID No: 291 & 292	414774	X02419	Hs.77274	plasminogen activator, urokinase

5	Seq ID No: 293 & 294	424629	M90656	Hs.151393	glutamate-cysteine ligase, catalytic sub
	Seq ID No: 295 & 296	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypothe
	Seq ID No: 297 & 298	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypothe
	Seq ID No: 299 & 300	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypothe
	Seq ID No: 301 & 302	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypothe
	Seq ID No: 303 & 304	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypothe
	Seq ID No: 305 & 306	453968	AA847843	Hs.62711	High mobility group (nonhistone chromoso
	Seq ID No: 307 & 308	403478			NM_022342:Homo sapiens kinesin protein 9
10	Seq ID No: 309	441525	AW241867	Hs.127728	ESTs
	Seq ID No: 310 & 311	434105	AW952124	Hs.13094	presenilins associated rhomboid-like pro
	Seq ID No: 312 & 313	428810	AF068236	Hs.193788	nitric oxide synthase 2A (inducible, hep
	Seq ID No: 314 & 315	413691	AB023173	Hs.75478	ATPase, Class VI, type 11B
	Seq ID No: 316 & 317	423934	U89995	Hs.159234	forkhead box E1 (thyroid transcription f
15	Seq ID No: 318 & 319	409228	R16811	Hs.22010	ESTs, Weakly similar to 2109260A B cell
	Seq ID No: 320 & 321	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg
	Seq ID No: 322 & 323	413582	AW295647	Hs.71331	hypothetical protein MGC5350
	Seq ID No: 324 & 325	438403	AA806607	Hs.292206	ESTs
	Seq ID No: 326 & 327	403329			unnamed protein product [Homo sapiens]
20	Seq ID No: 328 & 329	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.
	Seq ID No: 330 & 331	119073	BE245360	Hs.279477	v-ets erythroblastosis virus E26 oncogen
	Seq ID No: 332 & 333	113195	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom
	Seq ID No: 334 & 335	102283	AW161552	Hs.83381	guanine nucleotide binding protein 11
	Seq ID No: 336 & 337	101345	NM_005795	Hs.152175	calcitonin receptor-like
25	Seq ID No: 338 & 339	103280	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula
	Seq ID No: 340 & 341	102012	BE259035	Hs.118400	singed (Drosophila)-like (sea urchin fas
	Seq ID No: 342 & 343	105729	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds
	Seq ID No: 344 & 345	134299	AW580939	Hs.97199	complement component C1q receptor
	Seq ID No: 346 & 347	412719	AW016610	Hs.816	ESTs
30	Seq ID No: 348 & 349	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL
	Seq ID No: 350 & 351	128924	BE279383	Hs.26557	plakophilin 3
	Seq ID No: 352 & 353	100486	T19006	Hs.10842	RAN, member RAS oncogene family
	Seq ID No: 354 & 355	419121	AA374372	Hs.89626	parathyroid hormone-like hormone
	Seq ID No: 356 & 357	409459	D86407	Hs.54481	low density lipoprotein receptor-related
35	Seq ID No: 358 & 359	330493	M27826		endogenous retroviral protease
	Seq ID No: 360 & 361	417866	AW067903	Hs.82772	collagen, type XI, alpha 1
	Seq ID No: 362 & 363	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4
	Seq ID No: 364 & 365	437016	AU076916	Hs.5398	guanine monophosphate synthetase
	Seq ID No: 366 & 367	429612	AF062649	Hs.252587	pituitary tumor-transforming 1
40	Seq ID No: 368 & 369	440704	M69241	Hs.162	insulin-like growth factor binding prote
	Seq ID No: 370 & 371	431221	AA449015	Hs.286145	SRB7 (suppressor of RNA polymerase B, ye
	Seq ID No: 372 & 373	431565	AF161470	Hs.260622	butyrate-induced transcript 1
	Seq ID No: 374 & 375	431565	AF161470	Hs.260622	butyrate-induced transcript 1
	Seq ID No: 376 & 377	132354	BE185289	Hs.1076	small proline-rich protein 1B (comifin)
45	Seq ID No: 378 & 379	424441	X14850	Hs.147097	H2A histone family, member X
	Seq ID No: 380 & 381	103768	AF086009	Hs.296398	gb:Homo sapiens full length insert cDNA
	Seq ID No: 382 & 383	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb
	Seq ID No: 384 & 385	425266	J00077	Hs.155421	alpha-fetoprotein
	Seq ID No: 386 & 387	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,
50	Seq ID No: 388 & 389	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin
	Seq ID No: 390 & 391	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial
	Seq ID No: 392 & 393	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial
	Seq ID No: 394 & 395	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino
	Seq ID No: 396 & 397	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2
55	Seq ID No: 398 & 399	418506	AA084248	Hs.85339	G protein-coupled receptor 39
	Seq ID No: 400 & 401	423961	D13666	Hs.136348	periostin (OSF-2os)
	Seq ID No: 402 & 403	414812	X72755	Hs.77367	monokine induced by gamma interferon
	Seq ID No: 404 & 405	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein
60	Seq ID No: 406 & 407	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein
	Seq ID No: 408 & 409	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse
	Seq ID No: 410 & 411	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy
	Seq ID No: 412 & 413	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothe
	Seq ID No: 414 & 415	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated
	Seq ID No: 416 & 417	411789	AF245505	Hs.72157	Adican
65	Seq ID No: 418 & 419	428698	AA852773	Hs.334838	KIAA1866 protein
	Seq ID No: 420 & 421	450098	W27249	Hs.8109	hypothetical protein FLJ21080
	Seq ID No: 422 & 423	421552	AF026692	Hs.105700	secreted frizzled-related protein 4
	Seq ID No: 424 & 425	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR
	Seq ID No: 426 & 427	450375	AA009647		a disintegrin and metalloproteinase doma
70	Seq ID No: 428 & 429	426215	AW963419	Hs.155223	stanniocalcin 2
	Seq ID No: 430 & 431	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin
	Seq ID No: 432 & 433	432201	AI538613	Hs.298241	Transmembrane protease, serine 3
	Seq ID No: 434 & 435	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph
	Seq ID No: 436 & 437	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447
75	Seq ID No: 438 & 439	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn
	Seq ID No: 440 & 441	447033	AI357412	Hs.157601	ESTs
	Seq ID No: 442 & 443	447033	AI357412	Hs.157601	ESTs
	Seq ID No: 444 & 445	447033	AI357412	Hs.157601	ESTs
	Seq ID No: 446 & 447	115522	BE614387	Hs.333893	c-Myc target JPO1
	Seq ID No: 448 & 449	410418	D31382	Hs.63325	transmembrane protease, serine 4
80	Seq ID No: 450 & 451	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119
	Seq ID No: 452 & 453	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119
	Seq ID No: 454 & 455	452461	N78223	Hs.108106	transcription factor
	Seq ID No: 456 & 457	412420	AL035668	Hs.73853	bone morphogenetic protein 2
	Seq ID No: 458 & 459	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara
85	Seq ID No: 460 & 461	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antag

	Seq ID No: 462 & 463	437852	BE001836	Hs.256897	ESTs, Weakly similar to DJ365O12.1 [H.s.a
	Seq ID No: 464 & 465	402075			ENSP00000251056*:Plasma membrane calcium
	Seq ID No: 466 & 467	421110	AJ250717	Hs.1355	cathepsin E
5	Seq ID No: 468 & 469	451668	Z43948	Hs.326444	cartilage acidic protein 1
	Seq ID No: 470 & 471	451668	Z43948	Hs.326444	cartilage acidic protein 1
	Seq ID No: 472 & 473	451668	Z43948	Hs.326444	cartilage acidic protein 1
	Seq ID No: 474 & 475	422282	AF019225	Hs.114309	apolipoprotein L
	Seq ID No: 476 & 477	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member
10	Seq ID No: 478 & 479	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),
	Seq ID No: 480 & 481	427747	AW411425	Hs.180655	serine/threonine kinase 12
	Seq ID No: 482 & 483	420281	AI623693	Hs.323494	Predicted cation efflux pump
	Seq ID No: 484 & 485	405932			C15000305:gij3806122[gb]AAC69198.1 (AF0
	Seq ID No: 486 & 487	405932			C15000305:gij3806122[gb]AAC69198.1 (AF0
15	Seq ID No: 488 & 489	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane
	Seq ID No: 490 & 491	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy
	Seq ID No: 492 & 493	417079	U65590	Hs.81134	interleukin 1 receptor antagonist
	Seq ID No: 494 & 495	430890	X54232	Hs.2699	glypican 1
	Seq ID No: 496 & 497	419721	NM_001650	Hs.288650	aquaporin 4
20	Seq ID No: 498 & 499	444471	AB020684	Hs.11217	KIAA0877 protein
	Seq ID No: 500 & 501	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote
	Seq ID No: 502 & 503	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly
	Seq ID No: 504 & 505	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro
	Seq ID No: 506 & 507	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro
25	Seq ID No: 508 & 509	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitte
	Seq ID No: 510 & 511	410407	X66839	Hs.63287	carbonic anhydrase IX
	Seq ID No: 512 & 513	309931	AW341683		gb:hd13d01.x1 Soares_NFL_T_GBC_S1 Homo s
	Seq ID No: 514 & 515	412719	AW016610	Hs.816	ESTs
	Seq ID No: 516 & 517	417034	NM_006183	Hs.80962	neurotensin
30	Seq ID No: 518 & 519	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam
	Seq ID No: 520 & 521	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin
	Seq ID No: 522 & 523	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen
	Seq ID No: 524 & 525	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage
	Seq ID No: 526 & 527	418663	AK001100	Hs.41690	desmocollin 3
35	Seq ID No: 528 & 529	418663	AK001100	Hs.41690	desmocollin 3
	Seq ID No: 530 & 531	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas
	Seq ID No: 532 & 533	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad
	Seq ID No: 534 & 535	431846	BE019924	Hs.271580	uropod 1B
40	Seq ID No: 536 & 537	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL
	Seq ID No: 538 & 539	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta
	Seq ID No: 540 & 541	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an
	Seq ID No: 542 & 543	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino
	Seq ID No: 544 & 545	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3
45	Seq ID No: 546 & 547	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor
	Seq ID No: 548 & 549	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3
	Seq ID No: 550 & 551	417542	J04129	Hs.82269	progesterone-associated endometrial prote
	Seq ID No: 552 & 553	449230	BE613348	Hs.211579	melanoma cell adhesion molecule
	Seq ID No: 554 & 555	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma
	Seq ID No: 556 & 557	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma
50	Seq ID No: 558 & 559	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B
	Seq ID No: 560 & 561	418462	BE001596	Hs.85266	integrin, beta 4
	Seq ID No: 562 & 563	410274	AA381807	Hs.61762	hypoxia-inducible protein 2
	Seq ID No: 564 & 565	439606	W79123	Hs.58561	G protein-coupled receptor 87
	Seq ID No: 566 & 567	404877			NM_005365:Homo sapiens melanoma antigen,
55	Seq ID No: 568 & 569	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote
	Seq ID No: 570 & 571	418543	NM_005329	Hs.85962	hyaluronan synthase 3
	Seq ID No: 572 & 573	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 574 & 575	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 576 & 577	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
60	Seq ID No: 578 & 579	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 580 & 581	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 582 & 583	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 584 & 585	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR
	Seq ID No: 586 & 587	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)
65	Seq ID No: 588 & 589	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)
	Seq ID No: 590 & 591	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini
	Seq ID No: 592 & 593	332180	AF134160	Hs.7327	claudin 1
	Seq ID No: 594 & 595	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,
	Seq ID No: 596 & 597	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,
70	Seq ID No: 598 & 599	439223	AW238299	Hs.250618	UL16 binding protein 2
	Seq ID No: 600 & 601	409757	NM_001898	Hs.123114	cystatin SN
	Seq ID No: 602 & 603	428969	AF120274	Hs.194689	artemin
	Seq ID No: 604 & 605	428969	AF120274	Hs.194689	artemin
	Seq ID No: 606 & 607	428969	AF120274	Hs.194689	artemin
75	Seq ID No: 608 & 609	428969	AF120274	Hs.194689	artemin
	Seq ID No: 610 & 611	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-
	Seq ID No: 612 & 613	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-
	Seq ID No: 614 & 615	414774	X02419	Hs.77274	plasminogen activator, urokinase
	Seq ID No: 616 & 617	407944	R34008	Hs.239727	desmocollin 2
	Seq ID No: 618 & 619	407944	R34008	Hs.239727	desmocollin 2
80	Seq ID No: 620 & 621	457489	AI693815	Hs.127179	cryptic gene
	Seq ID No: 622 & 623	429547	AW009166	Hs.99376	ESTs
	Seq ID No: 624 & 625	407242	M18728		gb:Human nonspecific crossreacting antig
	Seq ID No: 626 & 627	407242	M18728		gb:Human nonspecific crossreacting antig
85	Seq ID No: 628 & 629	407242	M18728		gb:Human nonspecific crossreacting antig
	Seq ID No: 630 & 631	444006	BE395085	Hs.10086	type I transmembrane protein Fn14

Seq ID No: 632 & 633	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma
Seq ID No: 634 & 635	422109	S73265	Hs.1473	gastrin-releasing peptide
Seq ID No: 636 & 637	419235	AW470411	Hs.288433	neurotrimin
Seq ID No: 638 & 639	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc
Seq ID No: 640 & 641	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy
Seq ID No: 642 & 643	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu
Seq ID No: 644 & 645	448243	AW369771	Hs.52620	integrin, beta 8
Seq ID No: 646 & 647	426427	M86699	Hs.169840	TTK protein kinase
Seq ID No: 648 & 649	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6
Seq ID No: 650 & 651	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6
Seq ID No: 652 & 653	428450	NM_014791	Hs.184339	KIAA0175 gene product
Seq ID No: 654 & 655	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,
Seq ID No: 656 & 657	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11
Seq ID No: 658 & 659	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic
Seq ID No: 660 & 661	425776	U25128	Hs.159499	parathyroid hormone receptor 2
Seq ID No: 662 & 663	425776	U25128	Hs.159499	parathyroid hormone receptor 2
Seq ID No: 664 & 665	431515	NM_012152	Hs.258583	endothelial differentiation, lysophospha
Seq ID No: 666 & 667	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7
Seq ID No: 668 & 669	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci
Seq ID No: 670 & 671	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci
Seq ID No: 672 & 673	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci
Seq ID No: 674 & 675	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci
Seq ID No: 676 & 677	410001	AB041036	Hs.57771	kallikrein 11
Seq ID No: 678 & 679	426501	AW043782	Hs.293616	ESTs
Seq ID No: 680 & 681	408369	R38438	Hs.182575	solute carrier family 15 (H??? transport
Seq ID No: 682 & 683	445413	AA151342	Hs.12677	CGI-147 protein
Seq ID No: 684 & 685	422424	AI186431	Hs.296638	prostate differentiation factor
Seq ID No: 686 & 687	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,
Seq ID No: 688 & 689	420610	AI683183	Hs.99348	distal-less homeo box 5

TABLE 15B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
309931	AW341683	
330493	33264_5	M27826 R78416 AA307645 AW957879 AW957800 AA633529 H03662
439285	47065_1	AL133916 N79113 AF086101 N76721 AW950828 AA364013 AW955684 AI346341 AI867454 N54784 AI655270 AI421279 AW014882 AA775552 N62351 N59253 AA626243 AI341407 BE175639 AA456968 AI358918 AA457077
450375	83327_1	AA009647 AA131254 AA374293 AW954405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532 AA190993 H03231 H59605 H01642 AA852876 AA113758 AA626915 AA746952 AI161014 AA099554 R69067
451320	86576_1	AW118072 AI631982 T15734 AA224195 AI701458 W20198 F26326 AA890570 N90552 AW071907 AI671352 AI375892 T03517 R88265 AI124088 AA224388 AI084316 AI354686 T33652 AI140719 AI720211 T03490 AI372637 T15415 AW205836 AA630384 T03515 T33230 AA017131 AA443303 T33623 AI222556 T33511 T33785 AI419606 D55612

TABLE 15C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
403329	8516120	Plus	96450-96598
403478	9958258	Plus	116458-116564
404440	7528051	Plus	80430-81581
404877	1519284	Plus	1095-2107
405770	2735037	Plus	61057-62075
405932	7767812	Minus	123525-123713

Table 16

Seq ID NO: 1 DNA sequence
Nucleic Acid Accession #: NM_001216
Coding sequence: 43..1422

	1	11	21	31	41	51	
5							
10	GCCCGTACAC	ACCGTGTGCT	GGGACACCCC	ACAGTCAGCC	GCATGGCTCC	CCTGTGCCCC	60
	AGCCCCCTGGC	TCCCTCTGTT	GATCCCGGCC	CCTGCTCCAG	GCCTCACTGT	GCAACTGCTG	120
	CTGTCACTGC	TGCTTCTGAT	GCCTGTCCAT	CCCCAGAGGT	TGCCCCGGAT	GCAGGAGGAT	180
	TCCCCCTTGG	GAGGAGGCTC	TTCTGGGGAA	GATGACCCAC	TGGGCGAGGA	GGATCTGCCC	240
	AGTGAAGAGG	ATTACCCAG	AGAGGAGGAT	CCACCCGGAG	AGGAGGATCT	ACCTGGAGAG	300
15	GAGGATCTAC	CTGGAGAGGA	GGATCTACCT	GAAGTTAAGC	CTAAATCAGA	AGAAGAGGGC	360
	TCCCTGAAGT	TAGAGGATCT	ACCTACTGTT	GAGGCTCCTG	GAGATCTCTA	AGAACCCAG	420
	AATAATGCC	ACAGGGACAA	AGAAGGGGAT	GACCAGAGTC	ATTGGCGCTA	TGGAGGCGAC	480
	CCGCCCTGGC	CCCGGGTGTC	CCCAGCCTGC	GCGGGCCGCT	TCCAGTCCCC	GGTGGATATC	540
	CGCCCCCAGC	TCGCCCGCTT	CTGCCCGGCC	CTGGCCCCCC	TGGAACCTCT	GGGCTTCCAG	600
20	CTCCGCGCGC	TCCAGAACT	GCGCCTGCGC	AACAATGGCC	ACAGTGTGCA	ACTGACCTCG	660
	CCTCCTGGGC	TAGAGATGGC	TCTGGGTCCC	GGGCGGGAGT	ACCGGGCTCT	GCAGCTGCAT	720
	CTGCACTGGG	GGGTGCGAG	TCGTCCGGGC	TCGGAGCACA	CTGTGGAAGG	CCACCGTTTC	780
	CCTGCCGAGA	TCCACGTGGT	TCACCTCAGC	ACCGCCTTTG	CCAGAGTTGA	CGAGGCCTTG	840
	GGGGCCCGGG	GAGGCCTGGC	CGTGTGGCC	GCCTTTCTGG	AGGAGGGCCC	GGAGAGAAAC	900
25	AGTGCCTATG	AGCAGTTGCT	GTCCTCGCTT	GAAGAAATCG	CTGAGGAAGG	CTCAGAGACT	960
	CAGTCCCAG	GACTGGACAT	ATCTGCATC	CTGCCCTCTG	ACTTCAGCCG	CTACTTCCAA	1020
	TATGAGGGGT	CTCTGACTAC	ACCGCCCTGT	GCCAGGGTGG	TCATCTGGAC	TGTGTTTAAC	1080
	CAGACAGTGA	TGCTGAGTGC	TAAGCAGCTC	CACACCCCTC	CTGACACCCCT	TGGGGGACCT	1140
	GGTGACTCTC	GGCTACAGCT	GAACCTCCGA	GCGACGCAGC	CTTTGAATGG	GCGAGTGATT	1200
30	GAGGCCTCCT	TCCCTGCTGG	AGTGGACAGC	AGTCCTCGGG	CTGCTGAGCC	AGTCCAGCTG	1260
	AATTCCTGCC	TGGCTGCTGG	TGACATCCTA	GCCCTGGTTT	TTGGCCTCCT	TTTGTCTGTC	1320
	ACCAGCGTCG	CGTTCTTGT	GCAGATGAGA	AGGCAGCACA	GAAGGGGAAC	CAAAGGGGGT	1380
	GTGAGCTACC	GCCAGCCAGA	GGTAGCCGAG	ACTGGAGCCT	AGAGGCTGGA	TCTTGGAGAA	1440
	TGTGAGAAGC	CAGCCAGAGG	CATCTGAGGG	GGAGCCGGTA	ACTGTCCTGT	CCTGCTCATT	1500
35	ATGCCACTTC	CTTTTAACATG	CCAAGAAATT	TTTTAAAAATA	AATATTTATA	AT	

Seq ID NO: 2 Protein sequence:
Protein Accession #: NP_001207

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40							
	MAPLCPSPWL	PLLIPAPAPG	LTVQLLSLL	LLMPVHPQRL	PRMQEDSPLG	GGSSGEDDPL	60
	GEEDLPSEED	SPREEDPPGE	EDLPGEEDLP	GEEDLPPEVKP	KSEEEGSLKL	EDLPTVEAPG	120
	DPQEPQNNAH	RDKEGDDQSH	WRYGGDPPWP	RVSPACAGRF	QSPVDIRPQL	AAFCPALRPL	180
45	ELLGQLPLPL	PELLRLRNNGH	SVQLTLPPGL	EMALGPGREY	RALQLHLHWG	AAGRPGSEHT	240
	VEGHRFPABE	HVVHLSTAF	RVDEALGRPG	GLAVLAAPLE	EGPEENSAYE	QLLSRLEIEIA	300
	EESSETQVPG	LDISALLPSD	FSRYFQYEGS	LTPPCAQGV	IWTVFNQTVM	LSAKQLHTLS	360
	DTLWGPDSR	LQLNFRATQP	LNGRVIEASF	PAGVDSSPRA	AEPVQLNSCL	AAGDILALVF	420
	GLLFAVTSVA	FLVQMRRQHR	RGTKGGVSYR	PAEVAETGA			

Seq ID NO: 3 DNA sequence
Nucleic Acid Accession #: BC013923
Coding sequence: 438-1391

	1	11	21	31	41	51	
55							
	AGCGGGGTG	TCTATTAAC	TGTTCAAAAA	GTATCAGGAG	TGTCAAGGC	AGAGAAGAGA	60
	GTGTTTGCAA	AAGGGGGAAA	GTAGTTTGCT	GCCTCTTTAA	GACTAGGACT	GAGAGAAAGA	120
	AGAGGAGAGA	GAAAGAAAGG	GAGAGAAGTT	TGAGCCCCAG	GCTTAAGCCT	TTCCAAAAAA	180
60	TAATAATAAC	AATCATCGGC	GGCGGCAGGA	TCGGCCAGAG	GAGGAGGGAA	GCGCTTTTTT	240
	TGATCCTGAT	TCCAGTTTGC	CTCTCTCTTT	TTTTCCCCCA	AATTATTCTT	CGCCTGATTT	300
	TCTCGCGGA	GCCCTGCGCT	CCGACACCC	CCGCCCGCCT	CCCCTCTCTC	TCTCCCCCCC	360
	CCCGCGGGCC	CCCCAAGTC	CCGCGCGGCG	CGAGGGTCGG	CGGCCGCGCG	CGGGCCGGGC	420
	CCGCGCACAG	CGCCCGCATG	TACAACTGA	TGGAGACGGA	GCTGAAGCCG	CCGGGCCCGC	480
65	AGCAAACTTC	GGGGGGCGGC	GGCGGCAACT	CCACCGCGGC	GGCGGCCGCG	GGCAACCAGA	540
	AAAACAGCCC	GGACCGCGTC	AAGCGGCCCA	TGAATGCCTT	CATGGTGTGG	TCCCGCGGGC	600
	AGCGGCGCAA	GATGGCCAG	GAGAACCCCA	AGATGCACAA	CTCGGAGATC	AGCAAGCGCC	660
	TGGGCGCCGA	GTGGAACCTT	TTGTGCGAGA	CGGAGAAAGC	GCCGTTCATC	GACGAGGCTA	720
	AGCGGCTGCG	AGCGCTGCAC	ATGAAGGAGC	ACCCGGATTA	TAAATACCGG	CCCGCGCGGA	780
70	AAACCAAGAC	GCTCATGAAG	AAGGATAAGT	ACACGCTGCC	CGGCGGGCTG	CTGGCCCCCG	840
	GCGGCAATAG	CATGGCGAGC	GGGGTCGGGG	TGGGCGCCGG	CCTGGGCGCG	GGCGTGAACC	900
	AGCGCATGGA	CAGTTACGCG	CACATGAACG	GCTGGAGCAA	CGGCAGCTAC	AGCATGATGC	960
	AGGACCAAGT	GGGCTACCCG	CAGCACCCGG	GCCTCAATGC	GCACGGCGCA	GCGCAGATGC	1020
	AGCCCATGCA	CGCTACGAC	GTGAGCGCCC	TGCAGTACAA	CTCCATGACC	AGCTCGCAGA	1080
75	CCTACATGAA	CGGCTCGCCC	ACCTACAGCA	TGTCCTACTC	GCAGCAGGSC	ACCCCTGGCA	1140
	TGGCTCTTGG	CTCCATGGGT	TGCGTGGTCA	AGTCCGAGGC	CAGCTCCAGC	CCCCTGTGG	1200
	TTACCTCTTC	CTCCCACTCC	AGGGCGCCCT	GCCAGGCCGG	GGACCTCCGG	GACATGATCA	1260
	GCATGTATCT	CCCCGGCGCG	GAGGTGCGGG	AACCCGCGCG	CCCCAGCAGA	CTTCACATGT	1320
	CCCAGCACTA	CCAGAGCGGC	CCGGTGCCCG	GCACGGCCAT	TAACGGCACA	CTGCCCTCT	1380
80	CACACATGTG	AGGGCCGAGC	AGCGAACTGG	AGGGGGGAGA	AATTTTCAAA	GAAAAACGAG	1440
	GGAAATGGGA	GGGGTGCAAA	AGAGGAGAGT	AAGAAACAGC	ATGGAGAAAA	CCCGGTACGC	1500
	TCAAAAAAAA	AAAAAATAAA	AAAATCCCAT	CACCCACAGC	AAATGACAGC	TGCAAAAGAG	1560
	AACACCAATC	CCATCCACAC	TCACGCAAAA	ACCGCGATGC	CGACAAGAAA	ACTTTTATGA	1620
	GAGAGATCCT	GGACTTCTTT	TKGGGGGACT	ATTTTGTATC	AGAGAAAACC	TGGGGAGGGT	1680
	GGGGAGGGCG	GGGGAATGGA	CCTTGATATG	ATCTGGAGGA	AAGAAAGCTA	CGAAAAACTT	1740
85	TTTAAAGATT	TAGTGGTAC	GGTAGGAGCT	TTGCAGGAAG	TTTGCAAAAG	TCTTTACCAA	1800
	TAATATTTAG	AGCTAGTCTC	CAAGCGACGA	AAAAAATGTT	TTAATATTTG	CAAGCAACTT	1860
	TTGTACAGTA	TTTATCGAGA	TAAACATGGC	AATCAAAATG	TCCATTGTTT	ATAAGCTGAG	1920

AATTGTCCTA TATTTTTCCTA GGAGAGGCTT CTTGCTGAAT TTTGATTCTG CAGCTGAAAT 1980
 TTAGGACAGT TGCAAAACGTG AAAAGAAGAA AATTATTCAA ATTTGGACAT TTTAATTGTT 2040
 TAAAAATTGT ACAAAAAGGAA AAAATTAGAA TAAGTACTGG CGAACCATCT CTGTGGTCTT 2100
 GTTTAAAAAG GGCAAAAGTT TTAGACTGTA CTAATTTTAA TAACCTTACTG TTTAAAGCAA 2160
 AATATGCCAT CGAGGTTGAC ACCGTTGGTA ATTTATAATA GCTTTTGTTC GATCCCAACT 2220
 TTCCATTTTG TTCAGATAAA AAAAACCATG AATTTACTGT GTTTGAAATA TTTTCTTATG 2280
 GTTTGTAAATA TTTCTGTAAA TTTATTGTGA TATTTTAAAG TTTTCCCCCT TTTATTTTCC 2340
 GTAGTTGTAT TTTTAAAGAT TCGGCTCTGT ATTATTTGAA TCAGTCTGCC GAGAATCCAT 2400
 GTATATATTT GAACATAATAT CATCCTTATA ACAGGTACAT TTTCAACTTA AGTTTTTACT 2460
 CCATTATGCA CAGTTTGAGA TAAATAAATT TTTGAAATAT GGACACTGAA AAAAAAATAA 2520
 AAAAAAACAA AACAAAAAAA CAAAAACAA AACACAGAAA AACAAAAAAA AAAACAAAAA 2580
 CACAACACAA AACAAAAAAA AAAAAAAGA AACAAACACA CAACACAACA CAACACAATA 2640
 CCACAACACA AACACAACA CACAGAGGG

Seq ID NO: 4 Protein sequence:
 Protein Accession #: CAA83435.1

1 11 21 31 41 51
 MYNMMETELK PPGPQQTSGG GGGNSTAAAA GGNQKNSPDR VKRPMNAFMV WSRGQRRKMA 60
 QENPKMHNSE ISKRLGAEWK LLSETEKRPF IDEAKRLRAL HMKHEPDYKY RPRRKTKTLM 120
 KKDKYTLPGG LLAPGGNSMA SGVGVGAGLG AGVNQRMDSY AHMNGWSNGS YSMMQDQLGY 180
 PQHPGLNAHG AAQMQPMHRY DVSLALQNSM TSSQTYMNGS PTYSMSYSQQ GTPGMALGSM 240
 GSVVKSEASS SPPVVTSSSH SRAPCQAGDL RDMISMYLPG AEVPEPAAPS RLHMSQHYQS 300
 GPVPGTAING TLPLSHM

Seq ID NO: 5 DNA sequence
 Nucleic Acid Accession #: U91618
 Coding sequence: 29-541

1 11 21 31 41 51
 CGGACTTGGC TTGTTAGAAG GCTGAAAGAT GATGGCAGGA ATGAAAATCC AGCTTGTTATG 60
 CATGCTACTC CTGGCTTTCA GCTCCTGGAG TCTGTGCTCA GATTGAGAAG AGGAAATGAA 120
 AGCATTAGAA GCAGATTCTT TGACCAATAT GCATACATCA AAGATTAGTA AAGCACATGT 180
 TCCCTCTTGG AAGTAGACTC TGCTAAATGT TTGCAGTCTT GTAAATAAAT TGAACAGCCC 240
 AGCTGAGGAA ACAGGAGAAG TTTATGAAGA GGAGCTTGTT GCAAGAAGGA AACTTCCTAC 300
 TGCTTTAGAT GGCTTTAGCT TGGAGCAAT GTTGACAATA TACCAGCTCC ACAAATCTG 360
 TCACAGCAGG GCTTTTCAAC ACTGGGAGTT AATCCAGGAA GATATTCTTG ATACTGGAAA 420
 TGACAAAAAT GAAAGGAAG AAGTCATAAA GAGAAAAATT CCTTATATTC TGAACCGGCA 480
 GCTGTATGAG AATAAACCCA GAAGACCCCTA CATACTCAA AGAGATTCTT ACTATTACTG 540
 AGAGAATAAA TCATTTATTT ACATGTGATT GTGATTCATC ATCCCTTAAT TAAATATCAA 600
 ATTATATTGT TGTGAAATG TGACAAACAC ACTTATCTGT CTCTTCTACA ATTGTGGTTT 660
 ATTGAATGTG TTTTCTGCA CTAATAGAAA TTAGACTAAG TGTTTTCAA TAAATCTAAA 720
 TCTTCAAAAA AAAAAAATAA AAATGGGGCC GCAATT

Seq ID NO: 6 Protein sequence:
 Protein Accession #: AAB50564

1 11 21 31 41 51
 MMAGMKIQLV CMLLLAFSSW SLCSDSSEEM KALEADFLTN MHTSKISKAH VPSWKMTLLN 60
 VCSLVNMLNS PAETGVEVHE EELVARRKLP TALDGFSLFA MLTIYQLHKI CHSRAFQHWE 120
 LIQEDILDTG NDKNGKEEVI KRKIPYILKR QLYENKPRRP YILKRDSEYV

Seq ID NO: 7 DNA sequence
 Nucleic Acid Accession #: NM_006536.2
 Coding sequence: 109-2940

1 11 21 31 41 51
 ACCTAAAACC TTGCAAGTTC AGGAAGAAAC CATCTGCATC CATATTGAAA ACCTGACACA 60
 ATGTATGCAG CAGGCTCAGT GTGAGTGAAC TGGAGGCTTC TCTACAACAT GACCCAAAGG 120
 AGCATTGCAG GTCCTATTTC CAACCTGAAG TTTGTGACTC TCCTGGTTGC CTTAAGTTCA 180
 GAACTCCCAT TCCTGGGAGC TGGAGTACAG CTTCAAGACA ATGGGTATAA TGGATTGCTC 240
 ATTGCAATTA ATCCTCAGGT ACCTGAGAAT CAGAACCTCA TCTCAAACAT TAAGGAAATG 300
 ATAACTGAAG CTTCAATTTA CCTATTTAAT GCTACCAAGA GAAGAGTATT TTTGAGAAAT 360
 ATAAAGATTT TAATACCTGC CACATGGAAA GCTAATAATA ACAGCAAAAT AAAACAAGAA 420
 TCATATGAAA AGGCAAATGT CATAGTGACT GACTGGTATG GGGCACATGG AGATGATCCA 480
 TACACCCTAC AATACAGAGG GTGTGGAAAA GAGGAAAAAT ACATTCAAT CACACCTAAT 540
 TTCTACTGTA ATGATAACTT AACAGCTGGC TACGGATCAC GAGGCCGAGT GTTTGTCCAT 600
 GAATGGGGCC ACCTCCGTTG GGGTGTGTTC GATGAGTATA ACAATGACAA ACCTTTCTAC 660
 ATAAATGGGC AAAATCAAAT TAAAGTGACA AGGTGTTTCA CTGACATCAC AGGCATTTT 720
 GTGTGTGAAA AAGTCTCTTG CCCCCAAGAA AACTGTATTA TTAGTAAGCT TTTTAAAGAA 780
 GGATGCACCT TTATCTACAA TAGCACCCAA AATGCAACTG CATCAATAAT GTTCATGCAA 840
 AGTTTATCTT CTGTGGTTGA ATTTTGTAAAT GCAAGTACCC ACAACCAAGA AGCACCAAAC 900
 CTACAGAACCC AGATGTGCAG CCTCAGAAGT GCATGGGATG TAATCACAGA CTCTGCTGAC 960
 TTTCAACACA GCTTTCCTCC GAATGGGACT GAGCTTCCAC CTCTCCACAT ATTCTCGCTT 1020
 GTACAGGCTG GTGACAAAGT GGTCTGTTTA GTGCTGGATG TGTCCAGCAA GATGGCAGAG 1080
 GCTGACAGAC TCCTTCAACT ACAACAAGCC GCAGAATTTT ATTTGATGCA GATTGTTGAA 1140
 ATTCATACCT TCGTGGGCTT TGCCAGTTTC GACAGCAAAG GAGAGATCAG AGCCACGCTA 1200
 CACCAAAATTA ACAGCAATGA TGATCGAAAG TTGCTGGTTT CATATCTGCC CACCACTGTA 1260
 TCAGCTAAAA CAGCATCAG CATTTGTTCA GGGCTTAAGA AAGGATTGGA GGTGGTTGAA 1320
 AAAGTGAATG GAAAAGCTTA TGGCTCTGTG ATGATATTAG TGACCAGCGG AGATGATAAG 1380
 CTTCTGGCA ATTGCTTACC CACTGTGCTC AGCAGTGGTT CAACAATTCA CTCATTGCTC 1440

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CTGGGTTTCAT CTGCAGCCCC AAATCTGGAG GAATTATCAC GTCTTACAGG AGGTTTAAAG 1500
TTCTTTGTTC CAGATATATC AAATCTCCAAAT AGCATGATTG ATGCTTTTTC TAGAATTTCC 1560
TCTGGAACCTG GAGACATTTT CCAGCAACAT ATTCAGCTTG AAAGTACAGG TGAAAAATGTC 1620
AAACCTCACC ATCAATTGAA AAACACAGTG ACTGTGGATA ATACTGTGGG CAACGACACT 1680
5 ATGTTTCTAG TTACGTGGCA GGCCAGTGGT CCTCCTGAGA TTATATTATT TGATCCTGAT 1740
GGACGAAAAAT ACTACACAAA TAAATTTTATC ACCAATCTAA CTTTTCGGAC AGCTAGTCTT 1800
TGGATTCAGG GAACAGCTAA GCCTGGGCAC TGGACTTACA CCCTGAAACA TACCCATCAT 1860
TCTCTGCAAG CCCTGAAAGT GACAGTGACC TCTCGCGCCT CCAACTCAGC TGTGCCCCCA 1920
10 GCCACTGTGG AAGCCTTTGT GGAAGAGAC AGCCTCCATT TTCCTCATCC TGTGATGATT 1980
TATGCCAATG TGAACACAGG ATTTTATCCC ATTCTTAATG CCACTGTCTC TGCCACAGTT 2040
GAGCCAGAGA CTGGAGATCC TGTACGCTG AGACTCCTTG ATGATGGAGC AGGTGCTGAT 2100
GTTTAAAAAA ATGATGGAAT TTACTCGAGG TATTTTTTCT CCTTGTCTGC AAATGGTAGA 2160
TATAGCTTGA AAGTGCATGT CAATCACTCT CCCAGCATAA GCACCCCAAC CCACTCTATT 2220
15 CCAGGGAGTC ATGCTATGTA TGTACCAGGT TACACAGCAA ACGGTAATAT TCAGATGAAT 2280
GCTCCAAGGA AATCAGTAGG CAGAAATGAG GAGGAGCGAA AGTGGGGCTT TAGCCGAGTC 2340
AGCTCAGGAG GCTCCTTTTC AGTGCTGGGA GTTCCAGCTG GCCCCACCC TGATGTGTTT 2400
CCACCATGCA AAATTATTGA CCTGGAAGCT GTAAAAGTAG AAGAGGAATT GACCCATCT 2460
TGGACAGCAC CTGGAGAAGA CTTTGATCAG GGCCAGGCTA CAAGCTATGA AATAAGAATG 2520
AGTAAAAATG TACGAATAT CCAAGATGAC TTTAACAATG CTATTTTAGT AAATACATCA 2580
20 AAGCGAAATC CTGACGAGC TGGCATCAGG GAGATATTTA CGTCTCACC CCAGATTTCC 2640
ACGAATGGAC CTGAACATCA GCCAATGGA GAAACACATG AAAGCCACAG AATTATGTT 2700
GCAATACGAG CAATGGATAG GAACTCCTTA CAGTCTGCTG TATCTAACAT TGCCAGGCG 2760
CCTCTGTTTA TTCCCCCAA TTCTGATCCT GTACCTGCCA GAGATTATCT TATATTGAAA 2820
GGAGTTTAA CAGCAATGGG TTTGATAGGA ATCATTGCCC TTATTATAGT TGTGACACAT 2880
25 CATACTTTAA GCAGGAAAAA GAGAGCAGAC AAGAAAGAGA ATGGAACAAA ATTATTATAA 2940
ATAAATATCC AAAGTGTCTT CCTTCTTAGA TATAAGACCC ATGGCCTTCG ACTACAAAAA 3000
CATACTAACA AAGTCAAAAT AACATCAAAA CTGTATTAAA ATGCATTGAG TTTTGTGACA 3060
ATCAGATAAA GATTTTACA TGGTAGATCA ACAATCTTTT TTGGGGTAG ATTAGAAAAA 3120
30 CCTTACACTT TGGCTATGAA CAAATAATAA AAATTATCTT TTAAGTAAT GTCTTTAAAG 3180
GCAAAGGGAA GGGTAAAGTC GGACCAGTGT CAAGGAAAGT TTGTTTTATT GAGGTGGAAA 3240
AATAGCCCCA AGCAGAGAAA AGGAGGGTAG GTCTGCATTA TAACTGTCTG TGTGAAGCAA 3300
TCATTAGATT ACTTTGATTA ATTTTCTTTT TCTCCTTATC TGTGCAGTAC AGGTGCTGTT 3360
TTTACATGAA GATCATGCTA TATTTTATAT ATGTAGCCCC TAATGCAAAG CTCTTTACCT 3420
35 CTTGCTATTT TGTATATAT ATTTTCTGATG ACATCTCCCT GCTAATGCTC AGAGATCTTT 3480
TTTCACTGTA AGAGGTAACC TTTAACAATA TGGGTATTAC CTTTGTCTCT TCATACCGGT 3540
TTTATGACAA AGGTCTATTG AATTATTTG TNTGTAAGTT TCTACTCCCA TCAAAGCAGC 3600
TTTCTAAGTT TATGCTTTG GGTATTATG GAAATGATAG TATAGCCCN TATAATGCCT 3660
TACCTAGGAA A

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Seq ID NO: 8 Protein sequence:
Protein Accession #: NP_006527.1

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1      11      21      31      41      51
|      |      |      |      |      |
45 MTQRSIAGPI CNLKFTLLV ALSSELPFLG AGVQLQDNGY NGLLIAINPQ VPENQNLIISN 60
IKEMITEASF YLFNATKRRV FFRNIKILIP ATWKANNNSK IKQESYEKAN VIVTDWYGAH 120
GDDPYTLQYR CGCKEGKYIH FTPNFLNDN LTAGYGSRRG VVHEWAHLR WGVFDEYNND 180
KPFYINGQNO IKVTRCSSDI TGIHVCEKGP CPQENCIISK LFKRGCTFIY NSTQNATASI 240
50 MFMQSLSSVV EFCNASTHNQ EAPNLQNMCM SLRSAWDVIT DSADFHHSFP MNGTELPPPP 300
TFSLVQAGDK VVCLVLDVSS KMAEADRLLO LQQAEEFYLM QIVEIHTFVG IASFDSKGEI 360
RAQLHQINSN DDRKLLVSYL PTTVSAKTDI SICSGLKKGF EVVEKLNGKA YGSVMILVTS 420
GDDKLLGNCL PTVLSSGSTI HSIALGSSAA PNLEELSRLT GGLKFFVVDI SNSNSMIDAF 480
55 SRISGTDGI FQHQIQLBST GENVKPHHQL KNTVTVDNTV GNDTMFLVTW QASGPPPIIL 540
FDPDGRKYYT NNFITNLTFR TASLWIPGTA KPGHWYTYLN NTHHSLOALK VTVTSRASNS 600
AVPPATVEAF VERDSLHFPF PVMYIYANVKQ GFYPILNATV TATVEPETGD PVTLRLDDDG 660
AGADVIKNDG IYSRYFFSFA ANGRYSKLVH VNHSPTSSTP AHSIPGSHAM YVPGYTANGN 720
IQMNAPRKSV GRNEEERKWG FSRVSSGGSF SVLGVPAGPH PDVFPPCKII DLEAVKVVEE 780
LTLWSWTAPGE DFDQGGQATSY EIRMSKSLQN IQDDFNNAIL VNTSKRNPQQ AGIREIFTFS 840
60 PQISTNGPEH QPNGETHESH RIYVAIRAMD RNSLQSAVSN IAQAPLFIPP NSDPVPARDY 900
LILKGVLTAM GLIGIICLII VVTHHTLSRK KRADKKENG T KLL

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Seq ID NO: 9 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 336-632

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1      11      21      31      41      51
|      |      |      |      |      |
70 CTCCTCCAC CCCGGTCCAG GATGCCAGT CCCCACGACA CCTCCCACTT CCACTGTGG 60
CCTGGGTGGG CTCAGGGGCT GCCCTTGACC TGGCCTAGAG CCCTCCCCCA GCTGGTGGTG 120
GAGCTGGCAC TCTCTGGGAG GGAGGGGGCT GGGAGGGAAT GAGTGGGAAT GGCAAGAGGC 180
CAGGGTTTGG TGGGATCAGG TTGAGGCAGG TTTGGTTTCC TTAAAAATGCC AAGTTGGGGG 240
CCAGTGGGGC CCACATATAA ATCTTCACCC TGGGAGCCTG GCTGCCTTGC TCTCTTCCT 300
75 GGGTCTGTCT CTGCCACCTG GTCTGCCACA GATCCATGAT GTGCAGTTCT CTGGAGCAGG 360
CGCTGGCTGT GCTGCTCACT ACCTTCCACA AGTACTCCTG CCAAGAGGGG GACAAGTTCA 420
AGCTGAGTAA GGGGAAATG AAGGAACTTC TGCACAAGGA CCTGCCAGC TTTGTGGGGG 480
AGAAAGTGA TGGAGAGGGG CTGAAGAAGC TGATGGGCAG CTGGATGAG AACAGTGACC 540
AGCAGGTGGA CTTCCAGGAG TATGCTGTTT TCCTGGCACT CATCACTGTC ATGTGCAATG 600
ACTTCTTCCA GGGCTGCCCA GACCGACCTT GAAGCAGAAC TCTTGACTTC CTGCCATGGA 660
80 TCTCTGGGC CAGGACTGTG TGATGCCTTT GAGTTTGTGA TTCAATAAAC TTTTGTGTC 720
TGTTGATAAT ATTTTAAATG CTCAGTGATG TTCCATAACC CGGCTGGCTC AGCTGGAGTG 780
CTGGGAGATG AGGGCCTCCT GGATCCTGCT CCCCTCTGGG CTCTGACTCT CCGGAAATC 840
TCTCCAAGGC CAGAGCTATG CAATTTTGGG ATTTTCAACA CCAGCAAAAA 900
85 ATTGGAATC GAGATAGGTT GCTGACTTTT ATTTTGTCAA ATAAAGATAT TAAAAAGGC 960
AAATACCA

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Seq ID NO: 10 Protein sequence:

Protein Accession #: NP_005969.1

1 11 21 31 41 51
5 MMCSLEQAL AVLVTTFFHKY SCQEGDKFKL SKGEMKELLH KELPSFVGEK VDEEGLKKLM 60
GSLDENSQQ VDFQEYAVFL ALITVMCNDP FQGCPRP

Seq ID NO: 11 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 336-626

1 11 21 31 41 51
15 CTCCCTCAC CCCGCTCCAG GATGCCAGT CCCCACGACA CCTCCCACTT CCCACTGTGG 60
CCTGGGTGGG CTCAGGGGCT GCCCTTGACC TGGCTAGAG CCCTCCCCCA GCTGGTGGT 120
GAGCTGGCAC TCTCTGGGAG GGAGGGGCT GGGAGGGAAT GAGTGGGAAT GGCAAGAGGC 180
CAGGGTTTGG TGGGATCAGG TTGAGGCAGG TTTGGTTTCC TTAATATGCC AAGTGGGGG 240
CCAGTGGGGC CCACATATAA ATCCTCACCC TGGGAGCCTG GCTGCCCTTG TCTCCTCCT 300
20 GGGTCTGTCT CTGCCACCTG GTCTGCCACA GATCCATGAT GTGCAGTTCT CTGGAGCAGG 360
CGCTGGCTGT GCTGGTCACT ACCTCCACA AGTACTCCTG CCAAGAGGGC GACAAGTTCA 420
AGCTGAGTAA GGGGGAATG AAGGAACCTC TGCACAAGGA GCTGCCCAGC TTTGTGGGGC 480
ATTCACAGAG ACCATGTGCT GTGAGGGGCT TCCGAGTCCA TCTGTTTAAT CCTGTCTATG 540
25 GAGACTTGAG AAACACAGAG CCAGAAGGGA AAAGTGATTG TCCCAAGATC ACACAGCACT 600
GGAGAAATG GATGAGGAGG GGCTGAAGAA GCTGATGGGC AGCCTGGATG AGAACAGTGA 660
CCAGCAGGTG GACTTCCAGG AGTATGCTGT TTTCTGGCA CTCATCACTG TCATGTGCAA 720
TGACTTCTTC CAGGCTGCC CAGACCGACC CTGAAGCAGA ACTCTTGACT TCCTGCCATG 780
GATCTCTTGG GCCCAGGACT GTTGATGCCT TTGAGTTTGG TATTCAATAA ACTTTTGTG 840
30 TCTGTTGATA ATATTTTAAT TGCTCAGTGA TGTTCCATAA CCGGCTGGC TCAGCTGGAG 900
TGCTGGGAGA TGAGGGCCTC CTGGATCCTG CTCCTTCTG GGCTCTGACT CTCCTGGAAG 960
TCTCTCCAAG GCCAGAGCTA TGCTTTAGGT CTCATTTTGG GAATTTCAAA CACCAGCAAA 1020
AAATTGGAAA TCGAGATAGG TTGCTGACTT TTATTTTGTC AAATAAAGAT ATTAAAAAAG 1080
GCAATACCA

Seq ID NO: 12 Protein sequence:
Protein Accession #: Eos sequence

1 11 21 31 41 51
40 MMCSLEQAL AVLVTTFFHKY SCQEGDKFKL SKGEMKELLH KELPSFVGHG REPCAIVRAFR 60
VHLNPNVIGD LRNQSPGKGS DCPKITQHWR KWMRRG

Seq ID NO: 13 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 58-354

1 11 21 31 41 51
50 GTGAGCTCAC CATGTGGGGG TGAGGCTGAG AGAAAACAAG TACACAGCCA CAGATCCATG 60
ATGTGCAGTT CTCTGGAGCA GGCGCTGGCT GTGCTGGTCA CTACCTTCCA CAAGTACTCC 120
TGCCAAGAGG GCGACAAGTT CAAGCTGAGT AAGGGGGAAA TGAAGGAACT TCTGCACAAG 180
GAGCTGCCCA GCTTTGTGGG GGAGAAAGTG GATGAGGAGG GGCTGAAGAA GCTGATGGGC 240
55 AGCCTGGATG AGAACAGTGA CCAGCAGGTG GACTTCCAGG AGTATGCTGT TTTCTGGCA 300
CTCATCACTG TCATGTGCAA TGACTTCTTC CAGGGCTGCC CAGACCGACC CTGAAGCAGA 360
ACTCTTGACT TCCTGCCATG GATCTCTTGG GCCCAGGACT GTTGATGCCT TTGAGTTTGG 420
TATTCAATAA ACTTTTGTG TCTGTTGATA ATATTTTAAT TGCTCAGTGA TGTTCCATAA 480
CCCCGCTGGC TCAGCTGGAG TGCTGGGAGA TGAGGGCCTC CTGGATCCTG CTCCTTCTG 540
60 GGCTCTGACT CTCCTGGAAA TCTCTCCAAG GCCAGAGCTA TGCTTTAGGT CTCATTTTGG 600
GAATTTCAAA CACCAGCAAA AAATTGGAAA TCGAGATAGG TTGCTGACTT TTATTTTGTC 660
AAATAAAGAT ATTAAAAAAG GCAATACCA

Seq ID NO: 14 Protein sequence:
Protein Accession #: NP_005969.1

1 11 21 31 41 51
65 MMCSLEQAL AVLVTTFFHKY SCQEGDKFKL SKGEMKELLH KELPSFVGEK VDEEGLKKLM 60
GSLDENSQQ VDFQEYAVFL ALITVMCNDP FQGCPRP

Seq ID NO: 15 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 62-358

1 11 21 31 41 51
75 GGAGGGTGTG CCGCTGAGTC ACTGCCTGGG CATCTGGGCC TGGAACTCG GCCACAGATC 60
CATGATGTGC AGTTCTCTGG AGCAGGCGCT GGCTGTGCTG GTCACACTT TCCACAAGTA 120
80 CTCCTGCCAA GAGGCGGACA AGTTCAAGCT GAGTAAGGGG GAAATGAAGG AACTTCTGCA 180
CAAGGAGCTG CCCAGCTTTG TGGGGGAGAA AGTGGATGAG GAGGGGCTGA AGAAGCTGAT 240
GGGAGCCTG GATGAGAACA GTGACCAGCA GGTGGACTTC CAGGAGTATG CTGTTTCTCT 300
GGCACTCATC ACTGTCATGT GCAATGACTT CTTCCAGGCG TGCCAGACC GACCTGAAG 360
CAGAACTCTT GACTTCTGTC CATGGATCTC TTGGGCCAG GACTGTTGAT GCCTTTGAGT 420
TTTGTATTCA ATAACTTTT TTTGTCTGTT GATAATATTT TAATTGCTCA GTGATGTTCC 480
85 ATAACCCGGC TGGCTCAGCT GGAGTGTGG GAGATGAGGG CCTCCTGGAT CCTGCTCCCT 540
TCTGGGCTCT GACTCTCCTG GAAATCTCTC CAAGGCCAGA GCTATGCTTT AGGTCTCAAT 600
TTTGAATTT CAAACACCAG CAAAAAATTG GAAATCGAGA TAGGTTGCTG ACTTTTATTT 660

TGTCAAATAA AGATATTAAA AAAGGCAAAAT ACCA

Seq ID NO: 16 Protein sequence:
Protein Accession #: NP_005969.1

1	11	21	31	41	51	
MMCSSLEQAL	AVLVTTFFHKY	SCQEGDKFKL	SKGEMKELHH	KELPSFVGEK	VDEGLKKLM	60
GSLDENSQQ	VDFQYAVFL	ALITVMCNDP	FQGCDFRP			

Seq ID NO: 17 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 939-2372

1	11	21	31	41	51	
AAGACGGATT	CTCAGACAAG	GCTTGCAAAT	GCCCCGCAGC	CATCATTTAA	CTGCACCCGC	60
AGAATAGTTA	CGGTTTGTC	CCCAGACCCTC	CCGGATCGCC	TAATTTGTCC	CTAGTGAGAC	120
CCCGAGGCTC	TGCCCGCGCC	TGGCTTCTTC	GTAGCTGGAT	GCATATCGTG	CTCCGGGCAG	180
CGCGGGCGCA	GGGCACGGCT	TCGCGCACAC	CCTAGCACAC	ATGAACACGC	GCAAGAGCTG	240
AACCAAGCAC	GGTTTCCATT	TCAAAAGGG	AGACAGCCTC	TACCGCGATT	GTAGAAGAGA	300
CTGTGGTGTG	AATTAGGGAC	CGGGAGGCGT	CGAACGGAGG	AACGGTTCAT	CTTAGAGACT	360
AAATTTCTGG	AGTTTCTGCC	CCTGCTCTGC	GTACGCCCTC	ACGTCACTTC	GCCAGCAGTA	420
GCAGAGGCGG	CGGCGCGGCG	TCCCAGAAAT	GGGTGTGAGC	AGGAGCCTCG	CTGGCTGCTT	480
CGCTCGCGCT	CTACGCGCTC	AGTCCCCGGC	GGTAGCAGGA	GCCTGGACCC	AGGCGCGGCC	540
GGCGGGCGTG	AGGCGCCGGA	GCCCGGCCCTC	GAGGTGCATA	CCGGACCCCC	ATTGCGCATCT	600
AACAAGGAAT	CTGCGCCCCA	GAGAGTCCCG	GGAGCGCCCG	CGGTCCGTGC	CCGGCGCGCC	660
GGGCCATGCA	GCGACGGCGC	CCGCGGAGCT	CCGAGCAGCG	GTAGCGCCCC	CCTGTAAAGC	720
GGTTTCGTAT	GCCGGGGCCA	CTGTGAACCC	TGCCGCCTGC	CGGAACACTC	TTGCTCCGG	780
ACCAGCTCAG	CCTCTGATAA	GCTGGACTCG	GCACGCCCGC	AACAAGCACC	GAGGAGTTAA	840
GAGAGCCGCA	AGCGCAGGGA	AGGCCCTCCC	GCACGGGTGG	GGGAAAGCGG	CCGGTGCAGC	900
GCGGGGACAG	GCACCTCGGC	TGGCACTGGC	TGCTAGGGAT	GTCTGCTTGG	ATAAGGTGGC	960
ATGGACCCGC	CATGCGCGCG	CTCTGGGGCT	TCTGCTGGCT	GGTTGTGGGC	TTCTGGAGGG	1020
CCGTTTTCGC	CTGTCCCACG	TCCTGCAAAT	GCAGTGCCTC	TCGGATCTGG	TGCAGCGACC	1080
CTTCTCCTGG	CATCGTGCCA	TTTCCGAGAT	TGGAGCCTAA	CAGTGTAGAT	CCTGAGAACA	1140
TCACCGAAAT	TTTATCTGCA	AACCAAGAAA	GGTTAGAAAT	CATCAACGAA	GATGATGTTG	1200
AAGCTTATGT	GGGACTGAGA	AATCTGACAA	TTGTGGATTG	TGGATTAAAA	TTTGTGGCTC	1260
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CGAGTTTGTC	TAGGAAACAT	TTCCGTCAAC	TTGACTTGTC	TGAACTGATC	CTGGTGGGCA	1380
ATCCATTATC	ATGCTCCTGT	GACATTATGT	GGATCAAGAC	TCTCCAAGAG	GCTAAATCCA	1440
GTCCAGACAC	TCAGGATTGT	TACTGCCTGA	ATGAAAGCAG	CAAGAATATT	CCCCTGGCAA	1500
ACCTGCAGAT	ACCCAATTGT	GGTTTGCCAT	CTGCAAACTC	GGCCGCACCT	AACCTCACTG	1560
TGGAGGAAGG	AAAGTCTATG	ACATATATCT	GTAGTGTGGC	AGGTGATCCG	TTCTCTAATA	1620
TGTATTGGGA	TGTTGGTAAC	CTGGTTTCCA	AACATATGAA	TGAAACAAGC	CACACACAGG	1680
GCTCCTTAAG	GATAACTAAC	ATTTATCCG	ATGACAGTGG	GAAGCAGATC	TCTTGTGTGG	1740
CGGAAAATCT	TGTAGGAGAA	GATCAAGATT	CTGTCAACCT	CACTGTGCAT	TTTGCACCAA	1800
CTATCACATT	TCTCGAATCT	CCAACCTCAG	ACCACCACCTG	GTGCATTCCA	TTCACCTGTA	1860
AAGGCAACCC	CAAAACACGC	CTTCAGTGGT	TCTATAACCG	GGCAATATTG	AATGAGTCCA	1920
AATACATCTG	TACTAAAATA	CATGTTACCA	ATCACACGGA	GTACCACGGC	TGCCTCCAGC	1980
TGGATAATCC	CACACACATG	AACAATGGGG	ACTACACTCT	AATAGCCCAAG	AATGAGTATG	2040
GGAAAGGATGA	GAAACAGATT	TCTGCTCACT	TCATGGGCTG	GCCTGGAATT	GACGATGGTG	2100
CAAAACCCAAA	TTATCCTGAT	GTAATTTATG	AAGATTATGG	AACCTGCAGCG	AATGACATCG	2160
GGGACACAC	GACAGAGAT	AATGAAATCC	CTTCCACAGA	CGTCACTGAT	AAAACCCGTC	2220
GGGAACATCT	CTCGGTCTAT	GCTGTGGTGG	TGATTGCGTC	TGTGGTGGGA	TTTTGCCCTTT	2280
TGGTAATGCT	GTTTCTGCTT	AAGTTGGCAA	GACACTCCAA	GTTTGGCATG	AAAGGTTTGG	2340
TTTGTGTTCA	TAAGATCCCA	CTGGATGGGT	AGCTGAAATA	AAGGAAAAGA	CAGAGAAAAG	2400
GGCTGTGGTG	CTTGTGTGTT	GATGCTGCCA	TGTAAGCTGG	ACTCCTGGGA	CTGCTGTGTTG	2460
CTTATCCCGG	GAAGTGCTGC	TTATCTGGGG	TTTTCTGGTA	GATGTGGGCG	GTGTTTGGAG	2520
GCTGTACTAT	ATGAAGCTGC	CATATACTGT	GAGCTGTGAT	TGGGGAACAC	CAATGCAGAG	2580
GTAACCTCTA	GCGAGCTAAG	CAGCACTCA	AGAAAACATG	TTAAATTAAT	GCTTCTCTTC	2640
TTACAGTAGT	TCAATATAAG	AAATCCCAT	GGATTGTACT	TCTCTCTCTGA		2700
AAAGTGTGCT	TTTTGACCCT	ACTGGACATT	TATTGACTTA	ATTGCTTCTG	TTTATTAAAA	2760
TTGACCTGCA	AAGTTAAAAA	AAAATTAAAG	TTGAGAACAG	GTATAAGTGC	ACACTGAATA	2820
GTCTAATCTA	CATGTAACAC	ATATTTTAGT	GTGATTTTCT	ATACTCTAAT	CAGCACTGAA	2880
TTACAGAGGT	TTGACTTTT	CATCTATAAC	ACAGTGACTA	AAAGAGTTAA	GGGTATATAT	2940
ACCATCACTT	TGGGACTTGG	TAGTATTATT	AAAAGGTTAT	TTCCTTCACT	GTCAATAAAA	3000
GTCCAAATGT	TTAGCTTAGG	TCTGAGAGTC	AAACAATGTT	AAGGATTGTC	TTAAAGTTCC	3060
TTAGCCAGCA	AAACAAAACA	AAACAAAACA	AACAATGAA	AAACGTTTAA	AAAGAAGAAG	3120
AAGAAAAAAA	ACAAGAACAA	GCAGCAACAG	CTGTTTGTG	GGGGCTATAG	ATTTAAGTTA	3180
GGCATAGTCA	ATTTCAGAA	AACTAAGAGT	GGAAATATATG	CATATGGTGA	AATTATAACC	3240
TTGCCCTTTT	TTATTTGCC	TCTGCGATCC	ACCTGCTTTT	TAGAAGTCTG	CCGAGTGAGA	3300
AGGCCACAGT	ATCTCATGCT	GTTTGCATTA	CAGAACTGCA	GCTTTCTTAC	TCTGAAAAGG	3360
CCTGGGAGCA	GAATGGCTGG	CCTGCTGTGA	GCAGGAGAGG	AGATTCTAAG	AAGGATAGTC	3420
CCCCCTACAA	CATACTGTCA	TACTGCTGGG	TTTTCATGGG	TAGGAAAGCT	TGTCCTGACC	3480
CCAGCAGCAA	AGAGGTGCGA	GGTCGCTAAT	GAATATATGC	TTTATAATGT	CCTTCTTCAT	3540
TGCTGAGAGG	GCAGCCTTAG	AGCTGTGGAT	TTCTGCTATC	CCCCTGAGTC	TGACCCATGG	3600
ACACCTGTTT	GATTCACATT	AGCATCACAG	TGACCTTTGT	ATGCTCTGTT	CAGTCTGTGT	3660
CAGGCAGTAT	GCTTGTCTCG	AAGAGAGGTT	TGGCTATCCC	CACCCACCC	CACCCACCC	3720
TGTTCTTTT	TTATCAGAGG	GACTTCAGAG	CCAGGCTTGC	AGCATTTTGT	TTGAAAACAC	3780
AATCAGCTCT	GACAGTTAGA	CATGCACACA	GACGCCATAG	CTGGATTGGA	AACATTGATG	3840
TTTTAAAAAT	TTATTTT	TGGAATAGT	TGCACAAATG	CTGCAATTAA	GCTTTAAGGT	3900
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CAAGGCATTA	ATCTTAATAA	ACCAGGATCC	ATTTAGGTAC	CACCTGATAT	AAAAAGGATA	4020
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Seq ID NO: 18 Protein sequence:
 Protein Accession #: CAA53571

1 11 21 31 41 51
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 NFRNKLTSLS SRKFRHLDL SELLLVGNPF TCSCDIMWIK TLQEAQSSPD TDLYLCLNES 180
 SKNIPLANLQ IPNCGLPAN LAAPNLTVEE GKSTILSCSV AGDVPVPMYW DVGNLVSXHM 240
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 LIAKNEYGKD EKQISAHEFMG WPGIDDGANP NYPDVIYEDY GTAANDIGDT TNRSNEIPST 420
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Seq ID NO: 19 DNA sequence
 Nucleic Acid Accession #: NM_000228
 Coding sequence: 82-3600

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Seq ID NO: 20 Protein sequence:
 Protein Accession #: NP_000219

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 NARLNGGVQ LNLMDLVSGI PATQSQKIQE VGEITNLRVN FTRLAPVPQR GYHPPSAYYA 240
 VSQRLRLQGSC FCHGHADRC PKPGASAGPS TAVQVHDCV CQHNTAGPNC ERCAPFFYNR 300
 PWRPAEGQDA HECQRCDNCG HSETCHFDPA VFAASQGAYG GVCDNCRDHT EGKNCERCQL 360
 HYFNRNRRPGA SIQETLISCE CDDPGAVPGA PCDPVTGQCV CKEHVQGERC DLCKPGFTGL 420
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 RLRLNATASLW SGPGLDRLG ASRLLDKSK IEQIRAVLSS PAVTEQEVAV VASAILSLRR 660
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 AYEQSAQAAQ QVSDSSRLLD QLRDSREAE RLVRQAGGGG GTGSPKLVAL RLEMSSLPDL 780
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 GFNAQLQRT RMIKRAEESA SIQSSAQRL ETQVSASRSQ MEEDVRRTRL LIQVVRDFLT 900
 DDPDTAAITQ EVSEAVLALW LPTDSATVLQ KMNEIQAI A RLPNVDLVLS QTKQDIARAR 960
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 VLRPAEKLVMT SMTKQLGDFV TRMELRHQA RQQAEEAVQA QQLAEGASEQ ALSAEGFER 1080
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Seq ID NO: 21 DNA sequence
 Nucleic Acid Accession #: NM_003722
 Coding sequence: 145-1491

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Seq ID NO: 22 Protein sequence:
 Protein Accession #: NP_003713

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 FEARICACPG RDRKADEDSI RKQQVSDSTK NGDGTKRPFQ QNTHGIQMTS IKKRRSPDDE 360
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Seq ID NO: 24 Protein sequence:
 Protein Accession #: NP_001935.1

1 11 21 31 41 51

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	GEDNSKRNI	AKITSDYQAT	QKITVIRISGV	GIDQPPFGIF	VVDKNTGDIN	ITAIVDREET	120
5	PSFLITCRAL	NAQGLDVEKP	LILTVKILDI	NDNPPVFSQQ	IFMGEIEENS	ASNSLVMILN	180
	ATDADEPNHL	NSKIAFKIVS	QEPAGTFMFL	LSRNTGEVRT	LTNSLDREQA	SSYRLVVSGA	240
	DKDGEGLSTQ	CECNIKVKDV	NDNFPMFRDS	QYSARIEENI	LSSELRLRFQV	TDLDEEYTDN	300
	WLAVYFFTS	NEGNWFIEQT	DPRTNEGILK	VVKALDYEQ	QSVKLSIAVK	NKAEFHQSVI	360
	SRYRVQSTPV	TIQVINVRBG	IAFRPASKTF	TVQKGISSKK	LVDYILGTQ	AIDEDTNKAA	420
10	SNVKKVMGRN	DGGYLMIDSK	TAEIKFVKNM	NRDSTFIVNK	TITAEVLAI	EYTGKTSTGT	480
	VYVRVPDFND	NCPTAVLEKD	AVCSSSPSVV	VSARTLNNRY	TGPYTFALD	QPVKLPVWS	540
	ITTLNATSAL	LRAQEQIPPG	VYHISLVLD	SQNNRCMPR	SLTLEVQCQD	NRGICGTSYP	600
	TTSPGTRYGR	PHSGRLGPAA	IGLLLLGLLL	LLLAPLLLLT	CDCGAGSTGG	VTGGFIPVPD	660
	GSEGTIHQWG	IEGAHPDEKE	ITNICVPPVT	ANGADFMESS	EVCTNTYARG	TAVEGTSGME	720
15	MTTKLGAATE	SGGAAGFATG	TVSGAASGFG	AATGVGICSS	GQSGTMRTRH	STGGTNKDYA	780
	DGAISMNPLD	SYFSQKAFAC	AEEDDQGEAN	DCLLIYDNEG	ADATGSPVGS	VGCCSFIADD	840
	LDDSFLLSLG	PKFKKLAELS	LQVDGEGKEV	QPPSKDSGYG	IESCGHFIEV	QQTGFVKQCT	900
	LSGSQGSASL	SASGSVQPAV	SIPDPLQHGN	YLVTEYTSAS	GSLVQPFSTAG	FDPPLLTQNV	960
	VTERVICPIS	SVPGNLAGPT	QLRGSHTMLC	TEDPCSRILI			

Seq ID NO: 25 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 56-1642

25	1	11	21	31	41	51	
	AGTATCCCAG	GAGGAGCAAG	TGGCAGCTCT	TCGGACCTAG	GCTGCCCCTG	CCGTCATGTC	60
	GCAAGGGATC	CTTTCTCCGC	CAGCGGGCTT	GCTGTCCGAT	GACGATGTCG	TAGTTTCTCC	120
	CATGTTTGAG	TCCACAGCTG	CAGATTGCGG	GTCTGTGGTA	CGCAGAAGCC	TGCTATCAGA	180
30	CTGCTCTGTC	GTCTCTACCT	CCCTAGAGGA	CAAGCAGCAG	GTTCCATCTG	AGGACAGTAT	240
	GGAGAAAGTG	AAAGTATACT	TGAGGGTTAG	GCCCTTGTTA	CCTTCAGAGT	TGGAACGACA	300
	GGAAAGATCAG	GTTTGTGTCC	GTATTGAGAA	TGTGGAGACC	CTTGTTCTAC	AAGCACCCAA	360
	GGACTCTTTT	GCCCTGAAGA	GCAATGAACG	GGGAATTGGC	CAAGCCACAC	ACAGGTTTAC	420
	CTTTTCCCAG	ATCTTTGGGC	CAGAAAGTGG	ACAGGCATCC	TTCTTCAACC	TAACGTGTAA	480
35	GGAGATGGTA	AAGGATGTAC	TCAAAGGGCA	GAACCTGGCTC	ATCTATACAT	ATGGAGTCC	540
	TAACCTCAGG	AAAAACCCCA	CGATTCAAGG	TACCATCAAG	GATGGAGGGA	TTCTCCCCCG	600
	GTCCCTGGCG	CTGATCTTCA	ATAGCCTCCA	AGGCCAACTT	CATCCAACAC	CTGATCTGAA	660
	GCCCTTGCTC	TCCATGAGG	TAATCTGGCT	AGACAGCAAG	CAGATCCGAC	AGGAGGAAAT	720
	GAAGAAGCTG	TCCCTGCTAA	ATGGAGGCCT	CCAAGAGGAG	GAGCTGTCCA	CTTCTTGTA	780
40	GAGGAGTGT	TACATCGAAA	GTCCGATAGG	TACCAGCACC	AGCTTCGACA	GTGGCATTGC	840
	TGGGCTCTCT	TCTATCAGCT	AGTGATCCAG	CAGTAGCCAG	CTGGATGAAA	CAAGTCATCG	900
	ATGGGCACAG	CCAGACACTG	CCCCACTACC	TGTCCCGGCA	AACATTCCGT	TCTCCATCTG	960
	GATCTCATTC	TTTGAGATCT	ACAACGAACT	GCTTTATGAC	CTATTAGAAC	CGCCTAGCCA	1020
	ACAGCGCAAG	AGGCAGACTT	TGCGGCTATG	CGAGGATCAA	AATGGCAATC	CCTATGTGAA	1080
45	AGATCTCAAC	TGGATTCACT	TGCAAGATGC	TGAGGAGGCC	TGGAAGCTCC	TAAAGTGGG	1140
	TCGTAAAGAC	CAGAGCTTTG	CCAGCACCCA	CCTCAACCAG	AACTCCAGCC	GCAGTCACAG	1200
	CATCTTCTCA	ATCAGGATCC	TACACCTTCA	GGGGGAAGGA	GATATAGTCC	CCAAGATCAG	1260
	CGAGCTGTCA	CTCTGTGATC	TGGCTGGCTC	AGAGCGCTGC	AAAGATCAGA	AGAGTGGTGA	1320
	ACGGTTGAAG	GAAGCAGGAA	ACATTAAAC	CTCTCTACAC	ACCCCTGGGC	GCTGTATTGC	1380
50	TGCCCTTCTG	CAAAACACAG	AGAACCGGTC	AAAGCAGAAC	CTGGTTCCCT	TCCGTGACAG	1440
	CAAGTTGACT	CGAGTGTTCC	AAGGTTTCTT	CACAGGCCGA	GGCCGTTCC	GCATGATTGT	1500
	CAATGTGAAT	CCCTGTGCAT	CTACCTATGA	TGAAACTCTT	CATGTGGCCA	AGTTCTCAGC	1560
	CATTGCTAGC	CAGGTGACTT	GTGCATGCCC	CACCTATGCA	ACTGGGATTC	CCATCCCTGC	1620
	ACTCGTTCAT	CAAGGAACAT	AGTCTTCAGG	TATCCCCCAG	CTTAGAGAAA	GGGGCTAAGG	1680
55	CAGACACAGG	CCTTGATGAT	GATATTGAAA	ATGAAGCTGA	CATCTCCATG	TATGGCAAAG	1740
	AGGAGCTCCT	ACAAATTTGG	GAAGCCATGA	AGACACTGCT	TTTGAAGGAA	CGACAGGAAA	1800
	AGCTACAGCT	GAGATGCAAT	CTCCGAGATG	AAATTGCAA	TGAGATGGTA	GAACAGATGC	1860
	AACAGCGGGA	ACAGTGGTGC	AGTGAACATT	TGGACACCCA	AAAGGAACAT	TTGGAGGAAA	1920
	TGTATGAAGA	AAAACTAAAT	ATCCTCAAGG	AGTCACTGAC	AAGTTTTTAC	CAAGAAGAGA	1980
60	TTCAGGAGCG	GGATGAAAAG	ATTGAAGAGC	TAGAAGCTCT	CTTGACAGAA	GCCAGACAA	2040
	AGTCAGTGGC	CCATCAGCAA	TGAGGCTCTG	AATTGGCCCT	ACGGCGGTCA	CAAAGGTTGG	2100
	CAGCTTCTGC	CTCCACCCAG	CAGCTTCAGG	AGGTTAAAGC	TAAATTACAG	CAGTGCAAG	2160
	CAGAGCTAAA	CTCTACCACT	GAAGAGTTGC	ATAAGTATCA	GAAATGTTA	GAACCAACAC	2220
	CCTCAGCCAA	GCCCTTCACC	ATTGATGTGG	ACAAGAAATT	AGAAGAGGGC	CAGAAGATA	2280
65	TAAGGCTGTT	GCGGACAGAG	CTTCAGAAAC	TTGGTGAGTC	TCTCCAATCA	GCAGAGAGAG	2340
	CTTGTTGCCA	CAGCACTGGG	GCAGGAAAAC	TTCGTCAAGC	CTTGACCACT	TGTGATGACA	2400
	TCTTAATCAA	ACAGGACCAG	ACTCTGGCTG	AACTGCAGAA	CAACATGGTG	CTAGTGAAAC	2460
	TGGACCTTCG	GAAGAAGGCA	GCATGTATTG	CTGAGCAGTA	TCATACTGTG	TTGAAACTCC	2520
	AAGGCCAGGT	TTCTGCCAAA	AAGCGCCTTG	GTACCAACCA	GGAAATCAG	CAACCAAAAC	2580
70	AACAACCAAC	AGGGAAGAAA	CGATTCTTTC	GAAATTTACT	TCCCCGAACA	CCAACCTGCC	2640
	AAAGCTCAAC	AGACTGCAGC	CCTTATGCCC	GGATCCTACG	CTCACGGCGT	TCCCTTTTAC	2700
	TCAAATCTGG	GCCTTTTGGC	AAAAAGTACT	AAGGCTGTGG	GGAAAGAGAA	GAGCAGTCAT	2760
	GGCCCTGAGG	TGGGTCAGCT	ACTCTCCTGA	AGAAATAGGT	CTCTTTTATG	CTTTACCATA	2820
	TATCAGGAAT	TATATCCAGG	ATGCAATACT	CAGACACTAG	CTTTTCTCTC	ACTTTTGTAT	2880
75	TATAACCACC	TATGTAATCT	CATGTTGTTG	TTTTTTTTTA	TTTACTTATA	TGATTTCTAT	2940
	GCACACAAAA	ACAGTTATAT	TAAAGATATT	ATTGTTTACA	TTTTTTTATG	AATTCCAAAT	3000
	GTAGCAAAAT	CATTAACAAA	AATTATAAAA	GGGACAGAAA	AA		

Seq ID NO: 26 Protein sequence:
Protein Accession #: Eos sequence

80	1	11	21	31	41	51	
	MSQGILSPPA	GLLSDDDVVV	SPMFESTAAD	LGSVVRKNLL	SDCSVVSLSL	EDKQQVPS	60
	SMEKVKVYLR	VRPLLPSELE	RQEDQGCVR	ENVETLVLLQ	PKDSFALKSN	ERGIGQATHR	120
85	FTFSQIFGPE	VQGSFENLT	VKEMVKDVLK	GQNWLIYTYG	VTSNGKTHET	QGTIKDGGIL	180
	PRSLALIFNS	LQQQLHPTPD	LKPLLSNEVI	WLDKQIROE	EMKKLSLLNG	GLQBEELSTS	240
	LKRSVYIESR	IGTSTSFDSG	IAGLSSISQC	TSSSQLDETS	HRWAQPDTP	LPVPANIRFS	300

IWISFEEIYN ELLYDLEPP SQQRKQTLR LCEDQNGNPF VKDLNWIHVQ DAEBAWKLLK 360
 VGRKNQSPAS THLNQNSSRS HSIFSIRILH LQEGGDIVPK ISELSLCDLA GSERCKDQKS 420
 GERLKEAGNI NTLHLTLGRK IALRQNNQN RSKQNLVPPR DSKLTVRFQG FFTGRGRSCM 480
 IVNVNPCAST YDETLHVAKF SAIASQVTCA CPTYATGIPI PALVHQGT

Seq ID NO: 27 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 13-1424

1 11 21 31 41 51
 TAGAAGTTTA CAATGAAGTT TCTTCTAATA CTGCTCCTGC AGGCCACTGC TTCTGGAGCT 60
 CTTCCTCCGTA ACAGCTCTAC AAGCCTGGAA AAAAATAATG TGCTATTTGG TGAAAGATAC 120
 TTAGAAAAAT TTTATGGCCT TGAGATAAAC AAACCTCCAG TGACAAAAAT GAAATATAGT 180
 GGAAACTTAA TGAAGGAAAA AATCCAAGAA ATGCAGCACT TCTTGGGTCT GAAAGTGACC 240
 GGGCAACTGG ACACATCTAC CCTGGAGATG ATGCACGCAC CTCGATGTGG AGTCCCCGAT 300
 GTCCATCATT TCAGGGAAT GCCAGGGGGG CCGTATGGA GGAAACATTA TATCACTTAC 360
 AGAATCAATA ATTACACACC TGACATGAAC CGTGAGGATG TTGACTACGC AATCCGGAAG 420
 GCTTTCCAAG TATGAGTAA TGTTACCCCT TGAAATTCA GCAAGATTAA CACAGGCATG 480
 GCTGACATTT TGGTGGTTT TGCCCGTGA GCTCATGGAG ACTTCCATGC TTTTGATGGC 540
 AAAGGTGGA TCCTAGCCCA TGCTTTTGA CCTGGATCTG GCATTGGAGG GGATGCACAT 600
 TTCGATGAGG ACGAATTCG GACTACACAT TCAGGAGGCA CAACTTGT CTCTACTGCT 660
 GTTCACGAGA TTGGCCATTC CTTAGGTCTT GGCCATTCTA GTGATCCAAA GGCCGTAATG 720
 TTCCCCACCT ACAAAATCT TGACATCAAC ACATTTCGCC TCTCTGCTGA TGACATACGT 780
 GGCATTCACT CCCTGTATGG AGACCCAAA GAGAACCAAC GCTTGCCAAA TCCTGACAAT 840
 TCAGAACCCG CTCTCTGTGA CCCCAATTG AGTTTGTATG CTGTCACTAC CGTGGGAAAT 900
 AAGATCTTTT TCTTCAAGA CAGGTTCTTC TGGCTGAAGG TTTCTGAGAG ACCAAAGACC 960
 AGTGTAAAT TAATTTCTTC CTATGGCCA ACCTTGCCAT CTGGCATTGA AGCTGCTTAT 1020
 GAAATTGAAG CCAGAATCT AGTTTCTT TTTAAGATG ACAAATACTG GTTAATTAGC 1080
 AATTTAAGAC CAGAGCCAAA TTATCCCAAG AGCATACATT CTTTGTGTT TCCTAACTTT 1140
 GTGAAAAAAA TTGATGCAGC TGTTTTAAAC CCACGTTTT ATAGGACCTA CTCTTTTGT 1200
 GATAACCACT ATTGAGGTA TGATGAAAG AGACAGATGA TGGACCCCTG TTATCCCAAA 1260
 CTGATTACCA AGAATCTCCA AGGAATCGGG CCTAAATTG ATGCAGTCTT CTACTCTAAA 1320
 AACAAATACT ACTATTTCTT CCAAGGATCT AACCAATTG AATATGACTT CCTACTCCAA 1380
 CGTATCACCA AACCACTGAA AAGCAATAGC TGGTTTGGTT GTTGAAAATG GTGTAATTAA 1440
 TGGTTTTTGT TAGTTCACCT CAGCTTAATA AGTATTTATT GCATATTTCG TATGCTCTCA 1500
 GTGTACCCT ACTTAGCAT ATGTATCATA AAAATAAAT CTGTAAACCA TAGGTAATGA 1560
 TTATATAAAA TACATAATAT TTTTCAATTT TGAAACTCT AATTGTCCAT TCTTGCTTGA 1620
 CTCTACTATT AAGTTTGAAG ATAGTTACCT TCAAAGCAAG ATAATTCTAT TTGAAGCATG 1680
 CTCTGTAAGT TGCTTCCFAA CATCCTTGA CTGAGAAATT ATACTTACTT CTGGCATAAC 1740
 TAAATTAAG TATATATATT TTGGCTCAA TAAATTG

Seq ID NO: 28 Protein sequence:
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MKFLILLLLQ ATASGALPLN SSTSLEKNV LFGERYLEKF YGLEINKLPV TKMKYSGNLM 60
 KEKIQEMQH LGLKVTGQD TSTLEMMHAP RCGVPDVHVF REMPGGPVWR KHYITYRINN 120
 YTPDMNREDV DYAIRKAFQV WSNVTPKFPS KINTGMADIL VVFARGAHGD FHAFDGKGGI 180
 LAHAFPGSG IGGDAHFDDE EFWTTHSGGT NLFLTAVHEI GHSLLGLHSS DPKAVMFPTY 240
 KYVDINTFRL SADDIRGIQS LYGDPKENQR LPNPDNSEPA LCDPNLSFDA VTTVGNKIFF 300
 FKDRFPLKV SERPRTSVNL ISSLWPTLPS GIEAAYEIEA RNQVFLFKD KYWLISNLRP 360
 EPNYPKSIHS FGFPNFVKKI DAAVFNPRFY RTYFFVDNQY WRYDERRQMM DPGYPKLITK 420
 NFQGGIGPKID AVFYSKNKY YFFQGSNQFE YDFLLQRTK TLKSNWFGC

Seq ID NO: 29 DNA sequence
 Nucleic Acid Accession #: NM_006115.1
 Coding sequence: 236..1765

1 11 21 31 41 51
 GCTTCAGGGT ACAGCTCCCC CGCAGCCAGA AGCCGGGCCT GCAGCCCTC AGCACCCTC 60
 CGGGACACCC CACCCGCTTC CCAGGCGTGA CCTGTCAACA GCAACTTCGC GGTGTGGTGA 120
 ACTCTCTGAG GAAAAACCAT TTTGATTATT ACTCTCAGAC GTGCGTGGCA ACAAGTGA 180
 GAGACCTAGA AATCCAAGCG TTGGAGGTCC TGAGGCCAGC CTAAGTCGCT TCAAAATGGA 240
 ACGAAGCGGT TTGTGGGGTT CCATTACAGC CCGATACATC AGCATGAGTG TGTGGACAAG 300
 CCCACGGAGA CTGTGGGAGC TGGCAGGGCA GAGCCTGCTG AAGGATGAGG CCCTGGCCAT 360
 TGCCGCCCTG GAGTTGCTGC CCAGGGAGCT CTCCCGCCA CTCTTCATGG CAGCCTTTGA 420
 CGGGAGACAC AGCCAGACCC TGAAGGCAAT GGTGCAGGCC TGGCCCTTCA CCTGCCTCCC 480
 TCTGGGAGTG CTGATGAAGG GACAACATCT TCACCTGGAG ACCTTCAAAG CTGTGCTTGA 540
 TGGACTTGAT GTGCTCCTTG CCCAGGAGGT TCGCCCCAGG AGGTGGAAC TTCAAGTGCT 600
 GGATTACCG AAGAACTCTC ATCAGGACTT CTGACTGTA TGGTCTGGA ACAGGGCCAG 660
 TCTGTACTCA TTTCCAGAGC CAGAAGCAGC TCAGCCCATG ACAAGAGAGC GAAAAGTAGA 720
 TGGTTTGAGC ACAGAGCCAG AGCAGCCCTT CATTCAGTA GAGGTGCTGC TAGACCTGTT 780
 CCTCAAGGAA GGTGCTGTG ATGAATTGTT CTCCTACCTC ATTGAGAAAG TGAAGCGAAA 840
 GAAAAATGTA CTACGCTGT GCTGTAAGAA GCTGAAGATT TTTGCAATGC CCATGCAGGA 900
 TATCAAGATG ATCCTGAAA TGGTGCAGCT GGACTCTATT GAAGATTGG AAGTGACTTG 960
 TACCTGGAAG CTACCCACTT TGGCGAAATT TTCTCCTTAC CTGGGCCAGA GATTATATCT 1020
 GCGTAGACTC CTCCCTCTCC ACATCCATGC ATCTTCTTAC ATTTCCCCGG AGAAGGAAGA 1080
 GCAGTATATC GCCCAGTTCA CCTCTCAGTT CCTCAGTCTG CAGTGCCTGC AGGCTCTCTA 1140
 TGTGGACTCT TTATTTTCC TTAGAGGCCG CCTGGATCAG TTGCTCAGG ACCTGATGAA 1200
 CCCCTTGAAG ACCCTCTCAA TAACTAAGT CCGGCTTTCG GAAGGGGATG TGATGCATCT 1260
 GTCCAGAGT CCCAGCGTCA GTCAGCTAAG TGTCTGAGT CTAAGTGGGG TCATGCTGAC 1320
 CGATGTAAGT CCCGAGCCCC TCCAAGCTCT GCTGGAGAGA GCCTCTGCCA CCCTCCAGGA 1380
 CCTGGTCTTT GATGAGTGTG GGATCACGGA TGATCAGCTC CTGCCCCCTC TGCCTTCCCT 1440
 GAGCCACTGC TCCAGCTTA CAACCTAAG CTCTACGGG AATTCATCT CCATATCTGC 1500

CTTGCAGAGT CTCTCTGAGC ACCTCATCGG GCTGAGCAAT CTGACCCACG TGCTGTATCC 1560
 TGTCCCCTG GAGAGTTATG AGGACATCCA TGGTACCCTC CACCTGGAGA GGCTTGCCCTA 1620
 TCTGCATGCC AGGCTCAGGG AGTTGCTGTG TGAGTTGGGG CGGCCACGCA TGGTCTGGCT 1680
 TAGTGCCAAAC CCTGTCTCTC ACTGTGGGGA CAGAACCCTC TATGACCCGG AGCCCATCCT 1740
 GTGCCCTGT TTCATGCCTA ACTAGCTGGG TGCACATATC AAATGCTTCA TTCTGCATAC 1800
 TTGGACACTA AAGCCAGGAT GTGCATGCAT CTTGAAGCAA CAAAGCAGCC ACAGTTTTCAG 1860
 ACAAAATGTT AGTGTGAGTG AGGAAAACAT GTTCAGTGAG GAAAAAACAT TCAGACAAAT 1920
 GTTCAGTGAG GAAAAAAGG GGAAGTTGGG GATAGGCAGA TGTGACTTGG AGGAGTTAAT 1980
 GTGATCTTTG GGGAGATACA TCTTATAGAG TTAGAAATAG AATCTGAATT TCTAAAGGGA 2040
 GATTCTGGCT TGGGAAGTAC ATGTAGGAGT TAATCCCTGT GTAGACTGTT GTAAAGAAAC 2100
 TGTGAAAAT AAAGAGAAGC AATGTGAAGC AAAAAAAAAA AAAAAAAA

Seq ID NO: 30 Protein sequence:
 Protein Accession #: NP_006106.1

1 11 21 31 41 51
 | | | | | |
 GCTTCAGGGT ACAGCTCCCC CGCAGCCAGA AGCCGGGCCCT GCAGCGCCTC AGCACCCTC 60
 CGGGACACCC CACCCGCTTC CCAGGCGTGA CCTGTCAACA CCAACTTCGC GGTGTGGTGA 120
 ACTCTCTGAG GAAAAACCAT TTTGATTATT ACTCTCAGAC GTGCGTGGCA ACAAGTGACT 180
 GAGACCTAGA AATCCAAGCG TTGAGGTCC TGAGGCCAGC CTAAGTCGT TCAAAATGGA 240
 ACGAAGGCGT TTGTGGGGTT CCATTTCAGAG CCGATACATC AGCATGAGTG TGTGGACAAG 300
 CCCACGGAGA CTTGTGAGAG TGGCAGGGCA GAGCCTGCTG AAGGATGAGG CCCTGGCCAT 360
 TGGCGCCCTG GAGTTGCTGC CCAGGGAGCT CTTCCGCCCA CTCTTCATGG CAGCCTTTGA 420
 CGGGAGACAC AGCCAGACCC TGAAGGCAAT GGTGCAGGCC TGGCCCTTCA CCTGCCTCCC 480
 TCTGGGAGTG CTGATGAAGG GACAACATCT TCACCTGGAG ACCTTCAAAG CTGTGCTTGA 540
 TGGACTTGAT GTGCTCCTTG CCAGGAGGT TCGCCCCAGG AGGTGGAAC TTCAAGTGCT 600
 GGAATTTACG AAGAACTCTC ATCAGGACTT CTGGACTGTA TGGTCTGGAA ACAGGGCCAG 660
 TCTGTACTCA TTTCAGAGC CAGAAGCAGC TCAGCCCATG ACAGAAGAAGC GAAAAGTAGA 720
 TGGTTTGAGC ACAGAGGCAG AGCAGCCCTT CATTCAGTA GAGGTGCTCG TAGACCTGTT 780
 CCTCAAGGAA GGTGCTGTG ATGAATTGTT CTCCTACCTC ATTGAGAAAG TGAAGCGAAA 840
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 TATCAAGATG ATCTGAAAAA TGGTGCAGCT GGAATCTATT GAAGATTGGA AAGTGACTTG 960
 TACCTGGAGG CTACCCACCT TGGCGAAATT TTCCTCTTAC CTGGGCCAGA TGATTAATCT 1020
 GCGTAGACTC CTCCTCTCCC ACATCCATGC ATCTTCCTAC ATTTCCTCCG AGAAGGAAGA 1080
 GCAGTATATC GCCCAGTTCA CCTCTCAGTT CCTCAGTCTG CAGTGCCTGC AGGCTCTCTA 1140
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 CCCCTTGGAA ACCCTCTCAA TAACTAAGTG CCGGCTTTTC GAAGGGGATG TGATGCATCT 1260
 GTCCCAGAGT CCCAGCGTCA GTCAAGTAAG TGTCTGAGT CTAAGTGGGG TCATGCTGAC 1320
 CGATGTAAGT CCCAGAGCCC TCCAAGCTCT GCTGGAGAGA CCCTCTGCCA CCCTCCAGGA 1380
 CCTGGTCTTT GATGAGTGTG GGATCACGGA TGATCAGCTC CTGCCCCCTC TGCCTTCCCT 1440
 GAGCCACTGC TCCCAGCTTA CAACCTTAAG CTTCTACGGG AATTCCATCT CCATATCTGC 1500
 CTTGCAGAGT CTTCTGAGC ACCTCATCGG GCTGAGCAAT CTGACCCACG TGCTGTATCC 1560
 TGTCCCCTG GAGAGTTATG AGGACATCCA TGGTACCCTC CACCTGGAGA GGCTTGCCCTA 1620
 TCTGCATGCC AGGCTCAGGG AGTTGCTGTG TGAGTTGGGG CGGCCACGCA TGGTCTGGCT 1680
 TAGTGCCAAC CCTGTCTCTC ACTGTGGGGA CAGAACCCTC TATGACCCGG AGCCCATCCT 1740
 GTGCCCCTGT TTCATGCCTA ACTAGCTGGG TGCACATATC AAATGCTTCA TTCTGCATAC 1800
 TTGGACACTA AAGCCAGGAT GTGCATGCAT CTTGAAGCAA CAAAGCAGCC ACAGTTTTCAG 1860
 ACAAAATGTT AGTGTGAGTG AGGAAAACAT GTTCAGTGAG GAAAAAACAT TCAGACAAAT 1920
 GTTCAGTGAG GAAAAAAGG GGAAGTTGGG GATAGGCAGA TGTGACTTGG AGGAGTTAAT 1980
 GTGATCTTTG GGGAGATACA TCTTATAGAG TTAGAAATAG AATCTGAATT TCTAAAGGGA 2040
 GATTCTGGCT TGGGAAGTAC ATGTAGGAGT TAATCCCTGT GTAGACTGTT GTAAAGAAAC 2100
 TGTGAAAAT AAAGAGAAGC AATGTGAAGC AAAAAAAAAA AAAAAAAA

Seq ID NO: 31 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 64-2754

1 11 21 31 41 51
 | | | | | |
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 CCGATGGCCG CCGCTGGGCC CCGGCGCTCC GTGCGCGGAG CCGTCTGCCT GCATCTGCTG 120
 CTGACCCCTG TGATCTTCAG TCGTGATGGT GAAGCCTGCA AAAAGGTGAT ACTTAATGTA 180
 CCTTCTAAAC TAGAGGCAGA CAAAATAATT GGCAGAGTTA ATTTGGAAGA GTGCTTCAGG 240
 TCTGCAGACC TCATCCGGTC AAGTGATCCT GATTTCAGAG TTCTAAATGA TGGGTCACTG 300
 TACACAGCCA GGGCTGTTGC GCTGTCTGAT AAGAAAAGAT CATTTACCAT ATGGCTTTCT 360
 GACAAAAGGA AACAGACACA GAAAGAGGTT ACTGTGCTGC TAGAACATCA GAAGAAGGTA 420
 TCGAAGACAA GACACACTAG AGAAACTGTT CTCAGGCGTG CCAAGAGGAG ATGGGCACCT 480
 ATTCTTGTCT CTATGCAAGA GAATTCCTTG GGCCTTTTCC CATTTGTTCT TCAACAAGTT 540
 GAATCTGATG CAGCACAGAA CTATACTGTC TTCTACTCAA TAAGTGGACG TGGAGTTGAT 600
 AAAGAACCCT TAAATTTGTT TTATATAGAA AGAGACACTG GAAATCTATT TTGCACTCGG 660
 CCTGTGGATC GTGAAGAATA TGATGTTTTT GATTTGATTG CTTATGCTC AACTGCAGAT 720
 GGATATTTCAG CAGATCTGCC CCTCCACTA CCCATCAGGG TAGAGGATGA AAATGACAAC 780
 CACCTGTTT TACAGAGAAG AATTTATAAT TTTGAAGTTT TGGAAAGTAG TAGACCTGGT 840
 ACTACAGTGG GGTGGGTTTG TGCCACAGAC AGAGATGAAC CGGACACAAT GCATACCGCG 900
 CTGAAATACA GCATTTTTCG GCAGACACCA AGGTACCTCG GGCTCTTTC TGTGCATCCC 960
 AGCACAGGCG TAATCACCAC AGTCTCTCAT TATTTGGACA GAGAGGTTGT AGACAAGTAC 1020
 TCAATTGATAA TGAAGATACA AGACATGGAT GGCCAGTTT TGGATTGAT AGGCACATCA 1080
 ACTTGTATCA TAACAGTAAC AGATTCAAAT GATAATGCAC CCACCTTCAG ACAAAATGCT 1140
 TATGAAGCAT TTGTAGAGGA AAATGCATTC AATGTGGAAT TCTTACGAAT ACCTATAGAA 1200
 GATAAGGATT TAATTAACAC TGCCAATTGG AGAGTCAATT TTACCATTTT AAAGGGAAAT 1260
 GAAAATGGAC ATTTCAAAAT CAGACAGAC AAAGAACTA ATGAAGGTTT TCTTCTGTT 1320
 GTAAAGCCAC TGAATTATGA AGAAAACCGT CAAGTGAACC TGGAAATTGG AGTAAACAAAT 1380
 GAAGCGCCAT TTGCTAGAGA TATTTCCAGA GTGACAGCCT TGAACAGAGC CTTGGTTACA 1440
 GTTCATGTGA GGGATCTGGA TGAGGGGCCCT GAATGCACCT CTGCAGCCCA ATATGTGCGG 1500
 ATTAAGAGAA ACTTAGCAGT GGGGTCAAAG ATCAACGGCT ATAAGGCATA TGACCCCGAA 1560

	AATAGAAATG	GCAATGGTTT	AAGGTACAAA	AAATTGCATG	ATCCTAAAGG	TTGGATCACC	1620
	ATTGATGAAA	TTTCAGGGTC	AATCATAACT	TCCAAAATCC	TGGATAGGGA	GGTTGAAACT	1680
	CCCAAAAATG	AGTTGTATAA	TATTACAGTC	CTGGCAATAG	ACAAAGATGA	TAGATCATGT	1740
5	ACTGGAAACAC	TTGCTGTGAA	CATTGAAGAT	GTAATATGATA	ATCCACCAGA	AATACTTCAA	1800
	GAATATGTAG	TCATTTTGCAA	ACCAAAAATG	GGGTATACCG	ACATTTTAGC	TGTTGATCCT	1860
	GATGAACCTG	TCCATGGAGC	TCCATTTTAT	TTCAGTTTGC	CCAATACTTC	TCCAGAAATC	1920
	AGTAGACTGT	GGAGCCTCAC	CAAAGTTAAT	GATACAGCTG	CCCGTCTTTC	ATATCAGAAA	1980
	AATGCTGGAT	TTCAAGAATA	TACCATTCTT	ATTACTGTAA	AAGACAGGGC	CGGCCAAGCT	2040
10	GCAACAAAAT	TATTGAGAGT	TAATCTGTGT	GAATGTACTC	ATCCAACTCA	GTGTCGTGCG	2100
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	ATAGCACTGC	TCTTTTCTGT	ATTGCTAACT	TTAGTATGTG	GAGTTTTTGG	TGCAACTAAA	2220
	GGGAAACGTT	TTCTCTGAAGA	TTTAGCACAG	CAAAACTTAA	TTATATCAAA	CACAGAAGCA	2280
	CCTGGAGACG	ATAGAGTGTG	CTCTGCCAAT	GGATTTATGA	CCCAAACTAC	CAACAACTCT	2340
15	AGCCAAGGTT	TTTGTGGTAC	TATGGGATCA	GGAATGAAAA	ATGGAGGGCA	GSAAACCAT	2400
	GAAATGATGA	AAGGAGGAAA	CCAGACCTTG	GAATCCTGCC	GGGGGGCTGG	GCATCATCAT	2460
	ACCCTGGAGT	CCTGCAGGGG	AGGACACACG	GAGGTGGACA	ACTGCAGATA	CACCTTACTCG	2520
	GAGTGGCACA	GTTTTACTCA	ACCCCGTCTC	GGTGAAAAAT	TGCATCGATG	TAATCAGAAT	2580
	GAAGACCGCA	TGCCATCCCA	AGATTATGTC	CTCACTTATA	ACTATGAGGG	AAGAGGATCT	2640
20	CCAGCTGGTT	CTGCTGGCTG	CTGCAGTGAA	AAGCAGGAAG	AAGATTGGCT	TGACTTTTTA	2700
	AATAATTGTT	AACCCAAAT	TATTACATTA	GCAGAAGCAT	GCACAAAGAG	ATAATGTCAC	2760
	AGTGCTACAA	TTAGGTCCTT	GTCAGACATT	CTGGAGGTTT	CCAAAAATAA	TATTGTAAAG	2820
	TTCAATTTC	ACATGTATGT	ATATGATGAT	TTTTTTCTCA	ATTTTGAATT	ATGCTACTCA	2880
	CCRAATTATA	TTTTTAAAGC	CAGTTGTGTC	TTATCTTTTC	CAAAAAGTGA	AAAATGTTAA	2940
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	ATAAACAAAG	AATATTGAGT	ATCCTATGT	GAAGAAAAGT	TTGGAAAAGA	AACAATGAAG	3180
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	GAATACTCGC	TGCAGCTGGG	GTTCCCTGCT	TTTGGGTAGC	AAGGGTCCAG	AGATGAGGTG	3720
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	CAAGAAAATA	TATTTTTAAA	GCTTTCATTT	TTCCCCCAGT	GAATGATTTA	GAATTTTTTA	5640
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75	AATAGAAATA	CTCAATTATG	TCTTTGTGTT	ATTAATGGGG	AATATTTTGG	ACAATGTTTC	6000
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Seq ID NO: 34 Protein sequence:
 Protein Accession #: NP_077741.1

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 KPLNYEENRQ VNLEIGVNE PFARDIPRV TALNRALVTV HVRDLDEGPE CTPAAQVRI 480
 KENLAVGSKI NGYKAYDPEN RENGRLRYKK LHDPKGWITI DEISGSITS KILDBREVETP 540
 KNELYNITVL AIDKDRSCT GTLAVNIEDV NDNPPILQE YVVICPKMG YTDILAVDPD 600
 BPVHGAPFYF SLPTSPSIS RLWSLTKVND TAARLSYQKN AGFQYTIPI TVKDRAGQAA 660
 TKLLRVNLCE CTHPTQCRAT SRSTGVILGK WAILAILLGI ALLFSVLLTL VCGVFGATKG 720
 KRFPEDLAQQ NLIISNTEAP GDDRVCSANG FMTQTTNNSS QGFCGTMGSG MKNGGQETIE 780
 MMKGNGQTLN SLCRGGHHT LDSCRGGHTE VDNCRITYSE WHSFTQPRLG EESIRGHTG

Seq ID NO: 35 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 146-1273.

	1	11	21	31	41	51	
5	GGGAGTGGGC	GTGGCGGTGC	TGCCCAGGTG	AGCCACCGCT	GCTTCTGCCC	AGACACGGTC	60
	GCCTCCACAT	CCAGGTCTTT	GTGCTCCTCG	CTTGCTCTGT	CCTTTTCAC	GCATTTTCCA	120
	GGATAACTGT	GACTCCAGGC	CCGCAATGGA	TGCCCTGCAA	CTAGCAAATT	CGGCTTTTGC	180
	CGTTGATCTG	TTCAAACAAC	TATGTGAAAA	GGAGCCACTG	GGCAATGTCC	TCTTCTCTCC	240
	AATCTGTCTC	TCCACCTCTC	TGTCACCTTG	TCAAGTGGGT	GCTAAAGGTG	ACACTGCAAA	300
10	TGAAATTGGA	CAGGTTCTTC	ATTTTGAAAA	TGTCAAAGAT	ATACCCTTTG	GATTTCAAAC	360
	AGTAACATCG	GATGTAACA	AACTTAGTTC	CTTTTACTCA	CTGAAACTAA	TCAAGCGGCT	420
	CTACGTAGAC	AAATCTCTGA	ATCTTTCTAC	AGAGTTCATC	AGCTCTACGA	AGAGACCCTA	480
	TGCAAGGAA	TTGGAACATG	TTGACTTCAA	AGATAAATG	GAAAGAAACGA	AAGGTCAGAT	540
	CAACAACCTCA	ATTAAGGATC	TCACAGATGG	CCACTTTGAG	AACATTTTAG	CTGACAACAG	600
15	TGTGAACGAC	CAGACCAAAA	TCCTTGTGGT	TAATGCTGCC	TACTTTGTG	GCAAGTGGAT	660
	GAAGAAATTT	CCTGAATCAG	AAACAAAAGA	ATGTCCTTTC	AGACTCAACA	AGACAGACAC	720
	CAAAACAGTG	CAGATGATGA	ACATGGAGGC	CACGTTCTGT	ATGGGAAACA	TTGACAGTAT	780
	CAATTGTAA	ATCATAGAGC	TTCTTTTCA	AAATAAGCAT	CTCAGCATGT	TCATCCTACT	840
	ACCCAAGGAT	GTGGAGGATG	AGTCCACAGG	CTTGAGAGA	ATTGAAAAAC	AACTCAACTC	900
20	AGAGTCACTG	TCCAGTGGGA	CTAATCCCAG	CACCATGGCC	AATGCCAAGG	TCAAACCTCTC	960
	CATTCCAAAA	TTTAAAGTGG	AAAAGATGAT	TGATCCCAAG	GCTTGTCTGG	AAAACTTAGG	1020
	GCTGAAACAT	ATCTTCAGTG	AAGACACATC	TGATTTCTCT	GGAATGTCTG	AGACCAAGGG	1080
	AGTGGCCCTA	TCAAATGTTA	TCCACAAAGT	GTGCTTAGAA	ATAACTGAAG	ATGGTGGGGA	1140
	TTCCATAGAG	GTGCCAGGAG	CACGGATCCT	GCAGCACAA	GATGAATTGA	ATGCTGACCA	1200
25	TCCCTTTATT	TACATCATCA	GGCACAACAA	AACTCGAAAC	ATCATTTTCT	TTGGCAAATT	1260
	CTGTTCTCCT	TAAGTGGCAT	AGCCCATGTT	AAGTCTCTCC	TGACTTTTCT	GTGGATGCCG	1320
	ATTTCTGTAA	ACTCTGCATC	CAGAGATTCA	TTTTCTAGAT	ACAATAAATT	GCTAATGTTG	1380
	CTGGATCAGG	AAGCGCCAG	TACTTGTCTG	ATGTAGCCTT	CACACAGATA	GACCTTTTTT	1440
	TTTTTCCAAT	TCTATCTTTT	GTTTCTCTTT	TTCCCATAG	ACAATGACAT	ACGCTTTTAA	1500
30	TGAAAGGAA	TCACGTTAGA	GGAAAAATAT	TTATTCATTA	TTTGTCAAAT	TGTCGGGGT	1560
	AGTTGGCAGA	AATACAGTCT	TCCACAAAGA	AAATTCCTAT	AAGGAAGATT	TGGAAGCTCT	1620
	TCTTCCCAGC	ACTATGCTTT	CCTTCTTTGG	GATAGAGAAT	GTTCAGACA	TTCTCGCTTC	1680
	CCTGAAAGAC	TGAAGAAAGT	GTAGTGCATG	GGACCCACGA	AACTGCCCTG	GCTCCAGTGA	1740
	AACTTGGGCA	CATGCTCAGG	CTACTATAGG	TCCAGAAATC	CTTATGTTAA	GCCCTGGCAG	1800
35	GCAGGTGTTT	ATTAATAATC	TGAATTTTGG	GGATTTTCAA	AAGATAATAT	TTTACATACA	1860
	CTGTATGTTA	TAGAACTTCA	TGGATCAGAT	CTGGGGCAGC	AACCTATAAA	TCAACACCTT	1920
	AATATGCTGC	AACAAAATGT	AGAATATTCA	GACAAAATGG	ATACATAAAG	ACTAAGTAGC	1980
	CCATAAGGGG	TCAAAATTGG	CTGCCAAATG	CGTATGCCAC	CAACTTACAA	AAACACTTCG	2040
	TTCCGAGAGC	TTTTCAGATT	GTGGAATGTT	GGATAAGGAA	TTATAGACCT	CTAGTAGCTG	2100
40	AAATGCAAGA	CCCCAAGAGG	AAGTTCAGAT	CTTAATATAA	ATTCACCTTC	ATTTTGTGATA	2160
	GCTGTCCCAT	CTGTCATGTT	GGTTGGCATT	AGACTGGTGG	CAGGGGCTTC	TAGCTGACTC	2220
	GCACAGGGAT	TCTCAACAATA	GCCGATATCA	GAATTTGTGT	TGAAGGAACT	TGTCTCTTCA	2280
	TCTAATATGA	TAGCGGGAAA	AGGAGAGGAA	ACTACTGCCT	TTAGAAAATA	TAAGTAAAGT	2340
	GATTAAAGTG	CTACGTTTCA	CTTGACACAT	AGTTTTTCAG	TCTATGGGTT	TAGTTACTTT	2400
45	AGATTGGCAAG	CATGTAACCT	ATATTAAATG	TAATTTGTAA	AGTTGGGTGG	ATAAGCTATC	2460
	CCTGTTGCCG	GTTTCATGCT	TACTTCTCTA	TAAAAAATAT	ATATTATACCA	AAAAATTTTG	2520
	TGACATTCTCT	TCTCCCATGT	CTTCTCTGAC	ATGCATTGTA	AATAGGTTCT	TCTTGTCTCG	2580
	AGATTCAATA	TTGAATTTCT	CCTATGCTAT	TGACAATAAA	ATATTATTGA	ACTACC	

Seq ID NO: 36 Protein sequence:
Protein Accession #: NP_002630.1

	1	11	21	31	41	51	
55	MDALQLANSA	FAVDLFKQLC	EKEPLGNVLF	SPICLSTSL	LAQVGAKGDT	ANEIGQVLHF	60
	ENVKDIPFGF	QTVTSDVNKL	SSFYSLKLIK	RLYVDKSLNL	STEFISSTKR	PYAKELETVD	120
	FKDLLEETKG	QINNSIKDLT	DGHFENILAD	NSVNDQTKIL	VVNAAFYVVGK	WMKKFPESET	180
	KECPFRLNKT	DTKPVQMMNM	EATFCMGNID	SINCKIIELP	PQNKHLMSFI	LLPKDVEDES	240
	TGLEKIEKQL	NSESLSQWTN	PSTMANAKVK	LSIPKFKVEK	MIDPKACLEN	LGLKHIFSED	300
60	TSDFSGMSET	KGVALSNIH	KVCLIEITDG	GDSIEVPGAR	ILQHKDELNA	DHPFIYIIRH	360
	NKTRNIIFFG	KFCSP					

Seq ID NO: 37 DNA sequence
Nucleic Acid Accession #: NM_0168583
Coding sequence: 72-842

	1	11	21	31	41	51	
70	GGAGTGGGGG	AGAGAGAGGA	GACCAGGACA	GCTGCTGAGA	CCTCTAAGAA	GTCCAGATAC	60
	TAAGAGCAAA	GATGTTTCAA	ACTGGGGGCC	TCAATTGTCTT	CTACGGGCTG	TTAGCCCAGA	120
	CCATGGCCCA	GTTTGGAGGC	CTGCCCGTGC	CCCTGGACCA	GACCTGCCCC	TTGAATGTGA	180
	ATCCAGCCCT	GCCCTTGAGT	CCCACAGGTC	TTGCAGGAAG	CTTGACAAAT	GCCCTCAGCA	240
	ATGGCCTGCT	GTCGGGGGC	CTGTTGGGCA	TTCTGGAAAA	CCTTCCGCTC	CTGGACATCC	300
75	TGAAGCCTGG	AGGAGGTACT	TCTGGTGGCC	TCCTTGGGGG	ACTGCTTGGG	AAAGTGACGT	360
	CAGTGATTCC	TGGCCTGAAC	AACATCATTG	ACATAAAGGT	CAGTACCCCT	CAGCTGTGGG	420
	AACTTGGCCT	TGTGCAGAGC	CCTGATGGCC	ACCGTCTCTA	TGTCAACCATC	CCTCTCGGCA	480
	TAAAGCTCCA	AGTGAATACG	CCCCTGGTCG	GTGCAAGTCT	GTTGAGGCTG	GCTGTGAAGC	540
	TGGACATCAC	TGCAGAAATC	TTAGCTGTGA	GAGATAAGCA	GGAGAGGATC	CACCTGGTCC	600
80	TTGGTGAATG	CACCCATTCC	CCTGGAAGCC	TGCAAAATTC	TCTGCTTGAT	GGACTTGGCC	660
	CCCTCCCAT	TCAAGGTTCT	CTGGACAGCC	TCACAGGGAT	CTTGAATAAA	GTCCTGCGCTG	720
	AGTTGGTTCA	GGGCAACGTG	TGCCCTCTGG	TCAATGAGGT	TCTCAGAGGC	TTGGACATCA	780
	CCCTGGTGCA	TGACATTGTT	AACATGCTGA	TCCACGGACT	ACAGTTTGTG	ATCAAGGTCT	840
	AAGCCTTCCA	GGAAGGGGCT	GGCCTCTGCT	GAGCTGCTTC	CCAGTGGCTCA	CAGATGGCTG	900
	GCCCATGTGC	TGGAAGATGA	CACAGTTGCC	TTCTCTCCGA	GGAACCTGCC	CCCTCTCTTT	960
85	TCCACCCAGG	CGTGTGTAAC	ATCCCATGTG	CCTCACCTAA	TAAATGGGCT	CTTCTTCTGC	1020
	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA				

Seq ID NO: 38 Protein sequence:
Protein Accession #: NP_057667

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5      1      11      21      31      41      51
      |      |      |      |      |      |
MFQTGGILVF YGLLAQTMAG FGGLPVPLDQ TLPLNVNPFAL PLSPTGLAGS LTNALSNGLL 60
SGGLGLILEN LPLLDILKPG GGTSGGLLGG LLGKVTSVIP GLNNIIDIKV TDPQLLELGL 120
VQSPDGHRLY VTITPLGIKLQ VNTPLVGASL LRLAVKLDIT AEILAVRDKQ ERIHLVLGDC 180
THSPGSLQIS LLDGLGPIPI QGLLDSLTI LNKVLPELVQ GNVCPVNEV LRGLDITLVH 240
10    DIVNMLIHGL QFVIKV

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Seq ID NO: 39 DNA sequence
Nucleic Acid Accession #: NM_004363.1
Coding sequence: 115-2223

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15      1      11      21      31      41      51
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CTCAGGGCAG AGGGAGGAAG GACAGCAGAC CAGACAGTCA CAGCAGCCTT GACAAAACGT 60
TCCTGGAATC CAAGCTCTTC TCCACAGAGG AGGACAGAGC AGACAGCAGA GACCATGGAG 120
TCTCCCTCGG CCCCTCCCCA CAGATGGTGC ATCCCCTGGC AGAGGCTCCT GCTCACAGCC 180
TCACTTCTAA CCTTCTGGAA CCCGCCACC ACTGCCAAGC TCACTATTGA ATCCACGCCG 240
TTCAATGTCT CAGAGGGGAA GGAGGTGCTT CTACTTGTC ACAAATCTGC CCAGCATCTT 300
TTTGGCTACA GCTGGTACAA AGGTGAAAGA GTGGATGGCA ACCGTCAAAT TATAGGATAT 360
25    GTAATAGGAA CTCACAAGC TACCCAGGG CCCGCATACA GTGGTCGAGA GATAATATAC 420
CCCAATGCAT CCCTGCTGAT CCAGAATATC ATCCAGAATG ACACAGGATT CTACACCCTA 480
CACGTATATA AGTCAGATCT TGTGAATGAA GAAGCAACTG GCCAGTTCCG GGTATACCCG 540
GAGCTGCCCA AGCCTCCATC CTCAGCAAC AACTCCAAAC CCGTGGAGGA CAAGGATGCT 600
GTGGCCTTCA CCTGTGAACC TGAGACTCAG GACGCAACCT ACCTGTGGTG GGTAAACAAT 660
30    CAGAGCCTCC CGTCTAGTCC CAGGCTGCAG CTGTCCAATG GCAACAGGAC CCTCACTCTA 720
TTCATATGTC CAAGAAATGA CACAGCAAGC TACAAATGTG AAACCCAGAA CCCAGTGAGT 780
GCCAGGCGCA GTGATTCAGT CATCCTGAAT GTCTCTATG GCCCGGATGC CCCCAACATT 840
TCCCCTCTAA ACACATCTTA CAGATCAGGG GAAATCTGA ACCTCTCCTG CCACGCAGCC 900
TCTAACCCAC CTGCACAGTA CTCTTGGTTT GTCAATGGGA CTTTCCAGCA ATCCACCCAA 960
35    GAGCTCTTTA TCCCAACAT CACTGTGAAT AATAGTGGAT CCTATACGTG CCAAGCCCAT 1020
AACTCAGACA CTGGCCTCAA TAGGACCACA GTACGACGTA TCACAGTCTA TGCAGAGCCA 1080
CCCAACACCT TCATCACCAG CAACAACCTC AACCCTGGG AGGATGAGGA TGCTGTAGCC 1140
TTAACCTGTG AACCTGAGAT TCAGAACACA ACCTACCTGT GGTGGGTAAA TAATCAGAGC 1200
40    CTCGCCGTCA GTCCCGAGCT GCAGCTGTCC AATGACAACA GGACCTCAC TCTACTCAGT 1260
GTCAACAGGA ATGATGTAGG ACCCTATGAG TGTGGAATCC AGAACGAATT AAGTGTGAGT 1320
CACAGCGACC CAGTCATCCT GAATGTCTCT TATGGCCAG ACGACCCAC CATTTCCCCC 1380
TCATACACCT ATTACCGTCC AGGGGTGAAC CTCAGCCTCT CCTGCCATGC AGCCTCTAAC 1440
CCACTGACAC AGTATTCTTG GCTGATTGAT GGGAAACATCC AGCAACACAC ACAAGAGCTC 1500
45    TTTATCTCCA ACATCAGTGA GAAGAACAGC GGACTCTATA CCTGCCAGGC CAATAACTCA 1560
GCCAGTGGCC ACAGCAGGAC TACAGTCAAG ACAATCACAG TCTGTGCGGA GCTGCCCAAG 1620
CCCTCCATCT CCAGCAACAA CTCCAACCC GTGGAGGACA AGGATGCTGT GGCCTTCACC 1680
TGTGAACCTG AGGCTCAGAA CACAACCTAC CTGTGGTGGG TAAATGGTCA GAGCCTCCCA 1740
50    GTCAGTCCCA GGCTGCAGCT GTCCAATGGC AACAGGACCC TCACTCTATT CAATGTCA 1800
AGAAATGACG CAAGAGCCTA TGTATGTGGA ATCCAGAACT CAGTGAGTGC AAACCGCAGT 1860
GACCCAGTCA CCCTGGATGT CCTCTATGGG CCGGACACCC CCATCATTTT CCCCCAGAC 1920
TCGTCTTACC TTTGGGGAGC GAACCTCAAC CTCTCCTGCC ACTCGGCCTC TAACCCATCC 1980
CCGAGTATT CTGGCGTAT CAATGGGATA CCGCAGCAAC ACACACAAGT TCTCTTTATC 2040
55    GCCAAAATCA CGTCAAAATA TAACGGGACC TATGCCTGTT TTGTCTCTAA CTTGGCTACT 2100
GGCCGCAATA ATTCCATAGT CAAGAGCATC ACAGTCTCTG CATCTGGAAC TTCTCTCTGT 2160
CTCTCAGCTG GGGCCACTGT CGGCATCATG ATTGGAGTGC TGGTTGGGGT TGCTCTGATA 2220
TAGCAGCCCT GGTGTAGTTT CTTCAATTTA GGAAGACTGA CAGTTGTTT GCTTCTTCT 2280
TAAAGCATTT GCAACAGCTA CAGTCTAAA TTGCTTCTTT ACCAAGGATA TTTACAGAAA 2340
60    AGACTCTGAC CAGAGATCGA GACCATCCTA GCCAACATCG TGAACCCCA TCTCTACTAA 2400
AAATACAAAA ATGAGCTGGC CTGTGGTGGC GCACCTGTA GTCCAGTTA CTCGGGAGGC 2460
TGAGGCAGGA GAATCGCTTG AACCCGGGAG GTGGAGATG CAGTGAGCCC AGATCGCACC 2520
ACTGCATCC AGTCTGGCAA CAGAGCAAGA CTCATCTCA AAAAGAAAAG AAAAGAAGAC 2580
TCTGACCTGT ACTCTGAAT ACAAGTTTCT GATACCCTG CACTGCTGTA GAATTTCCAA 2640
65    AACTTTAATG AACTAATGTA CAGCTTCATG AAACCTGTCA CCAAGATCAA GCAGAGAAAA 2700
TAATTAATTT CATGGGACTA AATGAACATA TGAGGATTGC TGATTCTTTA AATGTCTTGT 2760
TTCACAGATT TCAGGAAACT TTTTCTCTT TAAGCTATCC ACTCTACAG CAATTGATA 2820
AAATATACTT TTGTGAACAA AAATTGAGAC ATTTACATTT TCTCCCTATG TGGTCGCTCC 2880
AGACTTGGGA AACTATTCTA GAATATTTAT ATTGTATGGT AATATAGTTA TTGCACAAGT 2940
70    TCAATAAAAA TCTGCTCTTT GTATAACAGA AAAA

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Seq ID NO: 40 Protein sequence:
Protein Accession #: NP_004354.1

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75      1      11      21      31      41      51
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MESPSAPPHR WCIWQRLLL TASLLTFWNP PTTAKLTIES TPFNVAEGKE VLLLHVNLPQ 60
HLFGYSWKYG ERVDGNRQII GYVIGTQAT PGPAYSGREI IYPNASLLIQ NIIQNDTGFI 120
TLHVIKSDLV NEEATGQFRV YPELPKPSIS SNNKPVEDK DAVAFCTCEPE TODATYLVWV 180
NNQSLFVSFR LQLSNGNRTL TLFNVTRNDT ASYKCETQNP VSARRSDSVI LNVLYGPDAP 240
TISPLNTSYR SGENLNLSCH AASNPPAQYS WFNVTGTFQS TQELFIPNIT VNNSGSYTCQ 300
AHNSDTGLNR TTVTTITVYA EPPKPFITSN NSNPVEDEDA VALTCEPEIQ NTTYLWVNN 360
70    QSLPVSPRLQ LSNDRNTLTL LSVTRNDVGP YECGIQNELS VDHSDFVILN VLYGDDPTI 420
SPSYTYRFPG VNLSLSCHAA SNPPAQYSWL IDGNIQQHTQ ELFISNITEK NSGLYTCQAN 480
NSASGHSRTT VKTITVSABL PKPSISSNNS KPVEDKDAYA FTCEPEAQNT TYLWVNGQS 540
LPVSPRLQLS NGRNRTLTLFN VTRNDARAYV CGIQNSVSAN RSDPVTLDVL YGPDPTIISP 600
85    PDSSYLSGAN LNLSCSASN PSPQYSWRIN GIPQOHTQVL FIAKITPNNN GTYACFVSNL 660
ATGRNNSIVK SITVSASGTS PGLSAGATVG IMIGVLVGVA LI

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Seq ID NO: 41 DNA sequence
Nucleic Acid Accession #: NM_006952.1
Coding sequence: 11-793

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1      11      21      31      41      51
|      |      |      |      |      |
AATCCCGACA ATGGCGAAAG ACAACTCAAC TGTTCTGTTGC TTCCAGGGCC TGCTGATTTT 60
TGGAAATGTG ATTATTGGTT GTTGCAGCAT TGCCCTGACT GCGGAGTGCA TCTTCTTTGT 120
ATCTGACCAA CACAGCCTCT ACCCACTGCT TGAAGCCACC GACAACGATG ACATCTATGG 180
GGCTGCCTGG ATCGGCATAT TTGTGGGCAT CTGCCTCTTC TGCCTGTCTG TTCTAGGCAT 240
TGTAGGCATC ATGAAGTCCA GCAGGAAAT TCTTCTGGCG TATTTTCATC TGATGTTTAT 300
AGTATATGCC TTTGAAGTGG CATCTGTAT CACAGCAGCA ACACAACGAG ACTTTTTCAC 360
ACCCAACCTC TTCCTGAAGC AGATGCTAGA GAGGTACCAA AACCAACGCC CTCCAACAA 420
TGATGACGAG TGGAAAAACA ATGGAGTCAC CAAACCTGG GACAGGCTCA TGCTCCAGGA 480
CAATTGCTGT GCGCTAAATG GTCCATCAGA CTGGCAAAAA TACACATCTG CCTTCCGGAC 540
TGAGAAATAT GATGCTGACT ATCCCTGGCC TCGTCAATGC TGTGTTATGA ACAATCTTAA 600
AGAACCTCTC AACCTGGAGG CTTGTAAACT AGGCGTGCCT GGTTTTATC ACAATCAGGG 660
CTGCTATGAA CTGATCTCTG GTCCAATGAA CCGACACGCC TGGGGGGTTG CCTGGTTTGG 720
ATTTGCCATT CTCTGCTGGA CTTTITGGGT TCTCCTGGGT ACCATGTTCT ACTGGAGCAG 780
AATTGAATAT TAAGAA

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Seq ID NO: 42 Protein sequence:
Protein Accession #: NP_008883.1

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1      11      21      31      41      51
|      |      |      |      |      |
MAKDNSTVRC FQGLLIFGNV IIGCCGIALT AECIFFVSDQ HSLYPLLEAT DNDDIYGAAW 60
IGIFVGLICLF CLSLVGIWGI MKSSRKILLA YFILMFIVYA FEVASCITAA TQRDFFTPNL 120
FLKQMLERYQ NNSPPNDDQ WKNNGVTKTW DRLMLQDNCC GVNGPSDWQK YTSAFRTENN 180
DADYFWRQC CVMNNLKBP NLEACKLGVP GFYHNGGCYE LISGPMNRHA WGVAWFGFAI 240
LCWTFWVLLG TMFWWSRIEY

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Seq ID NO: 43 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 83-2605

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1      11      21      31      41      51
|      |      |      |      |      |
GCCCGACAGA TCTGCGCGTA TCCTGGAGCC GGCCCAAGTTG TGAAGTAGGA GAGCTTTGGG 60
ACCTCTGTCC CAAGCAAGAG AGATGAATGG AGAGTATAGA GGCAGAGGAT TTGGACGAGG 120
AAGATTTCAA AGCTTGGAAA GGGGAAGAGG TGGTGGGAAC TTCTCAGGAA AATGGAGAGA 180
AAGAGAACAC AGACCTGATC TGAGTAAATC CACAGGAAAA CGTACTTCTG AACAAACCCC 240
ACAGTTTTTG CTTTCAACAA AGACCCACA GTCATGCAG TCAACATTGG ATCGATTCA 300
ACCATATAAA GGTGGAAGC TTTATTTCTC TGAAGTTTAC AGCGATAGCT CTCCTTTGAT 360
TGAGAAGATT CAAGCATTGG AAAAATTTT CACAGGCGAT ATTGATTGT ATGACAAGGA 420
TGAAATAGAA AGAAAGGGAA GTATTTTGGT AGATTTTAAA GAACTGACAG AAGGTGGTGA 480
AGTAACTAAC TTGATACCA ATATAGCAAC TGAACATAAG GATGCACCTG AGAAAACTT 540
GGCTTGCATG GGTTTGGCAA TACATCAGGT GTTAACTAAG GACCTTGAAA GGCATGCAGC 600
TGAGTTACAA GCCCAGGAAG GATTGTCTAA TGATGGAGAA ACAATGGTAA ATGTGCCACA 660
TATTCTATCA AGGGTGATCA ACTATGAGCC TTTGACACAG CTCAAGAAATG TCAGAGCAAA 720
TTACTATGGA AAATACATTG CTCTAAGAGG GACAGTGGTT CGTGTCACTA ATATAAAGCC 780
TCTTTGCACC AAGATGGCTT TTCTTTGTGC TGCATGTGGA GAAATTCAGA GCTTTCCTCT 840
TCCAGATGGA AAATACAGTC TTCCACAAA GTGTCTGTG CCTGTGTGTC GAGGCAGGTC 900
ATTTACTGCT CTCGCGAGCT CTCCTCTCAC AGTTACGATG GACTGGCAGT CAATCAAAAT 960
CCAGGAATTG ATGCTGATG ATCAGAGAGA AGCAGGTGCG ATTCACAGAA CAATAGAAATG 1020
TGAGCTTGTT CATGATCTTG TGGATAGCTG TGTCCCGGGA GACACAGTGA CTATTACTGG 1080
AATTGTCAAA GTCTCAATG CCGAAGAAGG TTCTCGAAAT AAGAATGACA AGTGTATGTT 1140
CCTTTTGTAT ATTGAAGCAA ATCTATTAG TAATAGCAAA GGACAGAAAA CAAAGAGTTC 1200
TGAGGATGGG TGTAAGCATG GAATGTTGAT GGAGTTCTCA CTTAAAGACC TTTATGCCAT 1260
CCAAGAGATT CAAGCTGAAG AAAACCTGTT TAAACTCATT GTCAACTCGC TTTGCCCTGT 1320
CATTTTGGT CATGAACCTG TTAAGCAGG TTTGGCATT GCACCTCTTG GAGGAAGCCA 1380
GAAATACGCA GATGACAAAA ACAGAATTCC AATTGCGGGA GACCCCCACA TCCTTGTGT 1440
TGGAGATCCA GGCCTAGGAA AAAGTCAAA GCTACAGGCA GCGTGCAATG TTGCCCCACG 1500
TGGCGTGTAT GTTTGTGGTA ACACCACGAC CACCTCTGGT CTGACGGTAA CTCCTTCAAA 1560
AGATAGTTCC TCTGGAGATT TTGCTTTGGA AGCTGGTGCC CTGGTACTTG GTGATCAAGG 1620
TATTTGTGGA ATCGATGAAT TTGATAAGAT GGGGAATCAA CATCAAGCCT TGTGGGAAGC 1680
CATGGAGCAG CAAAGTATTA GTCTTGCTAA GGCTGGTGTG GTTTGTAGCC TTCTGCAAG 1740
AACTTCCATT ATTGCTGCTG CAAATCCAGT TGGAGGACAT TACAATAAAG CCAAACAGT 1800
TTCTGAGAA TTAATAATGG GGAGTGCACT ACTATCCAGA TTTGATTGAG TCTTTATCCT 1860
GTTAGATACT CCAATGAGC ATCATGATCA CTTACTCTCT GAACATGTGA TTGCAATAAG 1920
AGCTGGAAG CAGAGAACCA TTAGCAGTGC CACAGTAGCT CGTATGAATA GTCAAGATTC 1980
AAATACTTCC GTACTTGAAG TAGTTTCTGA GAAGCCATTA TCAGAAAGAC TAAAGTGGT 2040
TCCTGGAGAA ACAATAGATC CCATTCCCCA CCAGCTATTG AGAAAGTACA TTGGCTATGC 2100
TCGGCAGTAT GTGTACCCAA GGCTATCCAC AGAAGCTGCT CGAGTTCTTC AAGATTTTAA 2160
CCTTGAGCTC CGGAACAGGA GCCAGAGGTT AAATAGCTCA CCAATCACTA CCAGGCAGCT 2220
GGAATCTTTG ATTCGTCTGA CAGAGGCACG AGCAAGGTTG GAATTGAGAG AGGAAGCAAC 2280
CAAAGAAGAC GCTGAGGATA TAGTGGAATAT TATGAAATAT AGCATGCTAG GAACCTTACT 2340
TGATGAATTT GGGAACTTAG ATTTTGAGCG ATCCAGCAT GGTTCCTGAA TGAGCAACAG 2400
GTCAACAGCG AAAAGATTTA TTTCTGCTCT CAACAACGTT GCTGAAAGAA CTTATAATAA 2460
TATATTTCAA TTTTCATCAAC TTCGGCAGAT TGCCAAAGAA CTAACATTTC AGGTTGCTGA 2520
TTTGAAAAAT TTTATTTGAT CACTAAATGA CCAGGGTTAC CTCTTGAAAA AAGGCCCAAA 2580
AGTTTACCAG CTTCAAACTA TGTAAAAGGA CTTCAACCAAG TTAGGGCTCT CTGGGTTTAT 2640
TGCGATTAA GTGCATCTCA GTGAAGATAT GCGTGACGCG ACAGACAGAC AGACACACAC 2700
ACACACACAC ACACACACAC ACACACACAC ACACACAGTC AAATACTGTT CTCTGAAAAA 2760
TGATGTCCCA AAAGTATTAT AATAGGAAAA AAGCATTAAA TATAATAAAC TAATTTAAGA 2820

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AGTGATAAAG TCTCCAGATG CAGTAGCTCA CACTGTAATC ACAGTGACTC AGGAGGCTGA 2880
GGTGAGAGGA TTCCTTGAGG CCAGGGTTCC AGACCAACCT TGGGCAACAT AGCAAGACCC 2940
CATTTCCTTAA AAAAAAATAA AAAAAAATTA AACTTAGCTG GGTATGGTGG CACATGCCTA 3000
TAGTCTCAGC TACTTGTGAG GCTGAGGCAG GAGGATTCTT TGAGCCGAGG AGTTTGAGGT 3060
TACAGTGAGC CACAATCACA CCAATCACTG CACTCCAGCC TGGGCAATAA AGTAACTCTT 3120
GACTCAAAAA AATAAAAAAA ATTGTAGTGG TAGCCATGTG TTAATTGTTA AATAAATCTT 3180
CCAAAGGGCT AAAAGTAAAT TACTTATAAA TTTTATTAG TTTGATTTT GACCTGCCTT 3240
TTATATGTAT GAATATTTC A TAGTTTTC TATCAGATGT AGGCATACAG ACAAATACAT 3300
AAACCAATGA ATATATTACA TATTCTGTGT TCCAATAAAA CTTTATTAT GGACACTAAA 3360
ATTTGAATTT CATAAAATTT TCCCATGTCA AGAATACAAA ATACTTGAGT TTTGTTTTTA 3420
GCTATTTAAT AATAGGCTTC ATTTATTCCA CAGGCTGTAG TTTGTAGTCT TGCTTGAAAC 3480
AATAGAAACA GACTGATTAA GCAGGAGAAG TTTTGTGAAA GAATTTTGT TGGCTCACGG 3540
AATTATTAGA AGGCAGGTGA ACCAGGAGGG TAAGCTTCCA GCAGCAATTT GTAAAAACCAT 3600
GCCTTAGAAT TGGACTAAGG AAGAAGCTGC TGACACTCCA CTGCCACACA GGGCACTGGA 3660
AGAAAGTGCT GCTGCCTCCC TGCCCCACCT TTGCCACTTC TGCAGCAGGA ATAGGCTAGAA 3720
GAATGCCCCC ACCCGCACCG GAACAGCAAC AAAAGGATTC TGCATGAGAT CCCTCCCTAA 3780
ATTGCTGAAT TCAAAAAAGA AGTTGCATAC AAAGACATCT GATTGAAAAA GGGTATGTTA 3840
TATGCCCTTT TCATAGGCTG CTAGGGAGTT TTCCTGGTTC TACTTTCAGG TGGTGGGATC 3900
AATAAGACCA GAATTTCTCA TATGTTGTGA GAGGATTCAA ATGTTACAGG GTTGCCAGCC 3960
AACTATCAA TCACTATATA ATCCAACAAA CACTTTGTAA CATACAAGAA CTCAGGAAAT 4020
GTGAACCATT TGTGGAGAA CTACTAAAT ACGGCTTCCC GCAACGAAAG ATGAATGGAA 4080
AATGTAAATA AAAAGAACTG GCAGTGTATA TCAGATGTTT AACTATAGGA CCAGAACTAA 4140
GATGTGGAGA CTATTGCCAT AGACACCAAT GTAAATTTT AAGTGAGGAA GGAATAATCA 4200
GGAATCAAAA GGGGCCAGGT GCAGTGGCTC ACATCTATA TCCAGAGCT TTGGGAGTTC 4260
GAGGCAGGAG GATCACTTGA AGCCAGTTT GAGACCAGCC TATGCAACAC ATTGAGACCC 4320
TATCTCTACA AAAAATAGAT TAGCTGGGCA CGGTGGTGCA TGCCTATTGT CCTACCTACT 4380
GTGGAGGCTG AAGTAGGAAA TCATTGAGC CCGAGAGTTT GAGGTTACAG TGAGCTATGA 4440
TTATACCACT GCATCCAGC CTGGGCAAGA GAGCAAGACC TTGCTCTT

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Seq ID NO: 44 Protein sequence:
Protein Accession #: CAB55276.2

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1      11      21      31      41      51
|      |      |      |      |      |
MNGEYRGRGF GRGRFQSWKR GRGGGNFSGK WREREHRPDL SKTTGKRTSE QTPQFLLSTK 60
TPQSMQSTLD RFIPYKWKVL YFSEVYSDSS PLIEKIQAFE KFFTRHIDLY DKDEIERKGS 120
ILVDFKELTE GGEVTNLTPD IATELRDAPE KTLACMGLAI HQVLTKDLER HAELQAEQEG 180
LSNDGETMVN VPHIHARVYN YEPLTQLKNV RANYYGKYIA LRGTVVVRVSN IKPLCTKMAF 240
LCAACGEIQS FPLPDGKYSL PTKCPVPVCR GRSFTALRSS PLVTMDWQS IKIQELMSDD 300
QREAGRIPRT IECCLVHDLV DSCVPGDTVT ITGIVKVSNA EEGSRNKNDK CMFLLYIEAN 360
SISNSKGQKT KSSBDGCKHG MLMEFSLKDL YAIQEIQAE NLFLKLVNSL CPVIFGHELV 420
KAGLALALFG GSQKYADDKN RPIRGDPHI LVVGDPLGLK SQMLQAACNV APRGVYVCGN 480
TTTTSGLTVT LSKDSSSDGF ALEAGALVLG DQIGICIDEF DKMGNHQHAL LEAMEQQSIS 540
LAKAGVVCSL PARTSIIAAA NPVGHHYNKA KTVSENLKMG SALLSRFDLV FILDTPNEH 600
HDHLLSEHVI AIRAGKQRTI SSATVARMNS QDSNTSVLEV VSEKPLSERL KVVPGETIDP 660
IPHQLLRKYI GYARQYVYPR LSTEARVLQ DFYLELRKQS QRLNSSPIIT RQLESILRLT 720
BARARLELRE BATKEDABDI VEIMKYSMLG TYSDEFGLND FERSQHSGSM SNRSTAKRFI 780
SALNNVAERT YNNIFQFQL RQIAKELNIQ VADFENFIGS LNDQGYLLKK GPVKYQLQTM

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Seq ID NO: 45 DNA sequence
Nucleic Acid Accession #: NM_005416.1
Coding sequence: 149..658

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1      11      21      31      41      51
|      |      |      |      |      |
ACCAGATCCC AGAGGCTGAA CACCTCGACC TTCTCTGCAC AGCAGATGAT CCCTGAGCAG 60
CTGAAGACCA GAAAGGCCAC TAAGACTTTC TGCTTAATTC AGGAGCTTAG AGGATTCTTC 120
AAAGAGTGTG TCCACGATCC TTTGAAGCAT GAGTTCCTAC CAGCAGAAGC AGACCTTTAC 180
CCCACCACTC CAGCTTCAAC AGCAGCAGGT GAAACAACCC AGCCAGCCTC CACCTCAGGA 240
AATATTGTGT CCCACAACCA AGGAGCCATG CCACTCAAAG GTTCCACAAC CTGGAACAC 300
AAAGATTCCA GAGCCAGGCT GTACCAAGGT CCCTGAGCCA GGCTGTACCA AGGTCCCTGA 360
GCCAGGCTGT ACCAAGGTCC CTGAGCCAGG TTGTACCAAG GTCCCTGAGC CAGGCTGTAC 420
CAAGGTCCCT GAGCCAGGTT GTACCAAGGT CCCTGAGCCA GGCTACACCA AGGTCCCTGA 480
ACCAGGCAGC ATCAGGTCC CTGACCAAGG CTTTATCAAG TTTCTGAGC CAGGTGCCAT 540
CAAAGTTCTT GAGCAAGGAT ACACCAAGT TCCTGTGCCA GGCTACACAA AGCTACCAGA 600
GCCATGTCTT TCAACGGTCA CTCCAGGCC AGCTCAGCAG AAGACCAAGC AGAAGTAATT 660
TGGTGACAG ACAAGCCCTT GAGAAGCCAA CCACCAGATG CTGGACACCC TCTTCCCATC 720
TGTTTCTGTG TCTTAATTGT CTGTAGACCT TGTAAATCAG ACATTGTAC CCAAGCCAT 780
AGTCTCTCTC TTATTGTAT CCTAAAAATA CGTACTATAA AGCTTTTGT CACACACACT 840
CTGAAGAATC CTGTAAGCCC CTGAATTAAG CAGAAAGTCT TCATGGCTTT TCTGGTCTTC 900
GGCTGCTCAG GGTTCATCTG AAGATTCGAA TGAAAAGAAA TGCATGTTTC CTGCTCTTCC 960
CTCATTAAT TGCTTTTAA TCCA

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Seq ID NO: 46 Protein sequence:
Protein Accession #: NP_005407.1

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1      11      21      31      41      51
|      |      |      |      |      |
MSSYQQKQTF TPPPQLQQQQ VKQPSQPPQ EIFVPTTKEP CHSKVPQPGN TKIPEPGCTK 60
VPEPGCTKVP EPGCTKVPEP GCTKVPEPGC TKVPEPGCTK VPEPGYTKVP EPGSIKVPDQ 120
GFIKFPPEGA IKVPEQGYTK VVPVGYTKLP EPCPSTVTPG PAQQKTKQK

```

Seq ID NO: 47 DNA sequence
Nucleic Acid Accession #: Eos sequence

1	11	21	31	41	51	
GCGTCGTGTG	CAGGCGTCCC	CGGGCTGTGG	ATAATTAGAC	ACGTTCTTCC	CTCATTGCCC	60
AAGGTCGTGT	AGAATTCGCC	CTAGAGCTGT	ATCATGTATT	TTCTTTCAA	TTAACTTTGC	120
TTGCAATTAA	GCTTAGGGAA	CCAGCAACAA	AAGCAAACCT	GGCCCGAGGT	CGTTCACCGC	180
GAAAAATGGAT	TAGAGAAACT	TCTTCCCCGA	TTTAAGGGGA	AAGATTCCTG	CGGCCAGCGC	240
TTTGGGGAAA	GTGCCCCGAC	CGCAGAGGCG	ACGACAGGGG	AGCAGGAAGC	TGCTCACGGT	300
AGTCGGCGTT	GGCGCGCAGC	GTGGCCTTCC	TCATCTGGGC	GATGTGGGCT	CCTAGAAGAG	360
TAAGGATAAC	ATCCTGGAAA	TGACTTCTGT	ACGGTTTGAG	CCCAACTGCA	CACTCATGAC	420
TTGGAGCTGC	CCTGTGGAGT	TACAGTTTAC	CAACACATT	CATGAACATA	ATCTCATTTA	480
CTAAAACTG	TGTGAGAAAT	TTCTTTTACT	AAAAATTTTT	CTTATTACAA	A	

Seq ID NO: 48 DNA sequence:

Nucleic Acid Accession #: CAT cluster

1	11	21	31	41	51	
TTCCAAATTT	TTTTTTTTGT	AATAAGAAAA	AATTTTAGTA	AAAGAAAAT	CTCAGAAAGT	60
TTTTAGTAAA	TGAGATTATG	TTCATGAATG	TGTTTGGTAA	ACTGTAACTC	CACAGGGCAG	120
CTCCAAGTCA	TGAGTGTGCA	GTTGGGCTCA	AACCGTACAG	AAGTCATTTC	CAGGATGTGA	180
TCCTTACTCT	TCTCGGAGCC	CACATCGCCC	AGATGAGGAA	GGCCACCGCT	GCCGCCAACG	240
CCGACTACCG	TGAGCAGCTT	CCTGCTCCCC	TGTCGTCGCC	TCTGCGGTGC	GGGCACTTTC	300
CCCAAGCGC	TGGCGCGAGG	AATCTTTCCC	CTTAATCGG	GGAAAGAAAT	TCTCTAATCC	360
ATTTTTCGGG	TGAACGACCT	CGGGCCAAAGT	TTGCTTTTGT	TGCTGGTTCC	CTAAGCTTAA	420
TTGCAAGCAA	AGTTAATTTG	AAAGAAAATA	CATGATACAG	CTCTAGGGCG	AATTCTAACG	480
AGCCTTGGGC	AATGAGGGAA	GAACGTGTCT	AGTTATCCAC	AGCCCGGGGA	CGCCTGCACA	540
CGACGCT						

Seq ID NO: 49 DNA sequence

Nucleic Acid Accession #: CAT cluster

1	11	21	31	41	51	
TCTTTCTTCT	GCTGCTCGTT	TGTCTCTCCT	GTGCTCTTCT	TCTTTCTTTC	CCTCGCCGCT	60
CCTGCGGACC	TCTGTGTGCT	CTTCTCTGAT	GGCGGGGGGC	GGGAGAAAGCT	GACCGGTGAG	120
ACCGTAGACC	CGAAACCAAT	GGGTGTCA	AGCCGGTCGC	CGGCTTTTTT	GGGAGAACCC	180
GACACATGCA	GACCACTTTT	CCTGGAACNG	CATGACCATG	TTATTACTAT	GGGCCGCCTC	240
CCCAACCAAA	GTGTTTAAAA	CTTTTATAGG	CACCCCCAAA	ATTTTTTTTT	TTTTTTTTTT	300
TTCAATTAAA	AAACTCTAAT	ATTTATATTA	AATACAAAGA	TACCCAAACC	CTTTATGCTT	360
CTTTCTCTGA	TCTGTGTCTT	TTTTCTTTGA	CAGCATCTCC	ATTTTTTTTT	TGCTGCTTCA	420
TCGCTGTAGC	CATGGGAATC	CGTTTTCATTA	TTATGGTAGC	AATATGGAGT	GCTGTATTCC	480
TAAAGAAACT	GACACAGGAG	AATCACTTGA	ACTTGGGAGG	CAGAGTTTGC	AGTGAGCCGA	540
GATTGAACCA	GTGCACTCCA	GCCTTGGCAG	CGGAGCAAGA	TTCTGTCCAC	GTTCTCTGAAG	600
TGCTGGTATC	GTCTGTGACG	CCCATCTCG	GTTCCATTGC	GCTGCCAGGC	AGGGTGTGCG	660
GACGTGGGGA	GAGCTGGTCT	ATATATCCGG	GTGAAGCTCA	GCTGTGGCAC	ACCTTGGATG	720
CCGGTCTCT	CCTGCCCCCG	GGGACCTAGT	ATTTTGGCCA	CGAGTGTACA	CCAAACAAAG	780
GAGACAGCAT	CATTATAGAG	CCTGCAGCAT	CCACCCTACT	GCTGTATCCA	GTTTCCATTG	840
ACTG						

Seq ID NO: 50 DNA sequence

Nucleic Acid Accession #: L05187

Coding sequence: 1991..2260

1	11	21	31	41	51	
CTGCAGGGAG	GCAGGTAGAA	AAGGCTTTTG	GGTTTTCAGG	TGGGGGGCAG	TCTAGCCTGA	60
TCAGAAAGGA	GGAAAAGGCC	AGGGCAGATG	TCTGGGTGGA	GTGAAGGGAA	AAAGTGATCC	120
CAGAAAGAGG	ATTAGCCCTT	GAAAGTCCCT	GAAGTAGGAG	AAGGGTAAAG	GTGTGGTTGG	180
TGAAGGAAG	CAGGTTTTCC	CAGATTAGCA	ACCAGTCAGG	GGGAGGAAGG	TGAGAGTGGG	240
AGAGTCATAA	GTAAATTAT	CTGAATGTGT	GTAGTTTAAT	GGAAATTGGGA	AAAAGATGGG	300
GGAAATGGAT	GGAAAGTCTT	GGACTCTGAG	ACAAGGGGTC	TATAATCAGT	CCATTTTCATT	360
ATTTCTAGCT	TCCACCTTCA	CCAAGGCAGA	CAAGGAGGGC	CCACCTCAGC	TCCTCTGCTC	420
CCCCTCCCTT	TCCCACCTAT	TCATGTGTGC	AAGAGTGCCC	TGTCCCAAG	AACACGGGGA	480
ACAACCATCT	CAATGACAAG	GACAGCAGGT	GGCAAGGCTC	AACAGGACTC	AGATGTCCCC	540
CCAGGGTTAA	CTCATGAAAC	CCTCCATGAA	GCCTGCTGCT	CACCCCTCCC	TCAAGGCAAG	600
CCCTGCACCT	GGGTCTGAGG	ATGAGGGTGG	CAGTGAAAT	TAGGCCAGTG	ACATCATTTT	660
CAGCCAGCTA	GTGCCAAAAA	ATATCAGGTG	GTGTTTCATCA	AATAAGCCGA	GCCAAACGGT	720
GATGAGGATG	TGAGTGTGAG	TCATGTGTGA	CAGGTGAGGA	ATGAAAAACAG	AGTGCCCGAG	780
AGCTTCTATT	TCCTTGAGGC	AGGGCTCATT	CATCTTATAA	AAGCCAGCTG	GCCATTGCCT	840
TCACACCAAA	CCCAAGGGAC	CACACAGCCC	ATTCGTCTCC	GTATACCAGG	TAAGTCTCTG	900
ATTGCAACAA	ACTGGCAATT	CTAGTGTAAT	TTTTCAATTAT	TAGAAATTAG	CTAAAGGCAA	960
ATATGTGTAA	GCAGGTAAAT	CCAGGGTTTC	AATGGGAGAT	AGAGAATAGT	GGAATATCTT	1020
TATTTTAAGT	TAAATTACAG	TCTGGATTTG	AAAGGACCTT	AGAGATGGTT	AGGGCTCCCA	1080
CCTCAGTAGA	TAGTCATTGA	ACTGGGAGTC	CTGGAGAAGA	TTGTTCAAAT	GCCCATGGGA	1140
AGTTCATAGC	AGAACTAGAA	CTCAGGCCAG	AGCACTCTCA	GTAACACTGC	AATTTCCCCC	1200
TGCAAGATA	TTTATAGAAA	TTTTAATTTA	TTAGATGGAT	CTCTACTGAG	CATTATTATC	1260
ATTTAAGGCA	GTATGCTAGG	CACTTTGGAC	AAATCAATGC	CCTAACGTAC	TTACTTAACA	1320
AACATAAAAC	CTAGCAGGAA	GGTAATACAT	ATATATAAAT	AAATGAAATG	CAAAAGTAGAT	1380
AGTAATTGGC	ATGACGGAGA	TGGGCAGAGA	AGGGCTGTGC	ACTTTTGGGA	GACTTGCTCA	1440
AGGAGACCTC	TAGGGTGTCA	AGTGATGTGA	GCTATGATGG	AGGGGTATTT	GGACAAGCAG	1500
AGATGGGAAG	AAAAGCATTT	GGAAGGGACT	GTGTAAGCAC	AGACCAGAAG	CAAAACCATA	1560
GAGGCTTAGA	TGAATATAAA	GCCATCCTAT	AAGTCACAGG	CTTTCTACAT	GGTACTAGGA	1620
GAGGAAAGTG	GTCTGATGCC	ATTTTCCAAA	AGACCTAATA	TGCGGACCTC	ATGTCCTCTC	1680
GAAGCCAGCT	TTAGCAGGCT	ATTTTCCAG	AACAGATATA	AGGTGCCITG	GGTAGGAAGG	1740
GAGCCAAGAA	GAGAACTCCA	ATAAATGGA	GCAGAAGAAA	TTGCCTTTTA	GCTCCTCCTC	1800
TTCAAAGGGC	CTGAAATTA	TCCAAGCTTA	TTTCATTTTT	AAATGTAATG	GGGGAGCTAA	1860

GGGAGATGAA AGGCTTTCTC TTCTAAAGGG TCCTGAAATA AAATCTGTTT GGCATTGAAT 1920
 TTGTATCCAT CTTTCTTTAA TTGAATCACT GTGTCACTT TCTGTCTCTA GAAAAAACA 1980
 CATTGAAGC ATGAATTCTC AGCAGCAGAA GCAGCCTTGC ACCCCACCCC CTCAGCCTCA 2040
 GCAGCAGCAG GTGAACAACA CTTGCCAGCC TCCACCCAG GAACCATGCA TCCCCAAAAC 2100
 CAAGGAGCCC TGCCAACCCA AGGTGCCTGA GCCCTGCCAC CCCAAAGTGC CTGAGCCCTG 2160
 CCAGCCCAAG ATTCCAGAGC CCTGCCAGCC CAAGGTGCCT GAGCCCTGCC CTTCAACGGT 2220
 CACTCCAGCA CCAGCCAGC AGAAGACCAA GCAGAAGTAA TGTGGTCCAC AGCCATGCCC 2280
 TTGAGGAGCT GGCCAGTGA TACTGAACAC CCTACTCCAT TCTGCTTATG AATCCCATT 2340
 GCCTATTGAC CCTGCAGTTA GCATGCTGTC ACCCTGAATC ATAATCGCTC CTTTGCACCT 2400
 CTAAGAGAT GTCCCTTACC CTCATTCTGG AGGCTCCTGA GCCTCTGCGT AAGGCTGAAC 2460
 GTCTCACTGA CTGAGCTAGT CTTCTTGTG CTCGGGTGCA TTTGAGGATG GATTTGGGGA 2520
 AGGTCAAATG ACCATCCCTA G

Seq ID NO: 51 Protein sequence:
 Protein Accession #: AAC26838

1 11 21 31 41 51
 MNSQQQKQPC TPPPQPPQQQ VKQPCQPPQ EPCIPKTKEP CQPKVPEPC PKVPEPCQPK 60
 IPEPCQPKVP EPCPSTVTPA PAQQTQKQK

Seq ID NO: 52 DNA sequence
 Nucleic Acid Accession #: NM_002638.1
 Coding sequence: 120-473

1 11 21 31 41 51
 CAATACAGCT AAGGAATTAT CCCTGTATAA TACCACAGAC CCGCCCTGGA GCCAGGCCAA 60
 GCTGGACTGC ATAAAGATTG GTATGGCCTT AGCTCTTAGC CAAACACCTT CCTGACACCA 120
 TGAGGGCCAG CAGCTTCTTG ATCGTGGTGG TGTTCCTCAT CGCTGGGACG CTGGTTCTAG 180
 AGGCAGCTGT CACGGGAGTT CCTGTTAAAG GTCAAGACAC TGTCAAAGGC CGTGTTCAT 240
 TCAATGGACA AGATCCCTTT AAAGGACAA TTTCAAGTAA AGGTCAAGAT AAAGTCAAAG 300
 CGCAAGAGCC AGTCAAAGGT CCAGTCTCCA CTAAGCCTGG CTCCTGCCCC ATTATCTTGA 360
 TCCGGTGGCG CATGTTGAAT CCCCCTAAC GCTGCTTGAA AGATACTGAC TGCCAGGAA 420
 TCAAGAAAGT CTGTGAAGGC TCTTGCGGGA TGGCCTGTT CGTTCCTCAG TGAAGGGAGC 480
 CGGTCTTTCG TGCACCTGTG CCGTCCCGAG AGCTACAGGC CCCATCTGGT CCTAAGTCCC 540
 TGCTGCCCTT CCCCTTCCCA CACTGTCCAT TCTTCTCTCC ATTCAAGATG CCCACGGCTG 600
 GAGCTGCCTC TCTCATCCAC TTCCAATAA A

Seq ID NO: 53 Protein sequence:
 Protein Accession #: NP_002629.1

1 11 21 31 41 51
 MRASSFLIVV VFLIAGTLVL EAAVTGVVVK GQDITVGRVP PNGQDPVKGQ VSVKGQDKVK 60
 AQEPVKGPVS TKPGSCP IIL IRCAMLNPPN RCLKDIDCFG IKKCEGSCG MACFVPQ

Seq ID NO: 54 DNA sequence
 Nucleic Acid Accession #: NM_019618
 Coding sequence: 75-584

1 11 21 31 41 51
 GGCACGAGCC ACGATTCACT CCCCTGGACT GTAGATAAAG ACCCTTTCTT GCCAGGTGCT 60
 GAGACAACCA CACTATGAGA GGCACCTCCAG GAGACGCTGA TGGTGGAGGA AGGGCCGTCT 120
 ATCAATCAAT GTGTAAACCT ATTACTGGGA CTATTAATGA TTTGAATCAG CAAGTGTGGA 180
 CCCTTCAGGG TCAGAACCTT GTGGCAGTTC CACGAAGTGA CAGTGTGACC CCAGTCACTG 240
 TTGCTGTTAT CACATGCAAG TATCCAGAGG CTCTTGAGCA AGGCAGAGGG GATCCCATT 300
 ATTTGGGAAT CCAGAATCCA GAAATGTGTT TGTATTGTGA GAAGGTGGA GAACAGCCCA 360
 CATTGCAGCT AAAAGAGCAG AAGATCATGG ATCTGTATGG CCAACCCGAG CCGGTGAAAC 420
 CCTTCCTTTT CTACCGTGCC AAGACTGGTA GGACCTCCAC CCTTGAGTCT GTGGCCTTCC 480
 CGGACTGTTT CATTGCCTCC TCCAAGAGAG ACCAGCCCAT CATTCTGACT TCAGAACTTG 540
 GGAAGTCATA CAACACTGCC TTTGAATTAA ATATAAATGA CTGAACCTAG CCTAGAGGTG 600
 GCAGCTGGT CTTTGTCTTA AAGTTTCTGG TTCCCAATGT GTTTTCGTCT ACATTTTCTT 660
 AGTGTCAATT TCACGCTGGT GCTGAGACAG GGGCAAGGCT GCTGTTATCA TCTCATTTTA 720
 TAATGAAGAA GAAGCAATTA CTTCATAGCA ACTGAAGAAC AGGATGTGTC CTCAGAAGCA 780
 GGAGAGCTGG GTGGTATAAG GCTGTCTCT CAAGCTGGTG CTGTGTAGGC CACAAGGCAT 840
 CTGCATGAGT GACTTTAAGA CTCAAAGACC AAACACTGAG CTTTCTTCTA GGGGTGGGTA 900
 TGAAGATGCT TCAGAGCTCA TGCGCGTTAC CCACGATGGC ATGACTAGCA CAGAGCTGAT 960
 CTCTGTTTCT GTTTTGTCTT ATTCCTCTT GGGATGATAT CATCCAGTCT TTATATGTTG 1020
 CCAATATACC TCATTGTGTG TAATAGAACC TTCTTAGCAT TAAGACCTTG TAAACAAAAA 1080
 TAATTCTTGT GTTAAGTTAA ATCATTTTGT TCCTAATTGT AATGTGTAAT CTTAAAGTTA 1140
 AATAAACTTT GTGATTTTAT ATAATAAAAA AAAAAAAAA AAA

Seq ID NO: 55 Protein sequence:
 Protein Accession #: NP_062564

1 11 21 31 41 51
 MRGTPGDADG GGRAVYQSMC KPITGTINDL NQQVWTLQGO NLVAVPRSDS VTPVTVAVIT 60
 CKYPEALEQG RGDPIYLGIO NPEMCLYCEK VGEQPTLQLK EQKINDLYGO PEPVKPFLFY 120
 RAKTGRSTSL ESVAFPDWFI ASSKRDQPII LTSELGKSYN TAFEININD

Seq ID NO: 56 DNA sequence
 Nucleic Acid Accession #: NM_003125
 Coding sequence: 65-334

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1      11      21      31      41      51
|      |      |      |      |      |
5  AGCAGTTCTA AGGGACCATA CAGAGTATTC CTCTCTTCAC ACCAGGACCA GCCACTGTGTG 60
   CAGCATGAGT TCCAGCAGC AGAAGCAGCC CTGCATCCCA CCCCTCAGC TTCAGCAGCA 120
   GCAGGTGAAA CAGCCTTGCC AGCCTCCACC TCAGGAACCA TGCATCCCA AAACCAAGGA 180
   GCCCTGCCAC CCCAAGGTGC CTGAGCCCTG CCACCCCAAA GTGCCCTGAGC CCTGCCAGCC 240
   CAAGCTTCCA GAGCCATGCC ACCCAAGGT GCCTGAGCCC TGCCCTTCAA TAGTCACTCC 300
   AGCACCAGCC CAGCAGAAGA CCAAGCAGAA GTAATGTGGT CCACAGCCAT GCCCTTGAGG 360
10  AGCCGGCCAC CAGATGCTGA ATCCCCATATC CCATTCTGTG TATGAGTCCC ATTTGCCTTG 420
   CAATTAGCAT TCTGTCTCCC CCAAAAAGA ATGTGCTATG AAGCTTTCTT TCCTACACAC 480
   TCTGAGTCTC TGAATGAAG TGAAGGTCTT AGTACCAGAG CTAGTTTTC A GCTGCTCAGA 540
   ATTCATCTGA AGAGAGACTT AAGATGAAAG CAAATGATTG AGTCCCTTA TACCCCATTT 600
15  AAATTCACAT TCAATTCCA

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Seq ID NO: 57 Protein sequence:
Protein Accession #: NP_003116

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1      11      21      31      41      51
|      |      |      |      |      |
20  MSSQQQKQPC IPPPQLQQQQ VKQPQPQQPQ EPCIPKTKEP CHPKVPEPCH PKVPEPCQPK 60
   LPEPCHPKVP EPCPSIVTPA PAQKTKQK

```

Seq ID NO: 58 DNA sequence
Nucleic Acid Accession #: NM_001793.2
Coding sequence: 71-2560

```

30  1      11      21      31      41      51
   |      |      |      |      |      |
   AAAGGGGCAA GAGCTGAGCG GAACACCGGC CCGCGGTCGC GGCAGCTGCT TCACCCCTCT 60
   CTCTGCAGCC ATGGGGCTCC CTCGTGACC TCTCGCTCT CTCTCTCTTC TCCAGGTTTG 120
   CTGGCTGCAG TGGCGCGCCT CCGAGCCGTG CCGGGCGGTC TTCAGGAGG CTGAAGTGAC 180
35  CTTGGAGGCG GAGGCGCGCG AGCAGGAGCC CGGCCAGGCG CTGGGGAAAG TATTCATGGG 240
   CTGCCCTGGG CAAGAGCCAG CTCTGTTTAG CACTGATAAT GATGACTTCA CTGTGCGGAA 300
   TGGCGAGACA GTCCAGGAAA GAAGGTCACT GAAGGAAAGG AATCCATTGA AGATCTTCCC 360
   ATCCAAACGT ATCTTACGAA GACACAAGAG AGATTGGGTG GTTGCTCAA TATCTGTCCC 420
   TGAATAATGGC AAGGGTCCCT TCCCCCAGAG ACTGAATCAG CTCAGTCTA ATAAAGATAG 480
40  AGACACCAAG ATTTTCTACA GCATCACGGG GCCGGGGGCA GACAGCCCCC CTGAGGGTGT 540
   CTTGCTGTGA GAGAAGGAGA CAGGCTGGTT GTTGTGAAT AAGCCACTGG ACCGGGAGGA 600
   GATTGCCAAG TATGAGTCTT TTGGCCACGC TGTGTCAGAG AATGGTGCCT CAGTGGAGGA 660
   CCCCATGAAC ATCTCCATCA TCGTGACCGA CCAGAATGAC CACAAGCCCA AGTTTACCCA 720
   GGACACCTTC CGAGGGAGTG TCTTAGAGGG AGTCTACCA GGTACTTCTG TGATGCAGGT 780
45  GACAGCCACG GATGAGGATG ATGCCATCTA CACCTACAAT GGGGTGGTTG CTTACTCCAT 840
   CCATAGCCAA GAACCAAAGG ACCCACACGA CCTCATGTTC ACCATTACCC GGAGCACAGG 900
   CACCATCAGC GTCATCTCCA GTGGCCTGGA CCGGGAAAAA GTCCCTGAGT ACACACTGAC 960
   CATCCAGGCC ACAGACATGG ATGGGGACGG CTCCACCACC ACGGCACTGG CAGTAGTGGA 1020
   GATCCTTGAT GCCAATGACA ATGCTCCCAT GTTTGACCCC CAGAAGTACG AGGCCCATGT 1080
50  GCCTGAGAAT GCAGTGGGCC ATGAGGTGCA GAGGCTGACG GTCACTGATC TGGACGCCCC 1140
   CAACTCACCA GCGTGGCGTG CCACCTACCT TATCATGGGC GGTGACGACG GGGACCATT 1200
   TACCATCACC ACCCACCTCG AGACAACCA GGGCATCCTG ACAACAGGA AGGGTTTGGA 1260
   TTTTGAGGCC AAAAACCCAG ACACCTGTGA CGTTGAAGTG ACCAACGAGG CCCCTTTTGT 1320
   GCTGAAGCTC CCAACCTCCA CAGCCACCAT AGTGGTCCAC GTGGAGGATG TGAATGAGGC 1380
55  ACCTGTGTTT GTCCCACCTT CCAAGTCTGT TGAGGTCCAG GAGGGCATCC CCACTGGGGA 1440
   GCCTGTGTGT GTCTTCTCTG CAGAAGACCC TGACAAGGAG AATCAAAAGA TCAGCTACCG 1500
   CATCTGAGA GACCCAGCAG GGTGGCTAGC CATGGACCCA GACAGTGGGC AGGTACACAGC 1560
   TGTGGGCACC CTCGACCGTG AGGATGAGCA GTTTGTGAGG AACAACATCT ATGAAGTCAT 1620
   GGTCTTGACC ATGACAAATG GAAGCCCTCC CACCACTGGC ACGGGAACCC TTCTGTAAAC 1680
60  ACTGATTGAT GTCAATGACC ATGGCCCACT CCCTGAGCCC CGTCAGATCA CCATCTGCAA 1740
   CCAAGCCCTT GTGCGCCAGG TGTGAAACAT CACGGACAAG GACCTGTCTC CCCACACCTC 1800
   CCTTTCCAG GCCCAGCTCA CAGATGACTC AGACATCTAC TGGACGCGAG AGGTCAACGA 1860
   GGAAGGTGAC ACAGTGGTCT TGTCCCTGAA GAAGTTCCTG AAGCAGGATA CATATGACGT 1920
   GCACCTTTCT CTGTCTGACC ATGGCAACAA AGAGCAGCTG ACGGTGATCA GGGCCACTGT 1980
65  GTGCGACTGC CATGGCCATG TCGAAACCTG CCCTGGACCC TGGAAAGGAG GTTTCATCCT 2040
   CCCTGTGCTG GGGGCTGTCC TGGCTCTGCT GTTCTCTCTG CTGGTGTGCT TTTTGTGGT 2100
   GAGAAAGAAG CGGAAGATCA AGGAGCCCTT CCTACTCCCA GAAGATGACA CCCGTGACAA 2160
   CGTCTTCTAC TATGGCAGAG AGGGGGGTGG CGAAGAGGAC CAGGACTATG ACATCACCCA 2220
70  GCTCCACCGA GGTCTGGAGG CCAGGCCGGA GGTGGTTCTC CGCAATGACG TGGCACCAAC 2280
   CATCATCCCG ACACCATGT ACCGTCTCG GCCAGCCAAC CCAGATGAAA TCGGCAACTT 2340
   TATAATTGAG AACCTGAAGG CGGCTAACAC AGACCCCAAC GCCCGGCCCT ACACACCCCT 2400
   CTTGGTGTTC GACTATGAGG GCAGCGGCTC CGACGCCGCG TCCCTGAGCT CCTCACCTC 2460
   CTCGCCCTCC GACCAAGACC AAGATTACGA TTATCTGAAC GAGTGGGGCA GCCGCTTCAA 2520
75  GAAGCTGGCA GACATGTACG GTGGCGGGGA GGACGACTAG GCGGCCTGCC TGCAGGGCTG 2580
   GGGACCAAAAC GTACAGCCAC AGAGCATCTC CAAGGGGTCT CAGTTCCTCC TTCACTGAG 2640
   GACTTCGGAG CTGTCTCAGG AGTGGCCGTA GCAACTTGGC GGAGACAGGC TATGAGTCTG 2700
   ACGTTAGAGT GGTGTGCTTC TTAGCCTTTC AGGATGGAGG AATGTGGGCA GTTTGACTTC 2760
   AGCACTGAAA ACCTCTCCAC CTGGGCCAGG GTTGCTCTAG AGGCCAAGTT TCCAGAAGCC 2820
   TCTTACCTGC CGTAAAAATG TCAACCTCTG GTCTTGGGCC TGGGCCTGCT GTGACTGACC 2880
80  TACAGTGAGC TTTCTCTCTG GAATGGAACC TTCTTAGGCC TCCTGGTGCA ACTTAATTTT 2940
   TTTTTTTAAAT GCTATCTTCA AAACGTTAGA GAAAGTTCTT CAAAGTGTCA GCCCAGAGCT 3000
   GCTGGGCCCA CTGGCCGTCC TGCATTTCTG GTTTCAGAC CCCAATGCCT CCCATTGCGA 3060
   TGGATCTCTG CGTTTATATA CTGAGTGTGC CTTTATTTT TATTTTCCCT 3120
85  GTTGCCTTGC TATAGATGAA GGGTGAGGAC AATCGTGTAT ATGTACTAGA ACTTTTTTAT 3180
   TAAAGAAACT TTTCCAGAAA AAAAA

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Seq ID NO: 59 Protein sequence:

Protein Accession #: NP_001784.2

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1      11      21      31      41      51
5  MGLPRGPLAS LLLQLQVCWLQ CAASEPCRAV FREAEVTLEA GGAEQEPGQA LGKVMGCPG 60
    QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIFPSKR ILRRHKRDWV VAPISVPENG 120
    KGPPFQRLNQ LKSNKDRDTK IFYSITGPGA DSPPEGVFAV EKETGWLLLN KPLDREEIAK 180
    YELFGHAVSE NGASVEDPMN ISIIIVTDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT 240
10 DEDDAIYTYN GVVAYSIHSQ BFKDPHDLMF TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300
    TDMDGDGSTT TAVAVVEILD ANDNAPMFDP QKYEAHVPEN AVGHEVQRLT VTDLDAPNSP 360
    AWRATYILMG GDDGDHFFIT THPENQGIIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL 420
    PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTEGPVC VYTAEDPDKE NQKISYRILR 480
    DPAGWLAMDP DSGQVAVGT LDREDEQFVR NNIEYVMVLA MDNGSPPTTG TGTLLLTLD 540
15 VNDHGPVPEP RQITICNQSP VRQVLNITDK DLSPHSTSPFQ AQLTDDSDIY WTAEVNEEGD 600
    TVVLSLKKFL KQPTYDVHLS LSDHGNKEQL TVIRATVDCD HGHVETCPGP WKGGFILPVL 660
    GAVLALLFL LVLVLLVRKK RKIKEPLLLP EDDTRDNVFI YGEEGGGEED QDYDITQLHR 720
    GLEARPEVVL RNDVAPTII PTPMYRPRAN PDEIGNFLIE NLKAANTDPT APPYDTLLVF 780
    DYEGSGSDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKKLA DMYGGEEDD

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Seq ID NO: 60 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 162-428

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    CATACGGACC GGATTGTTT CGCTGGCCCA GTGTCCCGG AGCTTGTGTG CGATACAGAG 120
    AGCACCTCGG AAGCTGAGGC AGCTGGTACT TGACAGAGAG GATGGCGCTG TCGACCATAG 180
    TCTCCAGAG GAAGCAGATA AAGCGGAAGG CTCCCGTGG CTTTCTAAAG CGAGTCTTCA 240
30 AGCGAAAGAA GCCTCAACTT CGTCTGGAGA AAAGTGGTGA CTTATTGGTC CATCTGAAC 300
    GTTACTGTT TGTTTCATCGA TTAGCAGAAG AGTCCAGGAC AAACGCTTGT GCGAGTAAAT 360
    GTAGAGTCAT TAACAAGGAG CATGTACTGG CCGCAGCAAA GGTAATTCTA AAGAAGAGCA 420
    GAGGTAGAA GTCAAAGAAC ATATTCTTGA AAGTTATGAT GCATTCTTTT GGGTGGTAAC 480
    AGATCATAAA GACATTTTTT ACACATCAGT TAATATGGGA TTATTAATA TTGG

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Seq ID NO: 61 Protein sequence:

Protein Accession #: Eos sequence

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1      11      21      31      41      51
40 MALSTIVSQR KQIKRKAPRG FLKRVFKRKK PQLRLEKSGD LLVHLNCLLF VHLRAEESRT 60
    NACASKCRVI NKEHVLAAAK VILKKSRRG

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Seq ID NO: 62 DNA sequence

Nucleic Acid Accession #: NM_000094.2

Coding sequence: 99-8933

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1      11      21      31      41      51
50 GGGCTGGAGG GCGCTGGGCG TCGGACCTGC CAAGGCCACC GCAGGGGGGA GCAAGGGACA 60
    GAGGCGGGGG TCCTAGCTGA CGGCTTTTAC TGCTTAGGAT GACGCTGCGG CTTCTGGTGG 120
    CCGCGCTCTG CGCCGGGATC CTGGCAGAGG CGCCCCGAGT GCGAGCCAG CACAGGGAGA 180
    GAGTGACCTG GACGCGCTT TACGCGCTG ACATTGTGTT CTTACTGGAT GGCTCCTCAT 240
55 CCATTGGCCG CAGCAATTTT CGCGAGGTCC GCAGCTTTCT CGAAGGGCTG GTGCTGCCTT 300
    TCTCTGGAGC AGCCAGTGCA CAGGGTGTGC GCTTTGCCAC AGTGCAGTAC AGCGATGACC 360
    CACGAGACAGA GTTCGGCTGC GATGCACCTG GCTCTGGGGG TGATGTGATC CGCGCCATCC 420
    GTGAGCTTAG CTACAAGGGG GGCAACACTC GCACAGGGGC TGCAATTCTC CATGTGGCTG 480
    ACCATGTCTT CCTGCCCGAC CTGGCCCGAC CTGGTGTCCC CAAGGTCTGC ATCCTGATCA 540
    CAGACGGGAA GTCCAGGAC CTGGTGGACA CAGCTGCCCA AAGGTGAAG GGGCAGGGGG 600
60 TCAAGCTATT TGCTGTGGGG ATCAAGAATG CTGACCCCTG GAGCTGAAG CGAGTTGCCT 660
    CACAGCCAA CTTCCGACTT TTCTTCTCG TCAATGACTT CAGCATCTTG AGGACACTAC 720
    TGCCCTCGT TTCCCGGAGA GTGTGCACGA CTGCTGGTGG CGTGCTGTG ACCCGACCTC 780
    CGGATGACTC GACCTCTGCT CCACGAGACC TGGTGTCTG TGAGCCAAGC AGCCAATCCT 840
    TGAGAGTACA GTGGACAGCG GCCAGTGGCC CTGTGACTGG CTACAAGGTC CAGTACACTC 900
65 CTCTGACGGG GCTGGGACAG CCACTGCCGA GTGAGCGGCA GGAGGTGAAC GTCCACAGCTG 960
    GTGAGACCAG TGTGCGGCTG CGGGGTCTCC GGCCACTGAC CGAGTACCAA GTGACTGTGA 1020
    TTGCCCTCTA CGCCAACAGC ATCGGGGAGG CTGTGAGCGG GACAGCTCGG ACCACTGCCC 1080
    TAGAAGGGCC GGAAGTGACC ATCCAGAATA CCACAGCCCA CAGCCTCTG GTGGCCTGGC 1140
    GGAGTGTGCC AGGTGCCACT GGCTACCGTG TGACATGGCG GGTCTCTCAGT GGTGGGCCCA 1200
70 CACAGCAGCA GGAGTGGGC CCTGGGCAGG GTTCAGTGTT GCTGCGTGAC TTGAGGCTG 1260
    GCACGGACTA TGAGGTGACC GTGAGACCCC TATTTTGGCCG CAGTGTGGGG CCCGCCACTT 1320
    CCCTGATGGC TCGCACTGAC GCTTCTGTTG AGCAGACCCT GCGCCCGGTC ATCCTGGGCC 1380
    CCACATCCAT CCTCTTTTCC TGGAACTTGG TGCCCTGAGGC CCGTGGCTAC CGGTGGAAT 1440
75 GCGGCGGTGA GACTGGCTTG GAGCCACCGC AGAAGGTGGT ACTGCCCTCT GATGTGACCC 1500
    GCTACCAAGT GGATGGGCTG CAGCCGGGCA CTGAGTACCG CCTCACACTC TACACTCTGC 1560
    TGGAGGGCCA CGAGGTGGCC ACCCTGCAA CCGTGGTTC CACTGGACCA GAGCTGCCTG 1620
    TGAGCCCTGT AACAGACTG CAAGCCACCG AGCTGCCCGG GCAGCGGGTG CGAGTGTCTC 1680
    GGAGCCAGT CCCTGGTGCC ACCCAGTACC GCATCATTGT GCGCAGCACC CAGGGGGTTG 1740
    AGCGGACCTT GGTGCTTCTT GGGAGTCAGA CAGCATTGCA CTTGGATGAC GTTCAGGCTG 1800
80 GGCTTAGCTA CACTGTGCGG GTGCTGTGTC GAGTGGGTCC CCGTAGAGGC AGTGCCAGTG 1860
    TCCTCACTGT CCGCCGGGAG CCGGAAACTC CACTTGCTGT TCCAGGGCTG CGGGTTGTGG 1920
    TGTGAGATGC AACCGGAGTG AGGGTGGCCT GGGGACCGCT CCCTGGAGCC AGTGGATTTC 1980
    GGATTAGCTG GAGCACAGGC AGTGGTCCGG AGTCCAGCCA GACACTGCCC CCAGACTCTA 2040
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85 TGCGAGGAGC AGAGGAGGGG CCGTGTGACG TCAGAACGAC CCACTGGGTC CCAGTGGGAC 2160
    CAGTGAGGAC GGTCCATGTG ACTCAGGCCA GCAGCTCATC TGTCAACATT ACCTGGACCA 2220
    GGGTTCTCTG CGCCACAGGA TACAGGGTTT CTGGCACTC AGCCACGGC CCAGAGAAAT 2280

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	CCCAGTTGGT	TTCITGGGGAG	GCCACGGTGG	CTGAGCTGGA	TGGACTGGAG	CCAGATACTG	2340
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	TTGTGAGGAC	TGCCCTTGAG	CCTGTGGGTC	GTGTGTGCGA	GCTGCAGATC	CTCAATGCTT	2460
5	CCAGCGAGCT	TCTACGGATC	ACCTGGGTAG	GGGTCACTGG	AGCCACAGCT	TACAGACTGG	2520
	CCTGGGGCGT	GAGTGAAGGC	GGCCCCATGA	GGCACCAGAT	ACTCCCAGGA	AACACAGACT	2580
	CTGCAGAGAT	CCGGGGTCTC	GAAGGTGGAG	TCAGTACTCT	AGTGCAGATG	ACTGCACTTG	2640
	TCGGGGACCG	CGAGGGGACA	CCTGTCTCCA	TTGTGTGTCAC	TACGCGCGCT	GAGGCTCCGC	2700
	CAGCCCTGGG	GACCCCTTAC	GTGGTGCAGC	GCGGGGAGCA	CTCGCTGAGG	CTGCGCTGGG	2760
10	AGCCGGTGCC	CAGAGCGCAG	GGCTTCCTTC	TGCACCTGGCA	ACCTGAGGGT	GGCCAGGAAC	2820
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	CACAGTACCG	CGTGAGGCTG	AGTGTCTTAG	GGCCGGCTGG	AGAAGGGCCC	TCTGCAGAGG	2940
	TGACTGCGCG	CAGTGAATCA	CCTCGTGTTC	CAAGCATTGA	ACTACGTGTG	GTGGACACCT	3000
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15	CCTGGCGGCC	ACTCAGAGGC	CCTGGCCAGG	AAGTGCCTGG	GTCCCGCCAG	ACACTTCCAG	3120
	GGATCTCAAG	CTCCAGCGGG	GTGACAGGGC	TAGAGCCTGG	CGTCTCTTAC	ATCTTCTCCC	3180
	TGACGCGTGT	CCTGGCTGGT	GTGCGGGGTC	CTGAGGCATC	TGTACACAGC	ACGCCAGTGT	3240
	GCCCCCGTGG	CCTGGCGGAT	GTGGTGTTC	TACCACATGC	CACTCAAGAC	AATGCTCACC	3300
	GTGCGGAGGC	TACGAGGAGG	GTCTGTGAGC	GTCTGGTGT	GGCACTTGGG	CCTCTTGGGC	3360
20	CACAGGCAGT	TCAGGTTGGC	CTGCTGTCTT	ACAGTCATCG	GCCCTCCCCA	CTGTTCCAC	3420
	TGAAATGGCTC	CCATGACCTT	GGCATTATCT	TGCAAAGGAT	CCGTGACATG	CCCTACATGG	3480
	ACCCAAGTGG	GAAACAACCT	GGCACAGCCG	TGGTCACAGC	TCACAGATAC	ATGTTGGCAG	3540
	CAGATGCTCC	TGGGCGCCGC	CAGCACGTAC	CAGGGGTGAT	GGTTCGTCTA	GTGGATGAAC	3600
	CCTTGAGAGG	TGACATATTC	AGCCCCATCC	GTGAGGCCCA	GGCTTCTGGG	CTTAATGTGG	3660
25	TGATTTGGGG	AATGGCTGGA	GCGGACCCAG	AGCAGCTGCG	TCGCTTGGCG	CCGGGTATGG	3720
	ACTCTGTCCA	GACCTTCTTC	GCCGTGGATG	ATGGGCCAAG	CCTGGACCAG	GCAGTCAGTG	3780
	GTCTGGCCAC	AGCCCTGTGT	CAGGCATCCT	TCACTACTCA	GCCCCGGCCA	GAGCCCTGCC	3840
	CAGTGTATTG	TCCAAAGGGG	CAGAAGGGGG	AACCTGGAGA	GATGGGCTGG	AGAGGACAAG	3900
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30	CCCCTGGGAG	GAACTGCTCC	AAGGGCGAGA	GGGGCTTCCC	TGGAGCAGAT	GGGCGTCCAG	4020
	GCAGCCCTGG	CCGCGCCGGG	AATCTTGGGA	CCCCTGGAGC	CCCTGGCCTA	AAGGGCTCTC	4080
	CAGGGTTGCC	TGGCCCTCGT	GGGGACCCGG	GAGAGCGAGG	ACCTCGAGGC	CCAAAGGGGG	4140
	AGCCGGGGGC	TCCCGGACAA	GTCAATCGGAG	GTGAAGGACC	TGGGCTTCTT	GGGCGGAAAG	4200
	GGGACCCCTG	ACCATCGGGC	CCCCCTGGAC	CTCGTGGACC	ACTGGGGGAC	CCAGGACCCC	4260
35	GTGGCCCCCC	AGGGCTTCTT	GGAACAGCCA	TGAAGGGTGA	CAAAGGCGAT	CGTGGGGAGC	4320
	GGGGTCCCCC	TGGACCAAGT	GAAGGTGGCA	TTGCTCTCTG	GGAGCCTGGG	CTGCCGGGTC	4380
	TTCCCGGAAG	CCCTGGAGCC	CAAGGCCCCG	TTGGCCCCCC	TGGAAGAGAA	GGAGAAAAAG	4440
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40	TGGGTGAGGC	TGGAGAGAGT	GGCGAACCTG	GACCCCCAGG	CCCAGCGGGA	TCCCGGGGGC	4620
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	GCCCGCAAGG	AGAGAAGGGG	GAGCCTGGTC	GCCCTGGGGA	CCCTGCAGTG	GTGGGACCTG	4740
	CTGTGTCTGG	ACCCAAAGGA	GAAAAGGGAG	ATGTGGGGCC	CGCTGGGCCC	AGAGGAGCTA	4800
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45	AGGGAGACCC	TGGAGACCGG	GGTCCCATTT	GCCTTACTGG	CAGAGCAGGA	CCCCCAGGTG	4920
	ACTCAGGGCC	TCCTGGAGAG	AAGGGAGACC	CTGGGCGGCC	TGGCCCCCCA	GGACCTGTGG	4980
	GCCCCCGAGG	ACGAGATGGT	GAAGTTGGAG	AGAAAGGTGA	CGAGGGTCTT	CCGGGTGACC	5040
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50	GATCATCTGG	ACCCAAGGGT	GACCGTGGGG	AGCCGGGTCC	CCCAGGACCC	CCGGGACGGC	5220
	TGGTAGACAC	AGGACCTGGA	GCCAGAGAGA	AGGGAGAGCC	TGGGGACCGC	GGACAAGAGG	5280
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	AAAAGGGTGA	CCGGGGTCCC	CCTGGGCTGG	ATGGCCGGAG	CGGACTGGAT	GGGAAACCAAG	5460
55	GAGCCGCTGG	GCCCTCTGGG	CCGAATGGTG	CTGCAGGCAG	AGCTGGGGAC	CCAGGGAGAG	5520
	ACGGGCTTCC	AGGCCCTCGT	GGAGAACAAG	GCCTCCCTGG	CCCCCTCTGT	CCCCCTGGAT	5580
	TACCCGGAAA	GCCAGGAGAG	GATGGGAAAC	CTGGCTTGAA	TGGAAAAAAC	GGAGAACCTG	5640
	GGGACCCCTG	AGAAAGACGG	AGGAAGGGAG	AGAAAGGAGA	TTCAGGCGCC	TCTGGGAGAG	5700
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60	CTCCAGGCCT	CCAGGGGCCA	CTGGGCCCTC	CTGGCCAGGG	TTTTCTCTGT	GTCCCAGGAG	5820
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	GAGAGCGTGG	CCTGCGAGGA	GAGCCTGGAA	GTGTGCCGAA	TGTGGATCGG	TTGCTGGAAA	5940
	CTGCTGGCAT	CAAGGCATCT	GCCCTGCGGG	AGATCGTGGA	GACCTGGGAT	GAGAGCTCTG	6000
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65	GCCCCCAGG	CAAGGAGGCG	CCCATCGGCT	TTCTTGAGAG	ACGCGGGCTG	AAGGGCGAGC	6120
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70	GACCCCTTGG	CCCCAAGGTG	TCTGTGGATG	AGCCAGGTCC	TGGACTTCTT	GGAGAACAGG	6420
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	GACAAAGTGG	GGAGACAGGG	AAGCCGGGAG	CCCCAGGTCC	AGATGGTGCC	AGTGGAAAAAG	6900
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80	CTAAAGGAGA	ACCTGGCCCC	ACGGGGGGCC	CTGGACAGGC	TGTGGTCCGG	CTCCCTGGAG	7020
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	CCAAAGGTGA	CCGAGGACTG	CCAGGGCCCG	GAGGCCAGAA	GGGTGAAGCT	GGCCGTGCAG	7140
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	GCCCCCAGG	GAGAGAAGGA	ATCCACAGGAC	CCCTGGGGCC	ACCTGGACCA	CCGGGGTCAG	7440
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	GTGATGTTGG	GAGTGCAGGA	CTAAGGGGTG	ACAAGGGAGA	CTCAGCTGTG	ATCCTGGGGC	7680
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10	GGGGAGTGAA	GGGAGCCTGT	GGCCTTGATG	GAGAGAAGGG	AGACAAGGGA	GAAGCTGGTC	8040
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	CCTGCCACCC	TGGCAGATGA	CTCACTGTGG	GGGGGTGGCT	GTGGGCAGTG	AGCGGATGTG	9180
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	GCATTAAAGC	TGCTGTTTTA	AAAGGCAAAA	AA			

Seq ID NO: 63 Protein sequence:
Protein Accession #: NP_000085.1

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	LEGLVLFPFS	AASAQGVRF	TVQYSDPRT	EFGLDALGSG	GDVIRAIREL	SYKGNTRTGT	120
40	AAILHVAHDV	FLPQLARPVG	PKVCILITDG	KSQDLVDTA	QRLKGQGVKL	FAVGKKNADP	180
	EELKRVASQP	TSDFFFVND	FSILRTLLEP	VSRRVCTTAG	GVPVTRPPDD	STSAPRDLVL	240
	SEPSQSRLRV	QWTAASGPVT	GKVKQYTPLT	GLGQPLPSER	QEVNVPAGET	SVRLRGLRPL	300
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	LRFVILGPTS	ILLWNVLVPE	ARGYRLEWR	ETGLEPPQKV	VLPSPDVTRYQ	LDGLQPGTEY	480
45	RLTLTYLLEG	HEVATPATVV	PTGPPLPVSP	VTDLQATELP	QORVRVSWSP	VPGATQYRII	540
	VRSTQGVERT	LVLPGSQATF	DLDDVQAGLS	YTVRVSVARV	PREGSASVLT	VRREPETPLA	600
	VPGLRVVSD	ATRVRVAVGP	VFGASGFRIS	WSTGSGPESS	QTLPPDSTAT	DITGLQPGTT	660
	YQVAVSVLRG	REEGPAIVIV	ARTDPLGPVR	TVHVTAQSSS	SVTITWTRVP	GATGYRVSWH	720
	SAHGPEKSQL	VSGEATVAEL	DGLEPDTEYT	VHVRAHVAGV	DGPPASVVVR	TAPEFVGRVS	780
50	RLQILNASSD	VLRTVWVGTV	GATAYRLAWG	RSEGGFMRHQ	ILPGNTDSAE	IRGLEGGVSY	840
	SVRVTLVGD	REGTPVSIIV	TTPPEAPPAL	GTLHVVRQGE	HSLRLRWEPV	PRAQGFLLHW	900
	QPEGQEQEIS	VLGPELSSYH	LDGLEPATQY	RVRLSVLPGA	GEGPSAEVTA	RTSEPRVPSI	960
	ELRVVDTSID	SVTLAWTPVS	RASSYILSWR	PLRGPQGEVP	GSPQTLPGIS	SSQRVTGLEP	1020
	GVSYIFSLTP	VLDGVRGPEA	SVTQTFVCPR	GLADVVLFP	ATQDNAHRAE	ATTRVLERLV	1080
55	LALGFLGPPA	VQVGLLSYSH	RPSLFLPLNG	SHDLGIILQR	IRDMFYMDPS	GNNLGTAVVT	1140
	AHRYMLAPDA	PGRRHQVPGV	MVLVDEPLR	GDIFSPIREA	QASGLNVVML	GMAGADPEQL	1200
	RRLAPGMDSV	QTFFAVDGDP	SLDQAVSGLA	TALCQASFTT	QPRPEPCPVY	CPKQKGEPPG	1260
	EMGLRGQVGP	PGDPGLPGRT	GAPGPQGPFG	SATAKGERGF	PGADGRPGSP	GRAGNPPTFG	1320
60	APGLKGSPLG	PGPRGDPGER	GPRGPKGEFG	APGQVIGGEG	PGLPGRKGDP	GPSGPPGPRG	1380
	PLGDPGPRGP	PGLPGTAMKG	DKGRGRGERG	PGPGGGIAP	GEPGLPGLFG	SFGPQGPVGP	1440
	PGKKEGKDS	EDGAPGLPGQ	PGSPGEQGPR	GPPGAIGPKG	DRGFPGLGE	AGEKGERGPP	1500
	GPAGSRGLPG	VAGRPGAAGP	EGPPGPTGRQ	GEKGEPRPG	DPAVVGPAVA	GPKGEKGDVG	1560
	PAGPRGATGV	QGERGPPGLV	LPGDPGPKGD	PGDRGPIGLT	GRAGPPGDSG	PPGEKGDPR	1620
65	PGPPGPVGP	GRDGEVGEKG	DEGPPGDPGL	PGKAGERGLR	GAPGVRGPVG	EKGQGDPEGE	1680
	DGRNGSPGSS	GPKGDRGEFG	PPGPPGRLVD	TGPGAREKGE	PGDRGQEGPR	GPKGDPGLPG	1740
	APGERGIEGF	RGPPGPQGDP	GVRGPAGEKG	DRGPPGLDGR	SGLDGKPGAA	GPSGPNGAAG	1800
	KAGDPGRDGL	PGLRGEQGLP	GPSGPPGLPG	KPGEDGKPLG	NGKNGEPGDP	GEDGRKGEKG	1860
	DSGASGREGR	DGPKGERGAP	GILGPQGPFG	LPGVPGPFGQ	GFPVPGGTG	PKGDRGETGS	1920
70	KGEQGLPGER	GLRGEFGSVP	NVDRLLETAG	IKASALREIV	ETWDESSGSF	LPVPERRRGP	1980
	KGDSGEQFPF	GKEGPIGFPF	ERGLKGRDGD	PGPQGPPLA	LGERGPPGFS	GLAGEPGKFG	2040
	IPGLPGRAGG	VGEAGRPERG	GERGEKGERG	EQGRDGPPLG	PGTPGPPGPP	GPKVSVDEPG	2100
	PGLSGEQGPP	GLKGAKEPFG	SNGDQCPKGD	RGVPGIKGDR	GEPGPRGQDG	NFGLPGERGM	2160
	AGPEKPKGLQ	GPRGPPGPVG	GHGDPGPPGA	PGLAGPAGPQ	GPSGLKGEFG	ETGPPGRGLT	2220
75	GFTGAVGLPG	PPGSPGLVGP	QGSPLPGQV	GETGKPGAPG	RDGASGKDGD	RGSPPVPGSP	2280
	GLPGVPVPGK	EPGPTGAPGQ	AVVGLPGAKG	EKGAPGGLAG	DLVGEPPGAKG	DRGLPGPRGE	2340
	KGEAGRAGEP	GDPGEDGQKG	APGPKGFKGD	PGVGVPGSPG	PPGPPGVKGD	LGLPGLPGAG	2400
	GVVGFPGQTG	PRGEMGQPGP	SGERGLAGPP	GREGIPGLPL	PPGPPGVSVP	PGASGLKGDG	2460
	GDPGVGLPGP	RGERGEPIGR	GEDGRPGQEG	PRGLTGPPGS	RGERGEKGDV	GSAGLKGDGK	2520
80	DSAVILGPPG	PRGAKGDMGE	RGPRLDGDG	GPRGDNPDG	DKGSKGEPGD	KGSAGLPGLR	2580
	GLLGPPQGPQ	AAGIPGDPGS	PGKDGVPGR	GEKGDVGMFG	PRGLKGERGV	KGACGLDGEK	2640
	GDKEGAGPPG	RPLAGLHKEG	MGEPPGVPGS	GAPGKEGLIG	PKGDRGFDGQ	PGPKGDQGEK	2700
	GERGTPGIGG	PPGSPGNDGS	GEAPPGPGSV	GPRGPEGLQG	QKGERGPPGE	RVVGAPGVFG	2760
	APGERGEQGR	PGPAGPRGEK	GAALTEDDI	RGFVRQEMSQ	HCACQGGFIA	SGSRPLPSYA	2820
85	ADTAGSQLHA	VPVLRVSHAE	EEERVPPEDD	EYSEYSEYSV	EYQDPEAPW	DSDDPCSLPL	2880
	DEGSCTATTL	RWYHRAVTGS	TEACHPFVYG	GCGGNANRFG	TREACERRCP	PRVVQSQTGT	2940
	TAQD						

Seq ID NO: 64 DNA sequence
Nucleic Acid Accession #: NM_006945
Coding sequence: 1-219

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      CCAAAGTGCC CAGAGCCATG TCCACCCCG AAGTGCCCTG AGCCCTGCCC ACCACCAAAG 120
10     TGTCCACAGC CCTGCCACC TCAGCAGTGC CAGCAGAAAT ATCCTCCTGT GACACCTTCC 180
      CCACCCTGCC AGCCAAAGTA TCCACCGAAG AGCAAGTAA

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Seq ID NO: 65 Protein sequence:
Protein Accession #: NP_008876

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      PPCQPKYPPK SK

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Seq ID NO: 66 DNA sequence
Nucleic Acid Accession #: NM_005629.1
Coding sequence: 639-2546

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      CCGCCGCGCG GAAAGAGAGG GCGAGGCGCG CCCGAGCCGC CGCGCCCGCC GCCACCGCCG 120
      CCGCCGCGCAC CACGCCACCC GGAGTCGCGG GCCAGCCGGG CAGCCTCCGC GGGCCCCGGC 180
      CGGGCGGGGG GCGCGGGGCG ACAGGCCCTT GCTCGGCGCG TCGTTTGAGC ACCGCGGGCG 240
30     CCGATGTGCG CCGCGCCCGG TTAGGATGAG TCTCGGGTCG GCGGAGGAGC CGCCGAGCCG 300
      GCCGCGCGCC GAGCCGCGGG CAGGAGCCTC GGGAGCCGCC GCGCGCCCGC CCGCCGCGCCG 360
      GCCGGGCCCC GACCCGCCCC GCGCGCCCCG GGGCCCCCGA CACACATGAG ATTCTTCAGG 420
      CTCACCTTCA AGTGCTTCGT GGACTGCTTC TGACTGCGCC GCCCGCGCCC CGCACCCCGC 480
      GGTCCGCGCG CCGCCCCGTC CCCCGGCCCG GCCCGCCCCC GGGCCCCGGC CGGCCCGCGC 540
35     CCTCGGGGCC CTCGCCGTGC CCGCCGCTGC CCCCGCCCTG ACCGCCCGCC CCCGTGAGGC 600
      GCCGCGACCC CGGCCCGCGG GTGCGGCCCG CCGGGGCCAT GCGGAAGAAG AGCGCCGAGA 660
      ACGGCATCTA TAGCGTGTCC GCGGACGAGA AGAAGGGCCC CCTCATCGCG CCCGGGCCCG 720
      ACGGGGCCCC GCGCAAGGGC GACGGCCCCG TGGGCTTGGG GACACCCGCG GGGCCGCTGG 780
      CCGTGCCGCC GCGCGAGACC TGGACGCGCC AGATGGACTT CATCATGTGC TGCCTGGGCT 840
40     TCGCGGTGGG CTGGGCAAC GTGTGGCGCT TCCCCTACCT GTGCTACAAG AACGGCGGAG 900
      GTGTGTTCTT TATTCCTTAC GTCTGTATCG CCTGTGTTGG AGGAATCCCC ATTTTCTTCT 960
      TAGAGATCTC GCTGGGCCAG TTCATGAAGG CCGGCAGCAT CAATGTCTGG AACATCTGTC 1020
      CCCTGTTCAA AGGCTTGGCG TACGCCTCCA TGGTGATCGT CTTCTACTGC AACACCTACT 1080
      ACATCATGGT GCTGGCCTGG GGCTTCTATT ACCTGGTCAA GTCCTTTACC ACCACGCTGC 1140
45     CTTGGGCCAC ATGTGGCCAC ACCTGGAACA CTCGCACTG CGTGAGATG TTCGCGCATG 1200
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      CCCCTGTCAAT CGAGTCTTGG GAGAACAAAG TCTTGAGGCT GTCTGGGGGA CTGGAGGTGC 1320
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50     CCTACGTGGT CCGGTCTGTG CTGCTGGTGC GTGGAGTGCT GCTGCCTGGC GCCCTGGATG 1500
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      GCCTCCTCGA CCTCCTCCCG GCCTCCTACT ACTTCCGTTT CCAAAGGAG ATCTCTGTGG 1980
      CCCTCTGTGT TGCCCTCTGC TTTGTCTATG ATCTCTCCAT GGTGACTGAT GCGGGGATGT 2040
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      CCTGTATGAT CGGGTACCGA CCTTGCCCTT GGATGAAATG GTGCTGTGCC TTCTTACCCC 2220
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      GAGGGGACAG AGAACCAAGG CAAATATTTC AGCTGGGCTA TACCCCTCTC CCCATCCCTG 3060
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      CCAGTATCAA TTGTGTGAGC TTGGGTGCGA GTGCACGCGT GCGTGAGTAC GGAGAGTATA 3180
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80     GGAGGCTTGT ATTTGTCACA TTTTATAAAA ACTTGAGAGA ATGAGATTTC TGCTTGATA 3300
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      CCTACCTTAC CCCTCTGCCC CTAGCCAAGG AGTGTGAATT TATAGATCTA ACTTTCATAG 3420
      GCAAAACAAA AGCTTCGAGC TGTTCGCTGT GTGTGGATG TGCGTGTGTG 3480
      GTCCCCAGCC CCAGACTGGA TTGAAAAAGT GCATGGTGGG GGCCTCGGGG CTGTCCCCAC 3540
85     GCTGTCCCTT TCCCACTGTA CTGTGGGCA AGAGGCTGCA ATATTCCGTC CTGGGTGTCT 3600
      GGGCTGCTAA CCTGGCCTGC TCAGGCTTCC CACCTGTGTC GGGGCACACC CCCAGGAAGG 3660
      GACCTTGGAC ACGGCTCCCA CGTCCAGGCT TAAGGTGGAT GCACCTCCCG CACCTCCAGT 3720

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CTTCTGTGTA GCAGCTTTAA CCCACGTTTG TCTGTACAGT CCAGTCCCGA GACGGCTGAG 3780
 TGACCCCAAG AAAGGCTTCC CCGACACCCA GACAGAGGCT GCAGGGCTGG GGGTGGGTGA 3840
 GGGTGGCGGG CCTGCGGGGA CATTCTACTG TGCTAAAAAG CCACTGCAGA CATAGCAATA 3900
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Seq ID NO: 67 Protein sequence:
 Protein Accession #: NP_005620.1

1 11 21 31 41 51
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 INVWNICPLF KGLGYASPMI VFYCNYYIM VLAWGFYVLV KSFTTTLFWA TCGHTWNTPD 180
 CVEIFRHEDC ANASLANLTC DQLADRRSPV IEFWENKVL RLSGGLEVPFA LNWEVTLCLL 240
 ACWLVVYFCV WKGVKSTGKI VYFATTFPYV VLVVLLVRGV LLPGALDGI IYYLKPDSKL 300
 GSPQVWIDAG TQIFFSYAIG LGALTALGSY NRFNNNCYKD AIILALINS GTSFFAGFVVF 360
 SILGFMAAEQ GVHISKVAES GPGLAFIAYP RAVTLMVPAP LWAAIFFFML LLLGLDSQFV 420
 GVEGFITGLL DLLPASYYFR FQREISVALC CALCFVIDLS MVTGGGMVVF QLFDDYSASG 480
 TTLWQAFWE CVVVAWYGA DRFMDDIACM IGYRCPWMK WCWSFFTLV CMGIFIFNVV 540
 YYEPLVYNNY VYVWVGWAM GWAFALSSML CVPLHLLGCL LRAKGTMAER WOHLTQPIWG 600
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Seq ID NO: 68 DNA sequence
 Nucleic Acid Accession #: NM_021953.1
 Coding sequence: 178-2469

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Seq ID NO: 69 Protein sequence:
Protein Accession #: NP_068772.1

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LRPQTQTSYD AKRTEVILET LGPKPAARDV NLPKPPGALC BQKRETCADG EAAGCTINNS 180
10     LSNIQWLKRM SSDGLGSRSI KQEMEKEKENC HLEQRQVKVE EPSRPSASWQ NSVSERPPYS 240
YMAMIQFAIN STERKRMTLK DIYTWIEDHF PYFKHIAKPG WKNSIRHNLS LHD MFVRETS 300
ANGKVSFTI HPSANRYLTL DQVFKPLDPG SPQLPEHLES QKRPNPPELR RNMTIKTELP 360
LGARRKMKPL LPRVSSYLVP IQFPVNQSLV LQPSVKVPLP LAASLMSEEL ARHSKRVRIA 420
15     PKVLLAEEGI APLSSAGPGK EEKLLFGEFG SPLLPVQTIK EEEIQPGHEM PHLARPIKVE 480
SPPLEEWSP APSFKESSH SWEDSSQSPT PRPKKSYSGL RSPTRCVSEM LVIQHRERRE 540
RSRSTRKQHL LPPCVDEPEL LFSEGPSTSR WAAELPPFAD SSDPASQLSY SQEVGGPFKT 600
PIKETLPISS TPKSVLERT PESWRLTPPA KVGGLDFSPV QTSQGASDPL PDLGLMDLS 660
TTPQLSAPPL ESPQRLLSSE PLDLISVPFG NSSPSDIDVP KGPSFEPQVS GLAANRSLTE 720
20     GLVLDTMNDS LSKILLDISF PGLDEDPLGP DNINWSQFIP ELQ

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Seq ID NO: 70 DNA sequence
Nucleic Acid Accession #: BC006529.1
Coding sequence: 178-2424

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30     CAGTCTGGAG GGTCCACACT TGTGATTCTC AATGGAGAGT GAAAACGCAG ATTCATAATG 180
AAAACTAGCC CCGTTCGGCC AGTATTCTCT AAAAGACGGA GGCTGCCCTT TCCTGTTCAA 240
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AATCAAGCAG AGGCTCCCAA GGAAGTGGCA GAGTCCAAC TTTGCAAGTT TCCAGCTGGG 360
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35     GCTAATATTC ACAGCATCTG CACAGCACTG ACTGCCAAGG GAAAAGAGAG TGGCAGTAGT 480
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CGGCTCCAAA CCTAACACAG CTATGATGCC AAAAGGACAG AAGTGACCCT GGAGACCTTG 600
GGACCAAAAC CTGCAGCTAG GGTGTGAAT CTTCTAGAC CACCTGGAGC CCTTTGCGAG 660
CAGAAACGGG AGACCTGTGC AGATGGTGAG GCAGCAGGCT GCACTATCAA CAATAGCCTA 720
40     TCCAAACATCC AGTGGCTTCG AAAGATGAGT TCTGATGGAC TGGGCTCCCG CAGCATCAAG 780
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CCTTCGAGAC CATCAGCGTC CTGGCAGAAC TCTGTGTCTG AGCGGCCACC CTACTCTTAC 900
ATGGCCATGA TACAAATTCG CATCAACAGC ACTGAGAGGA AGCGCATGAC TTTGAAAGAC 960
45     ATCTATACGT GGATGTAGGA CCACCTTCCC TACTTTAAGC ACATTGCCAA GCCAGGCTGG 1020
AAGAACTCCA TCCGCCACAA CCTTTCCCTG CACGACATGT TTGTCCGGGA GACGTCTGCG 1080
AATGGCAAGG TCTCCTTCTG GACCATTAC CCAGTGCCA ACCGCTACTT GACATTGGAC 1140
CAGGTGTTTA AGCAGCAGAA ACGACCGAAT CCAGAGCTCC GCCGGAACAT GACCATCAAA 1200
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50     TACCTGGTAC CTATCTCAGT CCCGGTGAAC CAGTCACTGG TGTTCAGGCC CTCGGTGAAG 1320
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GTCCGCAATTG CCCCAGGCTG GCTGCTAGCT GAGGAGGGGA TAGCTCCTCT TTCTTCTGCA 1440
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CAGCATATCA AGAGGAGGAA AATCCAGCCT GGGGAGGAAA TGCCACACTT AGCGAGACCC 1560
55     ATCAAAGTGG AGAGCCCTCC CTTGGAAGAG TGGCCCTCCC CGGCCCATC TTTCAAAGAG 1620
GAATCATCTC ACTCCTGGGA GGATTCGTCC CAATCTCCCA CCCCAAGACC CAAGAAGTCC 1680
TACAGTGGGC TTAGGTCCCC AACCGGTGT GTCTCGGAAA TGCTTGATGT TCAACACAGG 1740
GAGAGGAGGG AGAGGAGCCG GTCTCGGAGG AAACAGCATC TACTGCCTCC CTGTGTGGAT 1800
GAGCCGGAGC TGCTCTTCTC AGAGGGGGCC AGTACTTCCC GCTGGGCC3C AGAGCTCCCG 1860
TTCCAGCAGC ACTCCTCTGA CCCTGCCTCC CAGCTCAGCT ACTCCAGGA AGTGGGAGGA 1920
60     CCTTTAAGAA CACCCATTAA GGAACCGCTG CCCATCTCCT CCACCCCGAG CAAATCTGTC 1980
CTCCCAAGAA CCCCTGAATC CTGGAGGCTC ACGCCCCAG CCAAAGTAGG GGGACTGGAT 2040
TTCAGCCAG TACAAACCCC CCAGGGTGCC TCTGACCCTT TGCCTGACCC CCTGGGGCTG 2100
ATGGATCTCA GCACCACTCC CTGCAAAAGT GCTCCCCCCC TTGAATCACC GCAAAGGCTC 2160
CTCAGTTTCA AACCCCTAGA CCTCATCTCC GTCCCTTTTG GCAACTCTTC TCCCTCAGAT 2220
65     ATAGACGTCC CCAAGCCAGG CTCGCCGAG CCACAGGTTT CTGGCCTTGC AGCCAATCGT 2280
TCTCTGACAG AAGGCCTGGT CCTGGACACA ATGAATGACA GCCTCAGCAA GATCCTGCTG 2340
GACATCAGCT TTCTCTGGCT GGACGAGGAC CCAGTGGGCC CTGACAACAT CAACTGGTTC 2400
CAGTTTATTC CTGAGCTACA GTAGAGCCCT GCCCTTGCCC CTGTGCTCAA GCTGTCCACC 2460
ATCCCGGCA CTCGAAGGCT CAGTGCACCC CAAGCCTCTG AGTGAGGACA GCAGGCAGGG 2520
70     ACTGTTCTGC TCCTCATAGC TCCCTGCTGC CTGATTATGC AAAAGTAGCA GTCACACCCT 2580
AGCCACTGCT GGGACCTTGT GTTCCCCAAG AGTATCTGAT TCCTCTGCTG TCCCTGCCAG 2640
GAGCTGAAGG GTGGGAACAA CAAAGGCAAT GGTGAAAAGA GATTAGGAAC CCCCAGCCT 2700
GTTTCCATTC TCTGCCAGC AGTCTCTTAC CTTCCTGAT CTTTGAGGG TGCTCCGTGT 2760
75     AAATAGTATA AATTCCTCAA ATTATCTCT AATTTATAAT GTAAGCTTAT TTCCTTAGAT 2820
CATTATCCAG AGACTGCCAG AAGGTGGGTA GGATGACCTG GGGTTTCAAT TGACTTCTGT 2880
TCTTGTCTTT TAGTTTGTAG AGAAGGGAAG ACCTGCAGTG CACGGTTTCT TCCAGGCTGA 2940
GGTACCTGGA TCTTGGGTTT TTAAGTGAGG GAGCCAGAC AAGTGGATCT GCTTGCCAGA 3000
GTCCTTTTTC CCCCTCCCTG CCACCTCCCC GTGTTTCCAA GTCAGCTTTC CTGCAAGAAG 3060
80     AAATCCTGGT TAAAAAAGTC TTTTGTATTT GGTGAGGAGT TGAATTTGGG GTGGGAGGAT 3120
GGATGCAACT GAAGCAGAGT GTGGGTGCCC AGATGTGCGC TATTAGATGT TTCTCTGATA 3180
ATGTCCCAAA TCATACCAGG GAGACTGGCA TTGACGAGAA CTCAGGTGGA GGCTTGAGAA 3240
GGCCGAAAGG GCCCTGACC TGCCTGGCTT CCTTAGCTTG CCCCTCAGCT TTGCAAAGAG 3300
CCACCTAGG CCCAGCTGA CCGCATGGGT GTGAGCCAGC TTGAGAACAC TAACTACTCA 3360
85     ATAAAGCGA AGGTGAAAAA AAAAAA AAAAAA

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Seq ID NO: 71 Protein sequence:
Protein Accession #: AAH06529.1

1	11	21	31	41	51	
MKTSFRRPLI	LKRRRLPLPV	QNAPSETSEE	EPKRSPAQQE	SNQAEASKEV	AESNSCKFPA	60
GIIKIINHPTM	PNTQVVAIPN	NANIHSIITA	LTAKGKESGS	SGPNKFILIS	CGGAPTQPPG	120
LRPQTQTSYD	AKRTEVTLET	LGPKPAARDV	NLPRPPGALC	EQKRETCADG	EAAGCTINNS	180
LSNTQWLKRM	SSDGLGSRSI	KQEMEEKENC	HLEQRQVKVE	EPSRPSASWQ	NSVSERPPYS	240
YMAIIQFAIN	STERKRMTLK	DIYTWIEDHF	PYFKHIAKPG	WKNSIRHNLS	LHDMFVRETS	300
ANGKVSFWTI	HPSANRYLT	DQVFKQKRP	NPELRNMTI	KTELPLGARR	KMKPLLPRVS	360
SYLVPIQFPV	NQSLVLQPSV	KVPLPLAASL	MSSELARHSK	RVRIAPKVLL	AEEGIAPLSS	420
AGPGKEEKL	FGEGFSPLLP	VQTIKEEIQ	PGEEMPHLAR	PIKVESPPLE	EWSPSPSPFK	480
EESHSWEDS	SQSPTPRPKK	SYSGLRSPTR	CVSEMLVIQH	RERRERSRSR	RKQHLPLPCV	540
DEPELLFSEG	PSTRWAEL	PFPADSSDPA	SQLSYSQEVG	GPFKTPIKET	LPISTSPSKS	600
VLPRTPEWR	LTPPAKVGG	DFSPVQTPQG	ASDPLPDLG	LMDLSTTPLQ	SAPPLESPQR	660
LLSSEPLDLI	SVPPGNSPFS	DIDVFKPGSP	EPQVSGLAAN	RSLTEGLVLD	TMNDSLSKIL	720
LDISFPGDLE	DPLGPDNINW	SQFIEPLQ				

20 Seq ID NO: 72 DNA sequence
Nucleic Acid Accession #: U74612.1
Coding sequence: 178-2583

1	11	21	31	41	51	
GGCAGGAGGG	GGACCCGGCC	GGTCCGGCGC	GAGCCCCCGT	CCGGGGCCCT	GGCTCGGCC	60
CCAGGTTGGA	GGAGCCCGGA	GCCCGCCTTC	GGAGCTACGG	CCTAACGGCG	GCGCGGACTG	120
CAGTCTGGAG	GGTCCACACT	TGTGATTCTC	AATGGAGAGT	GAAAACGCGAG	ATTCTATAATG	180
AAAACATAGCC	CCCGTCGGCG	ACTGATTCTC	AAAAGACGGA	GGCTGCCCTC	TCCTGTTCAA	240
AATGCCCCAA	GTGAAACATC	AGAGGAGGAA	CCTAAGAGAT	CCCTGCCCA	ACAGGAGTCT	300
AATCAAGCAG	AGGCCTCCAA	GGAAGTGGCA	GAGTCCAAC	CTTGCAAGTT	TCCAGCTGGG	360
ATCAAGATTA	TTAACCACCC	CACCATGCCC	AACACGCAAG	TAGTGGCCAT	CCCCAACAA	420
GCTAATATTC	ACAGCATCAT	CACAGCACTG	ACTGCCAAGG	GAAAAGAGAG	TGGCAGTAGT	480
GGGCCCAACA	AATTCATCCT	CATCAGCTGT	GGGGGAGCCC	CAACTCAGCC	TCCAGGACTC	540
CGGCCTCAAA	CCCAACACG	CTATGATGCC	AAAAGGACAG	AAGTGACCTT	GGAGACCTTG	600
GGACCAAAAC	CTGCAGCTAG	GGATGTGAAT	CTTCTAGAC	CACCTGGAGC	CCTTTGCGAG	660
CAGAAACGGG	AGACTGTGCG	AGATGGTGAG	GCAGCAGGCT	GCACTATCAA	CAATAGCCTA	720
TCCAACATCC	AGTGGCTTCG	AAAGATGAGT	TCTGATGGAC	TGGGCTCCCG	CAGCATCAAG	780
CAAGAGATGG	AGGAAAAGGA	GAATTGTAC	CTGGAGCAGC	GACAGGTTAA	GGTTGAGGAG	840
CCTTCGAGAC	CATCAGCGTC	CTGGCAGAAC	TCTGTGTCTG	AGCGGCCACC	CTACTCTTAC	900
ATGGCCATGA	TACAATTGCG	CATCAACAGC	ACTGAGAGGA	AGCGCATGAC	TTTGAAGAC	960
ATCTATACGT	GGATTGAGGA	CCACTTTCCC	TACTTTAAGC	ACATTGCCAA	GCCAGGCTGG	1020
AAGAACTCCA	TCCGCCACAA	CCTTTCCCTG	CACGACATGT	TTGTCCGGGA	GACGCTCGCC	1080
AATGGCAAGG	TCTCCTTCTG	GACCATTCAC	CCCAGTGCCA	ACCGCTACTT	GACATTGGAC	1140
CAGGTGTTTA	AGCACTGGA	CCCAGGGTCT	CCACAATTGC	CCGAGCACTT	GGAATCACAG	1200
CAGAAACGAC	CGAATCCAGA	GCTCCGCGCG	AACATGACCA	TCAAAACCGA	ACTCCCCCTG	1260
GGCGCACGGC	GGAAGATGAA	GCCACTGCTA	CCACGGGTCA	GCTCATACCT	GGTACCTATC	1320
CAGTTCCCGG	TGAACCAAGT	ACTGGTGTG	CAGCCCTCGG	TGAAGGTGCC	ATTGCCCTTG	1380
GCGGCTTCCC	TCATGAGCTC	AGAGCTTGCC	CGCCATAGCA	AGCGAGTCCG	CATTGCCCCC	1440
AAGGTTTTTG	GGGAACAGGT	GGTGTGTTG	TACATGAGTA	AGTTCTTTAG	TGGCGATCTG	1500
CGAGATTTTG	GTACACCAT	CACCAAGCTG	TTTAATTTTA	TCTTTCTTTG	TTTATCAGTG	1560
CTGCTAGCTG	AGGAGGGGAT	AGCTCCTCTT	TCTTCTGCAG	GACCAGGGAA	AGAGGAGAAA	1620
CTCCTGTTTG	GAGAAGGGTT	TTCTCCTTTG	CTTCCAGTTC	AGACTATCAA	GGAGGAAGAA	1680
ATCCAGCCTG	GAGGGAATA	GCCACACTTA	GCGAGACCCA	TCAAAGTGGA	GAGCCCTCCC	1740
TTGGAAGAGT	GGCCCTCCCC	GGCCCATCT	TTCAAAGAGG	AATCATCTCA	CTCCTGGGAG	1800
GATTTCGTCCC	AATCTCCAC	CCCAGAGCCC	AAGAAGTCTT	ACAGTGGGCT	TAGGTCCCCA	1860
ACCCGGTGTG	TCTCGGAAAT	GCTTGTGATT	CAACACAGGG	AGAGGAGGGA	GAGGAGCCGG	1920
TCTCGGAGGA	AACAGCATCT	ACTGCCTCCC	TGTGTGGATG	AGCCGGAGCT	GCTCTTCTCA	1980
GAGGGGCCCA	GTACTTCCCG	CTGGGCCGCA	GAGCTCCCGT	TCCCAGCAGA	CTCCTCTGAC	2040
CCTGCCTCCC	AGCTTCAGCTA	CTCCCAGGAA	GTGGGAGGAC	CTTTTAAGAC	ACCCATTAA	2100
GAAACGCTGC	CCATCTCCTC	CACCCGAGC	AAATCTGTCC	TCCCCAGAAC	CCCTGAATCC	2160
TGGAGGCTCA	CGCCCCCAGC	CAAAGTAGGG	GGACTGGATT	TCAGCCCACT	ACAAACCTCC	2220
CAGGGTGCCT	CTGACCCCTT	GCCTGACCCC	CTGGGGCTGA	TGGATCTCAG	CACCACTCCC	2280
TTGCAAAAGT	CTCCCCCTCT	TGAATCACCG	CAAAGGCTCC	TCAGTTTCTG	ACCCCTTAG	2340
CTCATCTCCG	TCCCTTTTGG	CAACTCTTCT	CCCTCAGATA	TAGACGTCCC	CAAGCCAGGC	2400
TCCCCTGAGC	CACAGGTTTC	TGGCCTTGCA	GCCAACTCGT	CTCTGACAGA	AGGCCTGGTC	2460
CTGGACACAA	TGAATGACAG	CCTCAGCAAG	ATCTGCTGCT	ACATCAGCTT	TCTTGGCCTG	2520
GACGAGGACC	CACTGGGCCC	TGACAACATC	AACTGGTCCC	AGTTTATTCC	TGAGCTACAG	2580
TAGAGCCCTG	CCCTTGCCCC	TGTGCTCAAG	CTGTCCACCA	TCCCGGGCAC	TCCAAGGCTC	2640
AGTGCACCCC	AAGCCTCTGA	GTGAGGACAG	CAGGCAGGGA	CTGTCTGCT	CCTCATAGCT	2700
CCCTGCTGCC	TGATTATGCA	AAAGTAGCAG	TCACACCCTA	GCCACTGCTG	GGACCTTGTG	2760
TTCCCCAAGA	GTATCTGATT	CCTCTGCTGT	CCCTGCCAGG	AGCTGAAGGG	TGGGAACAAC	2820
AAAGGCAATG	GTGAAAAGAG	ATTAGGAACC	CCCCAGCCTG	TTTCCATTCT	CTGCCAGCA	2880
GTCTCTTACC	TTCCCTGATC	TTTGCAAGGT	GGTCCGTGTA	AATAGTATAA	ATTCTCCAAA	2940
TTATCCTCTA	ATTATAAATG	TAAGCTTATT	TCCTTAGATC	ATTATCCAGA	GACTGCCAGA	3000
AGGTGGGTAG	GATGACCTGG	GGTTTCAATT	GACTTCTGTT	CCTTGCTTTT	AGTTTGTGATA	3060
GAAGGGAAGA	CCTGCAGTGC	ACGTTTCTT	CCAGGCTGAG	GTACCTGGAT	CTTGGGTTCT	3120
TCACCTCAGG	GACCCAGCA	AGTGATCTG	CTTGCCAGAG	TCCTTTTGTG	CCCTCCCTGC	3180
CACCTCCCCG	TGTTTCCAAG	TCAGCTTTCC	TGCAAGAAGA	AATCTGGTT	AAAAAAGTCT	3240
TTTGATTGG	GTCAGGAGTT	GAATTGGGG	TGGGAGGATG	GATGCAACTG	AAGCAGAGTG	3300
TGGGTGCCCA	GATGCGCCT	ATTAGATGTT	TCTCTGATAA	TGTCCTCAAT	CATACCAGGG	3360
AGACTGGCAT	TGACGAGAAC	TCAGGTGGAG	GCTTGAGAAG	GCCGAAAGGG	CCCCTGACCT	3420
GCCTGGCTTC	CTTAGCTTGC	CCCTCAGCTT	TGCAAAAGAGC	CACCCTAGGC	CCCAGCTGAC	3480
CGCATGGGTG	TGAGCCAGCT	TGAGAACACT	AACTACTCAA	TAAAAGCGAA	GGTGGACAAA	3540
AAAAA	AAAAA					

Seq ID NO: 73 Protein sequence:
Protein Accession #: AAC51128.1


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1      11      21      31      41      51
|      |      |      |      |      |
5  MKTSPRRPLI LKRRRLPLPV QNAPSETSEE EPKRSPAQQE SNQAEASKEV AESNSCKFPA 60
   GIKIINHPTM PNTQVVAIPN NANIHSIITA LTAKGKESGS SGPKNKFILIS CGGAPTQPPG 120
   LRPTQTSTYD AKRTEVTLET LGPKPAARDV NLPRPPGALC EQKRETCADG EAAGCTINNS 180
   LSNIQWLKRM SSDGLGSSRSI KQEMEKEKENC HLEQRQVKVE EPSRPSASWQ NSVSEPPFYS 240
   YMAMIQFAIN STERKRMTLK DIYTWIEDHF PYFKHIAKPG WKNRIRHNLS LHDMPFVRETS 300
10  ANGKVSFWTI HPSANRYLTL DOVFKPLDPG SPQLPEHLES QOKRENPELR RNMTIKTELP 360
   LGARRKMKPL LPRVSSYLVP IQFPVNQSLV LQPSVKVPLP LAASLMSEL ARHSKRVRVA 420
   PKVFGQVVF GYMSKFFSGD LRDFGTPTS LFNFIPLCLS VLLAEEGIAP LSSAGPGKEE 480
   KLLFGEFSP LLPVQTIKEE EIQPGEEEMPH LARPIKVESP PLEEWPSAP SFKEESSHSW 540
   BDSSQSPFPR PKKSYSGLRS PTRCVSEMLV IQHRRERRS RSRKQHLLP PCVDEPELLF 600
15  SEGPSTSRWA AELPPPADSS DPASQLSYSQ EVGGPFKTP I KETLPISTP SKSVLPRTPE 660
   SWRLTPPAKV GGLDFSPVQT SQGASDPLPD PLGLMDLSTT PLQSAPPLES PQRLLSSEPL 720
   DLISVPFGNS SPDLIDVPKP GSPEPQVSGL AANRSLTEGL VLDTMNDSL S KILLDISFPG 780
   LDEDPLGPDN INWSQFIPEL Q

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Seq ID NO: 74 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 111-416

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1      11      21      31      41      51
|      |      |      |      |      |
25  GGGGAAGAGCC AGGCTGAGCC TTATAAAGGA CTGCTCTTTG TCCAAACACA CACATCTCAC 60
   TCATCCTTCT ACTCGTGACG CTTCCAGCT CTGGCTTTTT GAAAGCAAAG ATGAGCAACA 120
   CTAAGCTGA GAGGTCCATA ATAGGCATGA TCGACATGTT TCACAAATAC ACCGACGTG 180
   ATGACAAGAT TGAGAAGCCA AGCCTGCTGA CGATGATGAA GGAGAACTTC CCCAACTTCC 240
   TTAGTGCCCTG TGACAAAAAG GGCACAAATT ACCTCGCCGA TGTCTTTGAG AAAAAGGACA 300
30  AGAATGAGGA TAAGAAGATT GATTTTCTG AGTTTCTGTC CTTGCTGGGA GACATAGCCA 360
   CAGACTACCA CAAGCAGAGC CATGGAGCAG CGCCTGTTC CGGGGCGAGC CAGTGACCCA 420
   GCCCCACCAA TGGGCCTCCA GAGACCCAG GAACAATAA ATGTCTTCTC CCACCAGA

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Seq ID NO: 75 Protein sequence:
Protein Accession #: Eos sequence

```

1      11      21      31      41      51
|      |      |      |      |      |
40  MSNTQAERSI IGMIDMFHYK TRRDDKIEKP SLLTMMKENF PNFLSACDKK GTNYLADVFE 60
   KKDKNEDKKI DFSEFLSLLG DIATDYHKQS HGAAPCSGGS Q

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Seq ID NO: 76 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 111-416

```

1      11      21      31      41      51
|      |      |      |      |      |
50  GGGGAAGAGCC AGGCTGAGCC TTATAAAGGA CTGCTCTTTG TCCAAACACA CACATCTCAC 60
   TCATCCTTCT ACTCGTGACA CTTCCAGTT CTGGCTTTTT GAAAGCAAAG ATGAGCAACA 120
   CTAAGCTGA GAGGTCCATA ATAGGCATGA TCGACATGTT TCACAAATAC ACCGGACGTG 180
   ATGGCAAGAT TGAGAAGCCA AGCCTGCTGA CGATGATGAA GGAGAACTTC CCCAATTTC 240
   TCAGTGCCCTG TGACAAAAAG GGCATACATT ACCTCGCCAC TGTCTTTGAG AAAAAGGACA 300
55  AGAATGAGGA TAAGAAGATT GATTTTCTG AGTTTCTGTC CTTGCTGGGA GACATAGCCG 360
   CAGACTACCA CAAGCAGAGC CATGGAGCGG CGCCTGTTC TGGGGGAAGC CAGTGATCCA 420
   GCCCCACCAA GGGGCCTCCA GAGACCCAG GAACAATAAG TGTCTCTCTC CACCAGA

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Seq ID NO: 77 Protein sequence:
Protein Accession #: XP_048124.1

```

1      11      21      31      41      51
|      |      |      |      |      |
60  MSNTQAERSI IGMIDMFHYK TGRDGKIEKP SLLTMMKENF PNFLSACDKK GIHYLATVFE 60
   KKDKNEDKKI DFSEFLSLLG DIAADYHKQS HGAAPCSGGS Q

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Seq ID NO: 78 DNA sequence
Nucleic Acid Accession #: Z73678.1
Coding sequence: 253-2433

```

1      11      21      31      41      51
|      |      |      |      |      |
75  GGGGTGGTGC AGGGCAGGGG TGGTATATCC TGTCTGACGG AGGGCGGGCC TCGCCAGTGC 60
   CAGAGAGGGA CGAACCAGGG TGGAGCGGCC AGGAGCAGCT GCAGGGAGCC CTCACGCGGA 120
   CCTCGCACTC TATGGCCGTA GGGAGCCGCT GAGAGCGAGA AGAGCACGCT CCTGCCCGCC 180
   CGCTGCACCG CACCTCGCCT CGCCTCTCTG CTCTCCTAGG CCCCAGCCGC GCGCCACCCG 240
   CCTCCGCGCA CCATGAACCA CTCGCCGCTC AAGACCGCCT TGGCGTACGA ATGCTTCCAG 300
   GACCAGGACA ACTCCACGTT GGCTTTGCCG TCGGACCAA AGATGAAAC AGGCACGTCT 360
   GGCAGGCAGC GCGTGACGAG GCAGGTGATG ATGACCGTCA AGCGGCAGAA GTCCAAGTCT 420
   TCCAGTCCGT CCACCTGAG CCACTCCAAT CGAGGTTCCA TGTATGATGG CTTGGCTGAC 480
80  AATTCAACT ATGGGACCAC CAGCAGGAGC AGCTACTACT CCAAGTTCCA GGCAGGGAAT 540
   GGCTCATGGG GATATCCGAT CTACAATGGA ACCCTCAAGC GGGAGCCTGA CAACAGGCGC 600
   TTCAAGTCCCT ACAGCCAGAT GGAGAACTGG AGCCGGCACT ACCCCGGGG CAGCTGTAA 660
   ACCACCGGGC CAGGAGCGCA CATCTGCTTC ATGCAGAAAA TCAAGGCGAG CCGCAGTGAG 720
85  CCCGACCTCT ACTGTGACCC ACGGGGCACC CTGCGCAAGG GCACGCTGGG CAGCAAGGGC 780
   CAGAAGACCA CCCAGAACC CTACAGCTTT TACAGCACCT GCAGTGGTCA GAAGGCCATA 840
   AAGAAGTGCC CTGTGCGCCC GCCCTCTTGT GCCTCCAAGC AGGACCTGT GTATATCCCG 900

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	CCCATCTCCT	GCAACAAGGA	CCTGTCTCTT	GGCCACTCTA	GGGCCAGCTC	CAAGATCTGC	960
	AGTGAGGACA	TGAGTGCAG	TGGGTGACC	ATCCCAAGG	CTGTGCAGTA	CCTGAGCTCC	1020
	CAGGATGAGA	AGTACCAAGG	CATTGGGGCC	TATTACATCC	AGCATACCTG	CTTCCAGGAT	1080
5	GAATCTGCCA	AGCAACAGGT	CTATCAGCTG	GGAGGCATCT	GCAAGCTGGT	GGACCTCCTC	1140
	CGCAGCCCCA	ACCAACAAGT	CCAGCAGGCC	GCGGCAGGGG	CCCTGCGCAA	CCTGGTGTTC	1200
	AGGAGCACCA	CCAACAAGCT	GGAGACCCGG	AGGCAGAATG	GGATCCGCGA	GGCAGTCAGC	1260
	CTCCTGAGGA	GAACCGGGAA	CGCCGAGATC	CAGAAGCAGC	TGACTGGGCT	GCTCTGGAAC	1320
	CTGTCTTCCA	CTGACGAGCT	GAAGGAGGAA	CTCATTGCCG	ACGCCCTGCC	TGTTCTGGGC	1380
10	GACCCGCTCA	TCATTCCCTT	CTCTGGCTGG	TGCGATGGCA	ATAGCAACAT	GTCCCGGGAA	1440
	GTGGTGGACC	CTGAGGTCTT	CTTCAATGCC	ACAGGCTGCT	TGAGGAACCT	GAGCTCGGCC	1500
	GATGCAGGCC	GCCAGACCAT	GCGTAACTAC	TCAGGGCTCA	TTGATTCCCT	CATGGCCCTAT	1560
	GTCCAGAACT	GTGTAGCGGC	CAGCCGCTGT	GACGACAAGT	CTGTGGAAAA	CTGCATGTGT	1620
	GTTCGTGACA	ACCTCTCCTA	CCGCCTGGAC	GCCGAGGTGC	CCACCCGCTA	CCGCCAGCTG	1680
15	GAGTATAACG	CCCGCAACGC	CTACACCGAG	AAGTCTCTCA	CTGGCTGCTT	CAGCAACAAG	1740
	AGCGACAAGA	TGATGAACAA	CAACTATGAC	TGCCCCCTGC	CTGAGGAAGA	GACCAACCCC	1800
	AAGGGCAGCG	GCTGGTGTGA	CCATTCAAGT	GCCATCCGCA	CCTACCTGAA	CCTCATGGGC	1860
	AAGAGCAAGA	AAGATGCTAC	CCTGGAGGCC	TGTGCTGGTG	CCCTGCAGAA	CCTGACAGCC	1920
	AGCAAGGGGC	TGATGTCCAG	TGGCATGAGC	CAGTTGATTG	GGCTGAAGGA	AAAGGGCCTG	1980
20	CCACAAATTG	CCCGCTTCC	GCAATCTGGC	AACCTCTGAT	TGGTCCGGTG	CCGAGCCCTC	2040
	CTCCTGAGCA	ACATGTCCCG	CCACCTCTG	CTGCACAGAG	TGATGGGGAA	CCAGGTGTTC	2100
	CCGGAGGTGA	CCAGGCTCCT	CACCAGCCAC	ACTGGCAATA	CCAGCAACTC	GGAAGACATC	2160
	TTGTCTCTGG	CCTGCTACAC	TGTGAGGAAC	CTGATGGCCT	CGCAGCCACA	ACTGGCCAAG	2220
	CAGTACTTCT	CCAGCAGCAT	GCTCAACAAC	ATCATCAACC	TGTGCCGAGG	CAGTGCCTCA	2280
25	CCCAAGGCCG	CAGAGCTTGC	CCGGCTTCTC	CTGTCTGACA	TGTGGTCCAG	CAAGGAAGTG	2340
	CAGGGTGTCC	TCAGACAGCA	AGGTTTCGAT	AGGAACATGC	TGGGAACCTT	AGCTGGGGCC	2400
	AACAGCCTCA	GGAACTTCAC	CTCCCGATTG	TAAGAAGAGA	CTGTCCAAGC	AAGTTAGGCT	2460
	TGCAGGAAGA	TATGACCCAG	CTGAGAAGCC	CTCAGGCCCT	GCTGGATGGG	GTTTCTGTCT	2520
	CATCCTGTGC	AGTATTGGGA	AAAGTTTACA	AGAAACTGAG	AAGAAACCTA	AAAACCTGTG	2580
30	ATAGTGGAAA	GATTTTGTGA	TTTTTTTTTT	CCTTGGGGAA	ACTGGCAGGC	AATGGGGGTT	2640
	AGGGAGGTTG	GGGCGGGGGG	GGCTTTCTTG	AGTTAAAGGG	GCTTATATGT	GATGTCAATA	2700
	TTTCTTCTCT	TGAGAAATGG	TATATATATG	TGTCTAATGT	AAGTGTGTGC	ATGCATGTGC	2760
	GCGTGCATGT	GTGTGTGTGT	GAGTGTCTTA	AAGCATAACC	ACAAACTGCA	AAAAGCTAGG	2820
	TAAGCTATTT	TGTTGACAGT	CATAAGGTGG	TGAAAAGGAC	TCTCCTGTGT	TTCTTACTCA	2880
35	TAGGCAAGGA	CAACATGTGC	TTTTTGGTGA	GCTGCTCATA	ATTCCTGAAA	TGTGTGGTGC	2940
	CAGGGCAAGG	GGGCGATCAC	TGCAGTCAGG	CCCTCAGAGG	AGTCTGTGAG	GCTTCTTACC	3000
	AGTGTCTCTC	AAGGTGTCAG	GAGTAACTGG	GGCTGGGCCA	GCCTCCCCCC	TTACAAGGCT	3060
	GCTTTCCACG	AAGGAGGTTC	TGGTGTATCT	CATGGGAGAA	TCTGGGTGTG	CTGTAGTGTG	3120
	ACCCCTCCAG	CAGCGCCACA	AGGACTGAGG	TTGGGTAGGT	GTGAGGTTC	AGAGGACAGC	3180
40	AGGACACTCT	CGCATACTTT	GCCAAATGAG	GCCTGCTCAG	AGGAGTAGGA	GCTGAAAGAT	3240
	GGTGCTTCTC	ACCTCTTGG	GCTGTGTGCC	CATCAGAGCA	GGCTCAGCCT	GCAAGGGCCC	3300
	TGCATTACGA	GGTCTGTGTA	TCTACTTGTT	GCAGGAGAAA	GAAGGTAAAA	AATGATTTTT	3360
	TTAAGAAAAG	CTATTTTATT	GCAGCTCTTT	CCCAAGAGCT	GTTCTGGGAA	TGGCTGGTCT	3420
45	TCATATTTCC	AGTGGAGAGG	GGAAACAAGT	GGGCTGGGCA	TATACCTATT	CCGGTCTCTA	3480
	GTGGGATGGA	GTTGGGGTAT	AGAAATTAAC	CAGGAAGATG	TTTCCACCAA	GCCTGCTGTG	3540
	AGTCAATTGA	GGGAGTGTTT	GGGTCCACAG	AGACTTGGAC	GGGGGGAGTT	TGGGTAGACT	3600
	AGGAAAGGAA	AGTGGCCATAT	CAGGGTACCG	GTACCGGCAA	GCTCACATCT	CAGCCAGGGG	3660
	CCATGCCCCA	CTTCCCTTGA	CCCCAGCTGT	CTTGTCTCCA	CTCTGTGAAA	CCCACAGGGG	3720
	ATGTGATAAA	CAGGCTTATT	AGGGGTATCA	GCCACGTGCA	GCCCCAGAC	TCTGTGCACT	3780
50	TCAGACCAGC	AGCAGCAGGA	GGGCTCCCGA	GGGCTTATG	AGAAAACCTG	TGTGGACATC	3840
	CCTTGGTGTA	CACTAAGACA	GAGCAGAGCC	CAGCGCTCCC	AAGCCTTCTT	CCTTCCAGCT	3900
	TCTACCTCCA	TGCTAGCATT	GCTGGTGTTA	GAGAGGAATT	AACCTTCTGG	TCTGTGCCCT	3960
	TCTCTAGAAG	AATATAAGAT	GCTCCTCCTC	CTCACCCCTT	CTCAGCCTCC	TCCCAAGTCT	4020
	TCTCTTCTG	CACCAACCCC	GAGTCCAAAC	CCACCTCTTG	CCCCAGCATT	CAGGCTGGAA	4080
55	AACACTGATG	TGGACTCAGT	ATGACAACCT	AGATGGGGGA	AGCCAGACAT	GTGAGGACGC	4140
	TGTCTCTCCA	GAGGTGTCCC	CGGCTGTTAG	CCAGCTGTGC	TGTGGTGTCT	TGGGTCTGTC	4200
	ATACCTCTCC	TGCTTGTCTG	TCACACTGGG	AGGCCCACTC	CTGGCTCACC	TCTCCCTCTC	4260
	AGGGACCCAC	GTGGGAGCCT	GGATCCCTGG	ACTGTCTCTG	GCATAGGTTT	CAGGGGCCTC	4320
	CTTTGTTGTC	ATCAGAACCC	AGAGGAATTC	TTCTCCTAAA	AAATACGTAT	GGCATAACCA	4380
60	TCTGTGCGGG	GCAGTGTCTC	AAGCACTTAG	ACTACATCAG	GGAAAGAACAC	AGACCAACAT	4440
	CCCGTCTCTA	TGCGGCTTAT	GTTTTCTGGA	GGAAAGTGA	GACACAAGTC	CTTGGCTTTA	4500
	GGGCTCCCCC	GCTGGGGGCG	TGTGCACTCC	GGTCAGGGCG	GGAGGGGAAA	TGCACCGCTG	4560
	CATGTGAACC	TTACCAGCCC	AGGCGGATGC	CCCTTCCCCT	TAGCACTACC	CTGGCTCTCT	4620
	GCATCCCCCT	GCCTCATGTT	CCTCCCACCT	TCAAAGAATG	AAGAGCCCCA	TGGGCCCAGC	4680
65	CCCTGCCCTG	GGAAACCAAG	AGCCCTCCAG	ACCTCAGGGG	CTGAGGCAGA	CTATTAGGGC	4740
	AGGGCTGACT	TTGGTGACAC	TGCCCATTC	CTCTCAGGCC	AGCTCAGGTC	ACCCGGGCTC	4800
	CTGACCCAGG	CCTGTCACTT	TGAGAGGGGC	AAAACGTAGA	GGGGCTTTTC	CTAGAGAAAG	4860
	AGAAACAAGG	GCTTGCCAGG	CTTCATGTAG	CCGACACACG	TCTCAGGATT	TTAAGTCCAC	4920
	ATTGGCCTCA	CACTAGCCTA	GGCCAATGCC	CAAAATAAGG	AGTTCCAATT	TGGGGCCAAA	4980
70	TGAGGAAGGA	CACAGACTCT	GCCCTGGGAT	CTCCTGTGCT	AGCGGCCAAT	GACAAATCCA	5040
	GTCATTGGCC	ACCAGCCACC	TCTGCAGTGG	GGACCACACT	AGCAGCCCTG	ACTCCACACT	5100
	CCTCTTGGGG	ACCCAAGAGG	CAGTGTGTCT	GTCTGCGTGT	CCACCTTGGA	ATCTGGCTGA	5160
	ACTGGCTGGG	AGGACCAAGA	CTGCGGCTGG	GGTGGGCAGG	GAAGGGGAAG	CGGGGGCTGC	5220
	TGTGAGGGAT	CTTGAGCTTT	CCCTGTAGCC	CACCTTCCCC	TTGCTTCATG	TTGTAGAGGG	5280
75	AACCTTGTGC	CGGCCAGGCC	CAGTTTCCCT	GTGTGATACA	CTAATGTATT	TGCTTTTTTT	5340
	GGAATAGAG	AAAAACAATA	AATTGCTAGT	GTTTCTTTGA	AAAAAAAAAA		

Seq ID NO: 79 Protein sequence:
Protein Accession #: CAA98022.1

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	TLSHSNRSGM	YDGLADNYNY	GTTSRSSYS	KFQAGNGSWG	YPIYNGTLKR	EPDNRFFSSY	120
	QSMENWSRHY	PRGSCNNTGA	GDICFMQKI	KASRSEPDLY	CDPRGTLRKG	TLGSKGQKTT	180
85	QNRYSFYSTC	SQOKAIKKCP	VRPPSCASKQ	DPVYIPIISC	NKDLSPGHRS	ASSKICSEDI	240
	ECSGLTIPKA	VQYLSSQDEK	YQAI GAYYIQ	HTCFQDESAK	QVYQLGLGIC	KLVDLLRSPN	300
	QNVQQAAGGA	LRNLVFRSTT	NKLETRRQNG	IREAVSLLR	TGNAEIQKQL	TGLLWNLSST	360

DELKEELIAD ALPVLADRV I PFSGWCDGN SNMSREVVDV EVFFNATGCL RNLSSADAGR 420
 QTMRNYSGLI DSLMAYVQNC VAASRCDDKS VENCMLVHNL LSYRLDAEVP TRYRQLEYNA 480
 RNAYTEKSST GCFSNKSDKM MNMYDCPLP EETNPKGSG WLYHSDAIRT YLNLMGKSKK 540
 5 DATLEACAGA LQNLTASKGL MSSGMSQLIG LKEKGLPQIA RLLQSGNSDV VRSGASLLSN 600
 MSRHPLLRHV MGQVFFPEVT RLLTSHTGNT SNSDILSSA CYTVRNLMAS QPQLAKQYFS 660
 SSMNLNINIINL CRSSASPKAA EAARLLLSDM WSSKELQGV L RQQGFDRNML GTLAGANSLR 720
 NFTSRF

Seq ID NO: 80 DNA sequence
 Nucleic Acid Accession #: NM_006516.1
 Coding sequence: 180-1658

1 11 21 31 41 51
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 CGCACGCCCG TCGCCACCCG CGTACCCGGC GCAGCCAGAG CCACCAAGCG AGCGCTGCCA 180
 20 TGGAGCCCGAG CAGCAAGAGG CTGACGGGTC GCCTCATGCT GGCTGTGGGA GGAGCAGTGC 240
 TTGGCTCCCT GCAGTTTGGC TACAACACTG GAGTCATCAA TGCCCCCAG AAGGTGATCG 300
 AGGAGTTCTA CAACGAGACA TGGTCCACC GCTATGGGGA GAGCATCTTG CCCACCAAGC 360
 TCACCACGCT CTGGTCCCTC TCAGTGGCCA TCTTTTCTGT TGGGGGCATG ATTGGCTCCT 420
 TCTCTGTGGG CCTTTTCGTT AACCGCTTTG GCCGGCGGAA TTCATGCTG ATGATGAACC 480
 TGCTGGCCTT CGTGTCCGCC GTGCTCATGG GCTTCTCGAA ACTGGGCAAG TCCTTTGAGA 540
 25 TGCTGATCCT GGGCCGCTTC ATCATCGGTG TGTACTGCGG CCTGACCACA GGCTTCGTGC 600
 CCATGTATGT GGGTGAAGTG TCACCCACAG CCTTTCGTGG GGGCCTGGGC ACCCTGCACC 660
 AGCTGGGCAT CGTCGTCCGC ATCCTCATCG CCCAGGTGTT CGGCCTGGAC TCCATCATGG 720
 GCAACAAGGA CCTGTGCCCC CTGCTGCTGA GCATCATCTT CATCCCGGCC CTGCTGCAGT 780
 GCATCGTGCT GCCCTTCTGC CCCGAGAGTC CCCGCTTCTT GCTCATCAAC CGCAACGAGG 840
 30 AGAACCGGGC CAAGAGTGTG CTAAGAAGC TGGCGGGGAC AGCTGACGTG ACCCATGACC 900
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 35 CTGTCTGTGC GCTGTTTGTG GTGAGCGAG CAGGCCGGCG GACCCTGCAC CTCATAGGCC 1200
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 40 GCTTCCAGTA TGTGGAGCAA CTGTGTGGTC CCTACGTCTT CATCATCTTC ACTGTGCTCC 1500
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 45 AACCTGACAG ATGTGACCGG AGCCGGCCCT GGGGCTCCTT TCTCCAGCCA GCAATGATGT 1800
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 AAATCTATTG AGACAAGCAA CAGGTTTAT AATTTTATA TTACTGATTT TGTATTTTTT 1920
 ATATCAGCCT GAGTCTCCTG TGCCCAATC CCAGGCTTCA CCCTGAATGG TTCCATGCCT 1980
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 50 CTGGACCTAT GTCCTAAGGA CACACTAATC GAACATGAA CTACAAAGCT TCTATCCAG 2100
 GAGGTGGCTA TGGCCACCGG TTCTGTGGC CTGGATCTCC CCATCTAGG GGTGAGGCTC 2160
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 GCCGGGTCTT AGTCTCCTTT GCACTGAGGG CCACACTATT ACCATGAGAA GAGGGCCTGT 2340
 55 GGGAGCCTGC AAACCTACTG CTCAGAAGA CATGGAGACT CCTGCCCTGT TGTGTATAGA 2400
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 60 TTTGGATGG AGTGAGACAG AAGTAAAGTG GGTGCAACC ACTGCAACGG CTTAGACTTC 2640
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 TTTGATCCCT GTTACCAAGA GAATATATAC ATTCTTTATC TTGACATCA AGGCATTCTT 2760
 ATCACATATT TGATAGTTGG TGTTCAAAA AACACTAGTT TTGTGCCAGC CGTGATGCTC 2820
 AGGCTTGAAA TCGATTATT TTGAATGTGA AGGGAA

Seq ID NO: 81 Protein sequence:
 Protein Accession #: NP_006507.1

1 11 21 31 41 51
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 LTTWLSLSVA IFSVGGMIGS FSVGLFVNRF GRRNSMLMMN LLAPVSAVLM GFSKLGKSFE 120
 MLILGRFTIG VYCLTTFGV PMYVGEVSPT AFRGALGTLH QLGIIVGILI AQVFGLD SIM 180
 GNKDLWPLLL SIIFIPALLQ CIVLPFCPEP PRFLINRNE ENRAKSVLKK LRGTADVTHD 240
 75 LQEMKEESRQ MMREKKVITL ELFRSPAYRQ PILIAVVLQL SQQLSGINAV FYYSTSI FEK 300
 AGVQPVYAT IGSIVNTAF TVVSLFVVER AGRRTLHLIG LAGMAGCAIL MTIALALLEQ 360
 LPWMSYLSIV AIFGFVAFPE VGPPIPIWFI VAELEFSQGR PAATAVAGFS NWTNSNFIVGM 420
 CFQYVEQLCG PYVEIIFIVL LVLEFFIFTYF KVPETKGRTF DEIASGFRQG GASQSDKTPE 480
 ELFHPLGADS QV

Seq ID NO: 82 DNA sequence
 Nucleic Acid Accession #: BC001291
 Coding sequence: 44-541

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AGATCCAGAG GACTCCGAGC GAACGGACGA GGGTGACAAT AGAGTGTGGT GTCATGTTTG 180
 TGAGAGAGAA AACACTTTTC AGTGCCAGAA CCCAAGGAGG TGCAAAATGGA CAGAGCCATA 240
 CTGCGTTATA GCGGCCGTGA AAAATATTTCC ACGTTTTTTC ATGGTTGCGA AGCAGTGCTC 300
 CGCTGGTGTG CGAGCGATGG AGAGACCCAA GCCAGAGGAG AAGCGGTTTC TCCTGGGAAGA 360
 GCCCATGCCC TTCTTTTACC TCAAAGTGTG TAAATTCGC TACTGCAATT TAGAGGGGCC 420
 ACCTATCAAC TCATCAGTGT TCAAAGAATA TGCTGGGAGC ATGGGTGAGA GCTGTGGTGG 480
 GCTGTGGCTG GCCATCCTCC TGCTGCTGGC CTCCATTGCA GCGCGCCTCA GCCTGTCTTG 540
 AGCCACGGGA CTGCCACAGA CTGAGCCTTC CGGAGCATGG ACTCGCTCCA GACCGTTGTC 600
 ACCTGTTGCA TTAACACTGT TTTCTGTTGA TTACCTCTTG GTTTGACTTC CCAGGGTCTT 660
 GGGATGGGAG AGTGGGGATC AGGTGTCAGT GGCCTTTAAC CCTCAAGGGT TCTTTAACTC 720
 ACATTCAGAG GAAGTCCAGA TCTCCTGAGT AGTGATTTTG GTGACAAATT TTTCTCTTTG 780
 AAATCAAACC TTGTAACCTCA TTTATTGCTG ATGGCCACTC TTTTCTCTGA CTCCCCTCTG 840
 CCTCTGAGGG CTTCACTATT GATGGGGAGG GAGGCCTAAG TACCACTCAT GGAGAGTATG 900
 TGCTGAGATG CTTCCGACCT TTCAGGTGAC GCAGGAACAC TGGGGGAGTC TGAATGATTG 960
 GGGTGAAGAC ATCCCTGGAG TGAAGGACTC CTCAGCATGG GGGGCAGTGG GGCACACGTT 1020
 AGGGCTGCCC CCATTCCAGT GGTGGAGGCG CTGTGGATGG CTGCTTTTCC TCAACCTTTC 1080
 CTACCAGATT CCAGGAGGCA GAAGATAACT AATTGTGTTG AAGAACTTA GACTTCACCC 1140
 ACCAGCTGGC ACAGGTGCAC AGATTCTATA ATTCCACAC GTGTGTGTTT AACATCTGAA 1200
 ACTTAGGCCA AGTAGGAGAG ATCAGGTTAA ATGGCGTTCA TTTCTCTGTT AAGATGCAGC 1260
 CATCATGGG GAGCTGAGAA ATCAGACTCA AAGTTCACC AAAACAAAT ACAAGGGGAC 1320
 TTCAAAAGTT CACGAAAAA AAAAAAATA AAAAAAATA AAAAAAATA AAA

Seq ID NO: 83 Protein sequence:

Protein Accession #: AAH01291

1 11 21 31 41 51
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 KWTEPYCVIA AVKIFPRFFM VAKQCSAGCA AMERPKPEEK RFLLEEMPMPF FYLKCKCKIRY 120
 CNLEGGPPINS SVFKEYAGSM GESCGGLWLA ILLLLASIAA GLSLSL

Seq ID NO: 84 DNA sequence

Nucleic Acid Accession #: NM_022893.1

Coding sequence: 229-2726

1 11 21 31 41 51
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 CGCCCGCCGC CGCCCGCCGC GCCGCCCGCG CCCGCCCGCG AGCCCAACAT GTCTCGCCGC 240
 AAGCAAGGCA AACCCAGCA CTTAAGCAAA CGGGAATTCT CGCCCGAGCC TCTTGAAGCC 300
 ATTCTTACAG ATGATGAACC AGACCACGGC CCGTTGGGAG CTCACAGAAGG GGATCATGAC 360
 CTCCTCACCT TGCGGCAGTG CCAGATGAAC TTCCCATGCG GGGACATTCT TATTTTATC 420
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 GGAGCTCTAA TCCCCACGCC TGGGATGAGT GCAGAAATATG CCCCAGAGG TATTTGTAAA 720
 GATGAGCCCA GCAGCTACAC ATGTACAAT TGCAAAACAG CATTACACAG TGCATGGTTT 780
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 AGTCCCCTGA CCCCAGCGGT TGGTATCCCT TCAGGACTAG GTGCAGAAATG TCCTTCCCAG 900
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 GGATCAGTAT CGAGAGAGGC TTCCGGCCTG GCAGAAGGGC GCTTTCCACC CACTCCCCC 1020
 CTGTTTAGTC CACCCAGCAG ACATCACTTG GACCCCAACC GCATAGAGCG CCTGGGGGCG 1080
 GAAGAAATGG CCGTGGCCAG CCAATCCCGG AGTGCCCTTG ACAGGGTGCT GCGGTTGAAT 1140
 CCAATGGCTA TGGAGCCTCC CGCATGGAT TTCTCTAGGA GACTTAGAGA GCTGGCAGGG 1200
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 CACGAGAACA GCTCGCGGGG CGCGGTCTGT GGCCTGGGCG ACAGAGAGCG CGCCCTGCCC 1860
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 ACGGGCGAAA GGCCTTATAA ATGCGAGCTG TGCAACTATG CCGTGTGCCA GAGTAGCAAG 2580
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	TATTTTAAAT	TTGCCCTAAT	TCGTTGCTGA	GCAAACATGT	TGCTGTTTCC	AGTTCGGTTC	3180
	TGAGAGAAAA	AGAGAGAGAG	AGAGAAAAAG	ACCATGCTGC	ATACATTCTG	TAATACATAT	3240
5	CATGTACAGT	TTATTTTAT	AACGTGAGGA	GGAAAAACAG	TCITTGGATT	AACCCTCTAT	3300
	AGACAGAATA	GATAGCACTG	AAAAAAAATC	TCTATGAGCT	AAATGTCGT	CTCTAAAGGG	3360
	TTAAATGTAT	CAATTGGAAA	GGAGAGAAAA	AGGCCTTGAA	TTGACAAATT	AACAGAAAAA	3420
	CAGAACAGT	TTATTCATC	ATTTGGTTTT	AAAATATGAG	TGCCTTGGAT	CTATTAAAAA	3480
10	CACATCGATG	GTTCTTCTA	CTTGTATATA	ACTTGTAGCT	TAATTCAGCA	TTGGGTGAGG	3540
	TAATAAACCT	TAGGAACCTG	CATATAATTC	TATATTGTAT	TTCTCACAAC	AATGGCTACC	3600
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	AACAAAACCTG	ATTATACCAG	TATAAAAGCT	ACTTTGCTCC	TGGTGAGAGC	TTAAAAAGAA	3720
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15	TGCAAAAGCC	CTGGAACGCA	ATTAAATACA	CTAGTAAGGA	GTTCAATTTA	TGAAGATATT	3840
	TGCTTTAATA	ATGTCCTTTT	AAAAAATCTG	GCACCAAAAG	AAATAGATCC	AGATCTACTT	3900
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20	TGATGATTAA	CTATGAATTC	TTAAGACTTG	CATTAAATG	TGACATTCTT	AAAAAAGAA	4140
	GAGAAAGAA	TTTAAAGATA	GCAATATATA	TGTCTGTGCT	CCCTAAAAGT	TGTACTTCAT	4200
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	TTTTATTTTT	TTAATTTTTT	CTTTTTTATT	AAGCTAGCAT	CTGCCCCAGT	TGGTGTTC	4320
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25	TACAGGCTA	TACTTAAGGG	AAAAGTTGCA	AGAATGCTGA	AAAAAAATG	AACACAATCT	4500
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	TATTGAGCTT	ACTTACTTGG	ACGCAACATT	GCAAGCGCTG	TGAATGGAAA	CAGAATACAC	4620
	TTAACATAGA	AATGAATGAT	TGCTTTCGCT	TCTACAGTGC	AAGGATTTTT	TTGTACAAAA	4680
	CTTTTTTAAA	TATAAATGTT	AAGAAAAATT	TTTTTTAAAA	AACACTTCAT	TATGTTTAGG	4740
30	GGGGAACGTC	ATTTTAGGGT	TCCATTGTCT	TGGTGGTGT	ACAAGACTTG	TTATCCATTT	4800
	AAAAATGGTA	GTGGAAATTC	TATGCCTTGG	ATACACACCG	CTCTTCAGGT	TGTAAAAAAA	4860
	AAAAACATAC	ATTGGGGAAA	GGTTTAAAGT	TATATAGTAC	TTAAATATAG	GAAAAATGAC	4920
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35	GTATTTGAAT	TAAATGTTCA	TCTAGTGTTA	GGCACTATAG	TATTTATATT	GAAGCTTGTA	5040
	TTTTTAACCTG	TTGCTTGTTC	TCTTAAAAGG	TATCAATGTA	CCTTTTTTGG	TAGTGGAAAA	5100
	AAAAAAGACA	GGCTGCCACA	GTATATTTTT	TTAATTTGGC	AGGATAATAT	AGTGCAAAAT	5160
	ATTTGTATGC	TTCAAAAAAA	AAAAAAGAG	AGAAACAAAA	AAGTGTGACA	TTACAGATGA	5220
	GAAGCCATAT	AATGGCGGTT	TGGGGGAGCC	TGCTAGAAATG	TCACATGGAT	GGCTGTCTATA	5280
40	GGGGTTGTAC	ATATCCCTTT	TTGTTCCCTT	TTCTGCTGTC	CATACTGTAT	GCAGTACTGC	5340
	AAGCTAATAA	CGTGGCTTTC	TTATGTAGTG	TGCTTTTGT	CCCTTTCTCT	CTATCACCTC	5400
	ACATTCACAGC	ATCTTACCTT	CATATGCAGT	AAAAGAAAGA	AAGAAAAAAA	AAGGAAAAAA	5460
	AAAAAAAAC	CAATGTTTTG	CAGTTTTTTT	CATTGCCAAA	AACTAAATGG	TGCTTTATAT	5520
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45	ACTTTTTTGT	AAATGGCAAT	GCAGAAATAT	TTGTATTG	CCTTTCTAT	TCCTGTAATG	5640
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	GCTTATGTGC	CCTGTTCAAA	ACAGAGGCAC	TTAATTTGAT	CTTTTATTTT	TCTTTGTTTT	5760
	TATTTTTTTT	TTTTATTAGA	TGACCAAGG	TCATTACAAC	CTGGCTTTT	ATTGTATTG	5820
	TTTCTGGTCT	TTGTTAAGTT	CTATTGGAAA	AACCACTGTC	TGTGTTTTTT	TGGCAGTTGT	5880
50	CTGCATTAAC	CTGTTTCATAC	ACCCATTTTG	TCCCTTTATT	GAAAAATAA	AAAAAATAA	5940

Seq ID NO: 85 Protein sequence:
Protein Accession #: NP_075044.1

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60	CPKQEHIAADK	LLHWRLGLSSP	RSAGHALIPT	PGMSAEYAPQ	GICKDEPSSY	TCTTCKQPFT	180
	SAWFLLQHAQ	NTHGLRILE	SEHGSPLTPR	VGIPSGLGAE	CPSQPPPLHI	HIADNPNFNL	240
	LRIPGSVSRE	ASGLAEGRFP	PTPLFSPPP	RHLDPHRIE	RLGAEEMALA	THHPSAFDRV	300
	LRLNPMAMEP	PAMDFSRRRL	ELAGNTSSPP	LSPGRPSPMQ	RLLQPFQPGS	KPFPLATPPL	360
	PPLQSAPPPS	QPPVKSKECE	FCGKTFFKFS	NLVVHRRSHT	GEKPYKCNLC	DHACTQASKL	420
65	KRHMKTHMHK	SSPMTVKSDD	GLSTASSPEP	GTSDLVGSAS	SALKSVVAKF	KSENDPNLIP	480
	ENGDEEEED	DEEEEEE	EEBELTESER	VDYGFGLSLE	AARHHENSSR	GAVVGVGDES	540
	RALPDVMQGM	VLSSMQHFSE	AFHQVLGEKH	KRGHLAEAE	HRDTCDEDSV	AGESDRIDG	600
	TVNGRGCSPP	ESASGLLSKK	LLLGSPSSLS	PFSKRIKLEK	EFDLPPATMP	NTENVYSQWL	660
	AGYAASRLK	DPFLSFGDSR	QSPFASSEH	SENGSLRFS	TPPGELDGGI	SGRSGTSGSG	720
70	STPHISGPGT	GRSSKEGRR	SDTCEYCGKV	FKNCSNLTVH	RRSHTGERPY	KCELCNVACA	780
	QSSKLTRHMK	THGVQGVKDVY	KCEICKMPFS	VYSTLEKHMK	KWHSRDLVNN	DIKTE	

Seq ID NO: 86 DNA sequence
Nucleic Acid Accession #: XM_035292.2
Coding sequence: 53-1576

75	1	11	21	31	41	51	
80	GCTCGCTGGG	CCGCGGCTCC	CGGGTGTCCC	AGGCCCGGCC	GGTGCAGAGA	GCATGGCGGG	60
	TGCGGGCCCG	AAGCGGCGCG	CGCTAGCGGC	GCCGGCGGCC	GAGGAGAAGG	AAGAGGCGCG	120
	GGAGAAGATG	CTGCGCGCCA	AGAGCGCGGA	CGGCTCGGCG	CCGGCAGGCG	AGGGCGAGGG	180
	CGTGACCTCG	CAGCGGAACA	TCACGCTGCT	CAACGGCGTG	GCCATCATCG	TGGGGACCAT	240
	TATCGGCTCG	GGCATCTTCG	TGACGCCAC	GGCGTGCTC	AAGGAGGACG	GCTCGCGGG	300
85	GCTGGCGCTG	GTGTGTGGG	CCGCGTGGG	CGTCTTCTCC	ATCGTGGGCG	CGCTCTGCTA	360
	CGCGGAGCTC	GGCACATG	TCTCCAAATC	GGCGGCGGAC	TACGCTTACA	TGCTGGAGGT	420
	CTACGGCTCG	CTGCGCGCCT	TCCTCAAGCT	CTGGATCGAG	CTGCTCATCA	TCCGGCCTTC	480
	ATCGCAGTAC	ATCGTGGCCC	TGGTCTTCGC	CACCTACCTG	CTCAAGCCGC	TCTTCCCCAC	540

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CTGCCCCGGTG CCGCAGGAGG CAGCCAAGCT CGTGGCCTGC CTCTGCGTGC TGCTGCTCAC 600
GGCCGTGAAC TGCTACAGCG TGAAGGCCGC CACCCGGGTC CAGGATGCCT TTGCCGCCGC 660
CAAGCTCCTG GCCCTGGCCC TGATCATCCT GCTGGGCTTC GTCCAGATCG GGAAGGGTGA 720
TGTGTCCAAT CTAGATCCCA ACTTCTCATT TGAAGGCACC AAAGTGGATG TGGGGAACAT 780
5 TGCTGTGGCA TTATACAGCG GCCTCTTTGC CTATGGAGGA TGAATTACT TGAATTCGT 840
CACAGAGGAA ATGATCAACC CCTACAGAAA CCTGCCCTCG GCCATCATCA TCTCCCTGCC 900
CATCGTGACG CTGGTGACG TGCTGACCAA CCTGGCCTAC TTCACCACCC TGTCACCCGA 960
GCAGATGCTG TCGTCCGAGG CCGTGGCCGT GGACTTCGGG AACTATCACC TGGGCGTCAT 1020
10 GTCTTGATC ATCCCCGTCT TCGTGGGCTC GTCTGTCTTC GGCTCCGTCA ATGGGTCCCT 1080
GTTACATACC TCCAGGCTCT TCTTCGTGGG GTCCCGGGAA GGCCACCTGC CCTCCATCCT 1140
CTCCATGATC CACCCACAGC TCCTCACCCC CGTGCCGTCC CTCGTGTTCG CGTGTGTGAT 1200
GACGCTGCTC TACGCTTCTT CCAAGGACAT CTTCTCCGTC ATCAACTTCT TCAGCTTCTT 1260
CAACTGGCTC TCGTGGCCC TGGCCATCAT CGGCATGATC TGGCTGCGCC ACAGAAAGCC 1320
15 TGAGCTTGAG CGGCCCATCA AGGTGAACCT GGCCCTGCCT GTGTTCTTCA TCCTGGCCTG 1380
CCTCTTCTG ATCGCGCTCT CTTTCTGGAA GACACCCGTG GAGTGTGGCA TCGGCTTCAC 1440
CATCATCCTC AGCGGGCTGC CCGTCTACTT CTTGGGGGTC TGGTGGAAAA ACAAGCCCAA 1500
GTGGCTCCTC CAGGGCATCT TCTCCACGAC CGTCTGTGT CAGAAGCTCA TGCAGGTGGT 1560
CCCCCAGGAG ACATAGCCAG GAGGCCGAGT GGCTGCCGGA GGAGCATGC

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Seq ID NO: 87 Protein sequence:
Protein Accession #: XP_035292.2

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1      11      21      31      41      51
|      |      |      |      |      |
25 MAGAGPKRRA LAAPAAEKE EAREKMLAAK SADGSAPAGE GEGVTLQRNI TLLNGVAIIV 60
GTIIIGSIFV TPTGVLKEAG SPGLALVWVA ACGVFSIVGA LCYAEGLTTI SKSGGDYAYM 120
LEVYGSPLAF LKWIIELLII RPSSQYIVAL VFATYLLKPL FPTCPVPBEA AKLVACLCLV 180
LLTAVNCYSV KAATRVQDAF AAALKLLALAL IILLGFVQIG KGDVSNLDPN FSEFGTKLDV 240
30 GNVFLALYSG LFAYGWNLYL NFWTEEMINP YRNLPLAIII SLPIVTLVYV LTNLAYFTTL 300
STEQMLSSEA VAVDFGNHYL GVMSWIIPVF VGLSCFSGSVN GSLFTSSRLF FVGSREGHLP 360
SILSMIHPQL LTPVPSLVFT CVMTLLYAFS KDIPSVINFF SFFNWLVAL AIIGMIWLRH 420
RKPELERPIK VNLALPVFTI LACFLIAVS FWKTPVECGI GFTIILSGLP VYFFGVWVKN 480
KPKWLLQGIF STTVLCQKLM QVVPQET

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Seq ID NO: 88 DNA sequence
Nucleic Acid Accession #: NM_005268.1
Coding sequence: 168-989

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1      11      21      31      41      51
|      |      |      |      |      |
40 TAAAAAGCAA AAGAATTCGC GGCCGCGCTCG ACACGGGCTT CCCCAGAAAC CTTCCTCCGCT 60
TCTGGATATG AAATTCAGAG TGCTTGCTGA GTCTATTGTC CGGCTGCTGG GAGCCAGGAG 120
45 AGCCCTGAGG AGTAGTCACT CAGTAGCAGC TGACGCGTGG GTCCACCATG AACTGGAGTA 180
TCTTTGAGGG ACTCTGAGT GGGGTCAACA AGTACTCCAC AGCCTTTGGG CGCATCTGGC 240
TGTCTCTGGT CTTTCATCTTC CGCGTGCTGG TGTACCTGGT GACGGCCGAG CGTGTGTGGA 300
GTGATGACCA CAAGGACTTC GACTGCAATA CTCGCCAGCC CGGCTGCTCC AACGTCTGCT 360
TTGATGAGTT CTTCCCTGTG TCCCATGTGC GCCTCTGGGC CCTGAGCTT ATCCTGTGTA 420
50 CATGCCCTC ACTGCTCGTG GTCATGCACG TGGCCTACCG GGAGGTTTCA GAGAAGAGGC 480
ACCGAGAAGC CCATGGGGAG AACAGTGGGC GCCTCTACCT GAACCCCGGC AAGAAGCGGG 540
GTGGGCTCTG GTGGACATAT GTCTGCAGCC TAGTGTTCAA GCGGAGCGTG GACATCGCCT 600
TTCTCTATGT GTTCCACTCA TTCTACCCCA AATATATCCT CCTCCTGTG GTCAAGTGCC 660
ACGCAGATCC ATGTCCCAAT ATAGTGGACT GCTTCATCTC CAAGCCCTCA GAGAAGAACA 720
55 TTTTACCCTT CTTTCATGGT GCCACAGCTG CCATCTGCAT CCTGCTCAAC CTCGTGGAGC 780
TCATCTACCT GGTGAGCAAG AGATGCCACG AGTGCCCTGC AGCAAGGAAA GCTCAAGCCA 840
TGTGCACAGG TCATCACCCC CACGGTACCA CCTCTTCTTG CAAACAAGAC GACCTCCTTT 900
CGGGTGACCT CATCTTCTG GGCTCAGACA GTCATCTCTC TCTCTTACCA GACCGCCCCC 960
GAGACCATGT GAAGAAAACC ATCTTGTGAG GGGCTGCTCG GACTGCTCTG GCAGGTTGGG 1020
60 CCTGGATGGG GAGGCTCTAG CATCTCTCAT AGGTGCAACC TGAGAGTGGG GAGAGCTAAGC 1080
CATGAGGTAG GGGCAGGCAA GAGAGAGGAT TCAGACGCTC TGGGAGCCAG TTCCTAGTCC 1140
TCAACTCCAG CCACCTGCCC CAGTCTGACG GCACTGGGCC GATTCCCCCT CTGCTCTGCA 1200
GCTCGGTTTC CTTTTCTAGA ATGGAATAG TGAGGGCCAA TGC

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Seq ID NO: 89 Protein sequence:
Protein Accession #: NP_005259.1

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1      11      21      31      41      51
|      |      |      |      |      |
70 MNWSIFEGLL SGVNKYSTAF GRIWLSLVFI FRVLVYLVT A ERVWSDDHKD FDCNTRQPGC 60
SNVCFDEFFP VSHVRLWALQ LILVTCPSLL VVMHVAYREV QEKRHREAHG ENSGRLYLNP 120
GKKRGGGLWT YVCSLVFKAS VDIAFLYVFH SFYPKYILPP VVKCHADPCP NIVDCFISKP 180
SEKNIFTLFM VATAAICILL NLVELIYLV KRCHECLAAR KAQAMCTGHH PHGTTSSCKQ 240
DDLLSGDLIF LGSDSHPPLL PDRPRDHVKK TIL

```

Seq ID NO: 90 DNA sequence
Nucleic Acid Accession #: NM_002391.1
Coding sequence: 26-457

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1      11      21      31      41      51
|      |      |      |      |      |
80 CGGGCGAAGC AGCGCGGGCA GCGAGATGCA GCACCGAGGC TTCCTCCTCC TCACCCTCCT 60
CGCCCTGCTG CGGCTCACCT CCGCGGTGCG CAAAAAGAAA GATAAGGTGA AGAAGGGCGG 120
85 CCGGGGAGC GAGTGCGCTG AGTGGGCTG GGGGCCCTGC ACCCCAGCA GCAGGATG 180
CGGCGTGGGT TTCCGCGAGG GCACCTGCGG GGGCCAGACC CAGCGCATCC GGTGCAGGTG 240
GCCCTGCAAC TGAAGAAGG AGTTTGGAGC GCACTGCAAG TACAAGTTTG AGAACTGGGG 300
TGCGTGTGAT GGGGGCACAG GCACCAAAGT CCGCCAAGGC ACCCTGAAGA AGGCGCGCTA 360

```

CAATGCTCAG TGCCAGGAGA CCATCCGCGT CACCAAGCCC TGCACCCCA AGACCAAGGC 420
 AAAGGCCAAA GCCAAGAAAG GGAAGGGAAA GGACTAGACG CCAAGCCTGG ATGCCAAGGA 480
 GCCCTGTGTG TCACATGGGG CCTGGCCACG CCTCCCTCT CCCAGGCCCG AGATGTGACC 540
 CACCAGTGCC TTCTGTCTGC TCGTTAGCTT TAATCAATCA TGCCCTGCCT TGTCCCTCTC 600
 ACTCCCAAGC CCCACCCCTA AGTGCCCAAA GTGGGGAGGG ACAAGGGATT CTGGGAAGCT 660
 TGAGCCTCCC CCAAAGCAAT GTGAGTCCCA GAGCCCGCTT TTGTTCTTCC CCACAATTCC 720
 ATTACTAAGA AACACATCAA ATAAACTGAC TTTTTCCTCC CAATAAAGC TCTTCTTTT 780
 TAAATAT

Seq ID NO: 91 Protein sequence:
 Protein Accession #: NP_002382.1

1 11 21 31 41 51
 | | | | |
 15 MQHRGFLLLT LLALLAL TSA VAKKKDKVKK GPGSECAEW AWGPCTPSSK DCGVGFREGT 60
 CGAQTQRIRC RVPENWKKF GADCKYKFEN WGACDGGTGT KVRQGTLLKA RYNAQCQETI 120
 RVTKPCTPKT KAKAKAKGK GKD

Seq ID NO: 92 DNA sequence
 Nucleic Acid Accession #: NM_005130.1
 Coding sequence: 98-802

1 11 21 31 41 51
 | | | | |
 25 CTCTACCTGA CACAGCTGCA GCCTGCAATT CACTCCCACT GCCTGGGATT GCACTGGATC 60
 CGTGTGCTCA GAACAAGGTG AACGCCACG TGCAGCCATG AAGATCTGTA GCCTCACCCCT 120
 GCTCTCCTTC CTCTACTAGG CTGCTCAGGT GCTCCTGGTG GAGGGGAAAA AAAAAGTGAA 180
 GAATGGACTT CACAGCAAAG TGGTCTCAGA ACAAAGGAC ACTCTGGGCA ACACCCAGAT 240
 30 TAAGCAGAAA AGCAGGCCCG GGAACAAAGG CAAGTTTGTG ACCAAAGACC AAGCCAAC TG 300
 CAGATGGGCT GCTACTGAGC AGGAGGAGGG CATCTCTCTC AAGGTTGAGT GCACTCAATT 360
 GGACCATGAA TTTTCTGTG TCTTTGCTGG CAATCCAACC TCATGCCTAA AGCTCAAGGA 420
 TGAGAGAGTC TATTGGAAGC AAGTTGCCCG GAATCTGCGC TCACAGAAAG ACATCTGTAG 480
 35 ATATTCCAAG ACAGCTGTGA AAACCAGAGT GTGCAGAAAG GATTTTCCAG AATCCAGTCT 540
 TAAGCTAGTC AGCTCCAATC TATTGGGAA CACAAAGCCC AGGAAGGAGA AAACAGAGAT 600
 GTCCCCCAGG GAGCACATCA AGGGCAAAGA GACCACCCCT TCTAGCCTAG CAGTGACCCA 660
 GACCATGGCC ACCAAAGCTC CCGAGTGTGT GGAGGACCCA GATATGGCAA ACCAGAGGAA 720
 GACTGCCCTG GAGTCTGTG GAGAGACTTG GAGCTCTCTC TGCACATCTC TCCTCAGCAT 780
 40 AGTCAGGAC ACCTCATGCT AATGAGGTCA AAAGAGAACG GGTTCCTTTA AGAGATGTCA 840
 TGTGCTAAGT CCGTCTGTAT ACTTTAAAGC TCTCTACAGT CCCCCAAAA TATGAACCTT 900
 TGTGCTTAGT GAGTGCAACG AAATATTAA ACAAGTTTGT TATTTTGTG TTTTGTGTT 960
 TGGAATTGTC CTTATTTTTC TTGGATGCGA TGTTTCAGAG CTGTTTCTCT GAGCATGTAT 1020
 TTCCATGGCC CACACAGTCA TGTGTTGAG CAGCGAAGAG TCTTTGAGCT GAATGAGCCA 1080
 45 GAGTGATAAT TTCAGTGCAA CGAAGTTTCT GCTGAATTAA TGGAATAAAA ACTCTGGGTG 1140
 TTTTCAAAA AAAAAAAAAA AAA

Seq ID NO: 93 Protein sequence:
 Protein Accession #: NP_005121.1

1 11 21 31 41 51
 | | | | |
 50 MKICSLTLLS FLLLLAAQVLL VEGKKKVKNG LHSKVSEQK DTLGNTQIKQ KSRPGNKGKF 60
 VTKDQANCRW AATQEEGIG LKVECTQLDH EFSCVFAGNP TSCLKLKDER VYWKQVARNL 120
 55 RSQKIDICRY KTAVKTRVCR KDFPESSLKL VSSTLFGNTK PRKEKTEMSP REHIKKGKETT 180
 PSSLAVTQTM ATKAPCEVED PDMANQRKTA LEFCGETWSS LCTFFLSIVQ DTSC

Seq ID NO: 94 DNA sequence
 Nucleic Acid Accession #: NM_012101
 Coding sequence: 125-1891

1 11 21 31 41 51
 | | | | |
 60 CTCTCACAG GTGTGTCTCT AGTCCTCGTG GTTGCCCTGCC CCACTCCCTG CCGAGACGCC 60
 TGCCAGAAAG GTCACTATC CTGAACCCCA GCAAGCCTGA AACAGCTCAG CCAAGCACCC 120
 65 TGCATGGAA GCTGCAGATG CCTCCAGGAG CAACGGGTG AGCCCAAGAG CCAAGGATGC 180
 CCGAGGCCCG TCGGGCCCA GTGGCAGCCT GGAGAAATGGC ACCAAGGCTG ACGGCAAGGA 240
 TGCCAAGACC ACCAACGGGC ACGGCGGGGA GGCAGCTGAG GGCAAGAGCC TGGGCAGCGC 300
 CCTGAAGCCA GGGGAAGGTA GGAGCGCCCT GTTCGCGGGC AATGAGTGGC GGCAGCCAT 360
 CATCCAGTTT GTCGAGTCCG GGGACGACAA GAACTCCAAC TACTTCAGCA TGGACTCTAT 420
 70 GGAAGGCAAG AGGTGCGCGT ACGCAGGGCT CCAGCTGGGG GCTGCCAAGA AGCCACCCGT 480
 TACCTTTGCC GAAAGGGCG ACGTGCGCAA GTCCATTTC TCGGAGTCCC GGAAGCCAC 540
 GGTGTCCATC ATGGAGCCCG GGGAGACCCG GCGGAACAGC TACCCCGGG CCGACACGGG 600
 CCTTTTTTCA CGGTCCAAGT CCGGCTCCGA GGAGGTGCTG TCGCACTCCT GCATCGGCAA 660
 75 CAAGCAGAAG GCGGTCAAGT CCTGCCTGGT GTGCCAGGCC TCTTCTGCG AGCTGCATCT 720
 CAAGCCCAAC CTGGAGGGCG CCGCCTTCG AGACCACAG CTGCTCGAGC ACATCCGGGA 780
 CTTTGAGGCC CGCAAGTGT CCGTGATGAG CAAGACGATG GAGCTCTTCT GCCAGACCGA 840
 CCAGACCTGC ATCTGTCTAC TTGTCATGTT CCAGGAGCAC AAGAATCATA GCACCGTGAC 900
 AGTGGAGGAG GCCAAGGCCG AGAAGGAGAC GGAGCTGTCA CTGCAAAAGG AGCAGCTGCA 960
 80 GCTCAAGATC ATTGAGATTG AGGATGAAGC TGAGAAGTGG CAGAAGGAGA AGGACCGCAT 1020
 CAAGAGCTTC ACCACCAATG AGAAGGCCAT CCTGGAGCAG AACTTCCGGG ACCTGGTGG 1080
 GGACCTGGAG AAGCAAAAGG AGGAAGTGAG GGCTGCGCTG GAGCAGCGGG AGCAGGATGC 1140
 TGTGGACCAA GTGAAGGTGA TCATGGATGC TCTGGATGAG AGAGCCAAGG TGCTGCATGA 1200
 GGACAAGCAG ACCCGGGAGC AGCTGCATAG CATCAGCGAC TCTGTGTTGT TTCTGCAGGA 1260
 85 ATTTGGTGCA TTGATGAGCA ATTACTCTCT CCCCCACCC CTGCCCACCT ATCATGTCTCT 1320
 GCTGGAGGGG GAGGGCCTGG GACAGTCACT AGGCAACTTC AAGGACGACC TGCTCAATGT 1380
 ATGCATGCGC CACGTTGAGA AGATGTGCAA GCGGACCTG AGCCGTAACT TCATTGAGAG 1440
 GAACCACATG GAGAACGGTG GTGACCATCG CTATGTGAAC AACTACACGA ACAGCTTCGG 1500

	GGGTGAGTGG	AGTGCACCGG	ACACCATGAA	GAGATACTCC	ATGTACCTGA	CACCCAAAGG	1560
	TGGGGTCCGG	ACATCATACC	AGCCCTCGTC	TCCTGGCCGC	TCACCAAGG	AGACCACCCA	1620
	GAAGAATTTC	AACAATCTCT	ATGGCACCAA	AGGTAACCTAC	ACCTCCCGGG	TCTGGGAGTA	1680
5	CTCCTCCAGC	ATTGAGAACT	CTGACAATGA	CCTGCCCGTC	GTCCAAGGCA	GCTCCTCCTT	1740
	CTCCCTGAAA	GGCTATCCCT	CCCTCATGCG	GAGCCAAAGC	CCCAAGGCC	AGCCCCAGAC	1800
	TTGGAAATCT	GGCAAGCAGA	CTATGCTGTC	TCACTACCGG	CCATTCTACG	TCAACAAAGG	1860
	CAACGGGATG	GGGTCCAAAG	AAGCCCCATG	AGCTCCTGGC	GGAAAGGAACG	AGGCGCCACA	1920
	CCCTGCTCT	TCCTCCTGAC	CCTGCTGCTC	TTGCCCTTCTA	AGCTACTGTG	CTTGCTCTGG	1980
10	TGGGAGGGAG	CCTGGTCCCTG	CACCTGCCCT	CTGCAGCCCT	CTGCCAGCCT	CTTGGGGGCA	2040
	GTTCGGGCTT	CTCCGACTTC	CCCCTGCGC	ACACTCCAAT	CAGACTCCTT	TCCTGCCTTG	2100
	TGACCTCAGA	TGGTCACCAT	CATTCTCTGT	CTCAGAGGCC	AACCCATCAC	AGGGGTGAGA	2160
	TAGGTTGGGG	CCTGCCCTAA	CCCGCCAGCC	TCCTCCTCTC	GGGCTGGATC	TGGGGGCTAG	2220
	CAGTGAGTAC	CCGCATGGTA	TCAGCCTGCC	TCTCCCGCCC	ACGCCCTGCT	GTCTCCAGGC	2280
15	CTATAGACGT	TTCTCTCCAA	GGCCCTATCC	CCCAATGTTG	TCAGCAGATG	CCTGGACAGC	2340
	ACAGCCACCC	ATCTCCCATT	CACATGGCCC	ACCTCCTGCT	TCCCAGAGGA	CTGGCCCTAC	2400
	GTGCTCTCTC	TGCTCTTACC	TATCAATGCC	CAGCATGGCA	GAACCTGCAG	TGGCCAAAGG	2460
	CTGCAGATGG	AAACCTCTCA	GTGCTCTGAC	ATCACCTTAC	CCAGGCGGTG	GGTCTCCACC	2520
	ACAGCCACTT	TGAGTCTGTG	GTCCCTGGAG	GGTGGCTTCT	CCTGACTGGC	AGGATGACCT	2580
20	TAGCCAAGAT	ATTCTCTGTG	TCCTCTGCT	GAGATAAAGA	ATTCCCTTAA	CATGATATAA	2640
	TCCACCCATG	CAAATAGCTA	CTGGCCAGC	TACCATTTAC	CATTTCCTTA	CAGAATTTCA	2700
	TTCACTCTAC	ACTTTGGCAT	TCTCTCTGGC	GATGGAGTGT	GGCTGGGCTG	ACCGCAAAGG	2760
	GTGCCCTTACA	CACCTGCCCC	ACCCCTCAGC	GTGCCCCAT	CAGAGGCTGC	CTCCTCCTTC	2820
	TGATTACCCC	CCATGTTGCA	TATCAGGGTG	CTCAAGGATT	GGAGAGGAGA	CAAAACCAGG	2880
25	AGCAGCACAG	TGGGGACATC	TCCGTCTCA	ACAGCCCCAG	GCCTATGGGG	GCTCTGGAAG	2940
	GATGGGCCAG	CTTGCAGGGG	TTGGGGAGGG	AGACATCCAG	CTTGGGCTTT	CCCCTTTGGA	3000
	ATAAACCATT	GGTCTGTC					

Seq ID NO: 95 Protein sequence:
Protein Accession #: NP_036233.1

30							
	1	11	21	31	41	51	
35	MEAADASRSN	GSSPEARDAR	SPSGPSGSLE	NGTKADGKDA	KTTNGHGGEA	AEGKSLGSAL	60
	KPGEGRSALF	AGNEWRRPII	QFVESGGDDKN	SNYFSMDSME	GKRSPYAGLQ	LGAAKKPPVT	120
	FAEKGDVRKS	IFSESRRPTV	SIMEPGETRR	NSYPRADTGL	FSRSKSGSEE	VLCDSICGNK	180
	QKAVKSCSLVC	QASFCEBLHLK	PHLEGAAFRD	HQLLEPIRDF	EARKCPVHGK	TMELFCQTDQ	240
	TCICYLCMFQ	EHNHSTVTV	EEAKAEKETE	LSLQKEQLQL	KIEIEDEAE	KWQKEKDRIK	300
40	SFTTNEKAIL	EQNFRDLVRD	LEKQKEEVRA	ALBQREQDAV	DQVKVIMDAL	DERAKVLHED	360
	KQTRQLHSI	SDSVLFLQEF	GALMSNYSLP	PPLPTYHVLL	EGEGLGQSLG	NFKDDLNLNV	420
	MRHVEKMKCA	DLSRNFIERN	HMENGGDHRV	VNNYTNISFGG	EWASAPDTMKR	YSMYLTPKGG	480
	VRTSYQSPSP	GRFTKETTKQ	NFNLYLGTGK	NYTSRVWEYS	SSIQNSDNDL	PVVQSSSFS	540
	LKGYPSLMRS	QSPKAQPTW	KSGKQTMLSH	YRPFYVKNKN	GIGSNEAP		

45 Seq ID NO: 96 DNA sequence
Nucleic Acid Accession #: NM_080668.1
Coding sequence: 83-841

50	1	11	21	31	41	51	
	GGCACGAGGG	CAGCGAGTGG	CCTTCCCGGT	TGGCGCGCGC	CCGGGGCGGC	GGCGCTGGAG	60
	GAGCTCGAGA	CGGAGCCTAG	TTATGTCTGG	GAGGCGAAGC	CGGTCCCGAG	GAGCCGCTCA	120
	GCGCTCCGGG	CCAAGGGCCC	CATCTCTTAC	TAAGCCTCTG	CGGAGGTCCC	AGCGGAAATC	180
55	AGGCTCTGAA	CTCCCGAGCA	TCCTCCCTGA	AATCTGGCCG	AAGACACCCA	GTGCGGCTGC	240
	AGTCAGAAAG	CCCATCGTCT	TAAAGAGGAT	CGTGGCCCAT	GCTGTAGAGG	TCCCAGCTGT	300
	CCAATCACCT	CGCAGGAGCC	CTAGGATTTT	CTTTTCTTTG	GAGAAAGAAA	ACGAGCCCCC	360
	TGGCAGGGAG	CTTACTAAGG	AGGACCTTTT	CAAGACACAC	AGCGTCCCTG	CCACCCCCAC	420
	CAGCACTCCT	GTGCCGAACC	CTGAGGCCGA	GTCCAGCTCC	AAGGAAGGAG	AGCTGGACGC	480
60	CAGAGACTTG	GAAATGTCTA	AGAAAGTCAG	GCCTTCTTAC	AGCCGGCTGG	AGACCTTGGG	540
	CTCTGCCTCT	ACCTCCACCC	CAGGCCGCGC	GTCCTGCTTT	GGCTTCGAGG	GGCTGTGGGG	600
	GGCAGAAGAC	TTGTCCGGAG	TCTCGCCAGT	GGTGTGCTCC	AAACTCACCG	AGGTCCCCAG	660
	GGTTTGTGCA	AAGCCCTGGG	CCCCAGACAT	GACTCTCCCT	GGAATCTCCC	CACCACCCGA	720
	GAAACAGAAA	CGTAAGAGAA	AGAAATGCC	AGAGATCTTG	AAAACGGAGC	TGGATGAGTG	780
65	GGCTGCGGCC	ATGAATGCCG	AGTTTGAAGC	TGCTGAGCAG	TTTGATCTCC	TGGTTGAATG	840
	AGATGCAATG	GGGGGTGCAC	CTGGCCAGAC	TCTCCCTCCT	GTCCTGTACA	TAGCCACCTC	900
	CCTGTGGAGA	GGACACTTAG	GGTCCCCCTC	CCTGGTCTTG	TTACCTGTGT	GTGTGCTGGT	960
	GCTGCGCATG	AGGACTGTCT	GCCTTTGAGG	GCTTGGGCAG	CAGCGGCAGC	CATCTTGGTT	1020
	TTAGGAAATG	GGGCCGCTG	GCCACGCCAC	TCACTGGTGT	CCTGTCTCTT	GTCTGCTCTG	1080
70	CCTTCCTATC	TCCCCAAAGT	ACCATAGCCA	GTTTCCAGAT	GGGCCACAGA	CTGGGGAGGA	1140
	GAATCAGTGG	CCCAGCCAGA	AGTTAAAGGG	CTGAGGGTTG	AGGTGAGAGG	CACCTCTGCT	1200
	CTTGTGGGGA	GGGGTGGCTG	CTTGGAAATA	GGCCAGGGGG	CTCTGCCAGC	CTCGGCTCTT	1260
	CCCTCTGAG	TTGCCTTCTG	TTGGTGGCTT	TCTTCTTGAA	CCCACCTGTG	TAAAGAGGTT	1320
	TTCACTTCCG	TGGGTTTCCC	CTTTGATTCT	GTAATAGTCT	CCAGAGAGAA	TTCTGTTGGT	1380
75	GAGGGCAATT	CTGTCTTGGA	GGAAGAAGCT	GGACATTTCAG	CCTGTGGAGT	CTGAGTTTGT	1440
	AAGGATGTAG	GGAGCCTTAG	TTGGGTCTCA	GACCATAAGT	GTGTACTACA	CAGAAGCTGT	1500
	GTTTTCTAGT	TCTGTCTGTC	TGTTGAGATG	TTTGGTAAAT	GCCAGGTTGA	TAGGGCGCTG	1560
	GCTGCTTGGA	GCAAGGGTGT	CATTTAGGGG	TGTGGCCACC	AGGTGCTGTG	AGTTTCTGTG	1620
	GCTCATGGCC	TCTGGGCTGG	TCCCTTGCAC	AGGGCCACG	CTGGAGTCTT	ACCACTCTGC	1680
80	TGCAGGGGTG	GAAGGTGGCC	CCTCTTGTCA	CCCATACCCA	TTTCTTACAA	AATAAGTTAC	1740
	ACCGAGTCTA	CTTGGCCCTA	GAAGAGAAAG	TGAAGAGTCT	CCAGACCTAC	TAGCATTTTG	1800
	CAACTATGCT	TGTAAAGTCC	TCGGAAAGTT	TCTTCGCTGA	CCAGACAGCG	GCGGGGGCTG	1860
	ATAGCAATTT	TAGTTTTTGG	CCTCCCTATC	CTCTCACATG	AGAAACACTGC	CTGGATGCAT	1920
	CTCATGATCT	CTGGAGAAAT	TCCCATCTT	TCTCTTCTTT	CCATCGTGTG	GATTCAATAG	1980
	TTTGGATTGG	AAGGCTGCC	TGCCCCGAC	TCTCTGCGC	CACCCCTGGC	CATTGTACCT	2040
85	TTTGTATGTT	AGAAGTTCCT	GGAAGTAGAC	GCTGAGGTGT	GCAGAGGAGC	TGGTGGATAA	2100
	CAGAGAATGC	CAGGAAGAT	GAGTGCTGGG	TCAGGGTACT	TGGATGAAAC	GGTGCAGGCC	2160
	AGGGGGGCC	TAATAAAACC	CTCTGCCAGG	TCTGGGAGTC	CCAGGCCATC	TGCTCAACGC	2220

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	GCCGCGTTGG	AGTGTACAA	CACGTTTCATT	GGCGAGAGAA	CTGTAGGAGC	GCTCCAGGTC	3900
	CTAGGTACTG	AAGCCCAGTC	TTCACCTTTT	AAAGCAGTGG	CTTCTCTCTT	AGAAAGCATT	3960
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10	AAAATAACAG	CACAGAGCAT	TGAGGAGCTT	TGTGCCGTCA	ACTTGTATGG	CCCTGACGCG	4380
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	TTCCCATGTC	AGTCCAGGGA	ATTTCTCCA	GGAACCTCGC	GGTTCAATTA	TTATGTGGAC	5280
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	CCTGCTGAGC	TGCTGCGCAA	GCGAGTCCGT	GGGAAGGCC	GCCTCCCTTC	TGATGTCTCT	8820
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Seq ID NO: 99 Protein sequence:
Protein Accession #: NP_008835.5

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85	LGEVHPSEMI	NKENLFRAP	LGELKTQMTS	AVREPKLPLV	AGCLKGLSSL	LCNFTKSMEE	240
	DPQTSREIFN	FVLKAIRPQI	DLKRYAVPSA	GLRLFALHAS	QFSTCLLDNY	VSLFEVLLKW	300
	CAHTNVELKK	AALSALSFL	KQVSNMVAKN	AEMHKNKLQY	FMEQFYGIIR	NVDSNNKELS	360

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5	MDSLILADEAF	FSVNSSSESL	NHLLYDEFVK	SVLKIVEKLD	LTLEIQTVGE	QENGDEAPGV	600
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	SQDFSTGVQ	SYSYSSQDPR	PATGRFRRE	QRDPTVHDDV	LELEMDLNR	HECMAPLTAL	2100
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	AKHWLSPILL	LAASENNNGE	GIHYMVVEIV	ATILSWTGLA	TPTGVPKDEV	LANRLNLFM	2220
	KHVFHPKRAV	FRHNLIIKT	LVECKWKCLS	IPYRLIFEKF	SGKDPNSKDN	SVGIQLLGIV	2280
	MANDLPPYDP	QCGIOSSEYF	QALVNMSFV	RYKEVYAAAA	EVLGLILRYV	MERNKILEES	2340
35	LCELVAQQLK	QHQNLTMEDF	IVCLNKVTKS	FPPLADRFMN	AVFLLPKFHF	GVLKTLCLV	2400
	VLCRVEGTE	LYFQLKSKDF	VQVMRHRDDE	RQKVCGLDIY	KMPKPKPVE	LRELLNPVVE	2460
	FVSHSTTCR	BQMNILMWI	HDNVRDPESE	TDNDSQEIFK	LAKDVLIQGL	IDENPGLQLI	2520
	IRNFWSHETR	LPSNTLDRL	ALNSLYSPKI	EVHFLSLATN	FLEMTSMSP	DYPNPMFHP	2580
	LSECEFEYET	IDSDFWRFRST	VLTMPFVETQ	ASQGTQLQTRT	QEGSLSARWP	VAGQIRATQQ	2640
40	QHDFTLTQTA	DGRSSFDWLT	GSSTDPVLVDH	TSPSSDLSLF	AHKRSERLQR	APLKSVPDF	2700
	GKKRLGLPGD	EVDNKNVKGAA	GRTDLLRLRR	RFMRDQEKLS	LMYARKGVAE	QKREKEIKSE	2760
	LKMKQDAQVV	LYRSYRHGDL	PDIQIKHSSL	ITPLQAVAQ	DPITAKQLFS	SLFSGILKEM	2820
	DKFKTLSEKN	NITQKLLQDF	NRFLNTTFSF	FPFVSCIQD	ISQHAALLS	LDPAASVAGC	2880
	LASLQQPVG	RLLEALLRL	LPAELPAKRV	RGKARLPD	LRWVELAKLY	RSIGEYDVL	2940
45	GIFTSEIGTK	QITQSALLAE	ARSDYSEAAK	QYDEALNKQD	WVDGEPTAE	KDFWELASLD	3000
	CYNHLAEWKS	LEYCSTASID	SENPPDLNKI	WSEPFYQETY	LFYMRSLKL	LLQGEADQS	3060
	LLTFIDKAMH	GELQKAILLE	HYSQELSLY	LLQDDVDRAK	YYIQNGIQSF	MQNYSSIDVL	3120
	LHQSRLLTKL	SVQALTEQF	FISFISKQGN	LSSQVPLKRL	LNTWTNRYPD	AKMDPMNIWD	3180
50	DIITNRCFFL	SKIEEKLTP	PEDNSMNVQD	DGDPSSDRMEV	QEQUEEDISSL	IRSCFKFSMKM	3240
	KMIDSARKQN	NFSLAMKLLK	ELHKESKTRD	DWLVSQVQSY	CRLSHCRSRS	QGCSEQVLT	3300
	LKTVSLLDEN	NVSSYLSKNI	LAFRDQNIL	GTTYRIIANA	LSSEPACLAE	IEEDKARRIL	3360
	ELSGSSSEDS	EKVYAGLVQ	AFQHLSEAVQ	AAEEEAQPPS	WSCGPAAGVI	DAYMTLADFC	3420
	DQQLRKEEEN	ASVDSAELO	AYPALVVEKM	LKALKLNSNE	ARLKFPRLQ	IIERYPEETL	3480
	SLMTKEISSV	NCKQFISWIS	HMVALLDKDQ	AVAVQHSVEE	ITDNYPPQAI	YPFIISSESY	3540
55	SFKDTSTGHK	NKEFVARIKS	KLDQGGVIQD	FINALDQLSN	PELLFKDWSN	DVRAELAKTP	3600
	VNKNIEIKMY	BRMYAALGDP	KAPGLGAFRR	KFIQTFGKEF	DKHFGKGGSK	LLRMKLSDFN	3660
	DITNMLLLKM	NKDSKPPGNL	KECESPMSDF	KVEFLRNELE	IPGQYDGRGK	PLPEYHVRIA	3720
	GFDERTVMA	SLRRPKRII	RGHDEREHPF	LVKGGEDLRQ	DQVEQLFQV	MNGILAQDSA	3780
	CSQRLQLRT	YSVVPMTSRK	GLIEWLENTV	TLKDLLNTM	SQEEKAAYLS	DPRAPPCEYK	3840
60	DWLTKMSGKH	DVGAYMLMYL	GANTTETVTS	FRKRESKVA	DLLKRAFRVM	STSPFAFLAL	3900
	RSHFASSHAL	ICISHWILGI	GDRHLNFMV	AMETGGVIGI	DFGHAFGSAT	QFLPVPPELMP	3960
	FRLTRQFINL	MLPMKETGLM	YSIMVHALRA	FRSDPGLLTN	TMDVVFVKPS	FDWKNFEQKM	4020
	LKKGGSWIQE	INVAEKNWYP	RQKICYAKRK	LAGANPAVIT	CDELLLGHEK	APAFRDYVAV	4080
	ARGSKDHNR	AQEPESGLSE	ETQVKCLMDQ	ATDPNILGRT	WEGNEPWW		

Seq ID NO: 100 DNA sequence
Nucleic Acid Accession #: NM_000673
Coding sequence: 101-1225

	1	11	21	31	41	51	
70	ATGTGAAGGC	ACAAGCTGCT	GTTATATACA	ACAGAGTGAA	CTGAGCATCA	GTCAGAAAAA	60
	GTCTATGTTT	GCAGAAATAC	AGATCCAAGA	CAAAGACAGG	ATGGGCACCTG	CTGGAAAGT	120
	TATTAAATGC	AAAGCAGCTG	TGCTTTGGGA	GCAGAAGCAA	CCCTTCTCCA	TTGAGGAAAT	180
	AGAAGTTGCC	CCACCAAAGA	CTAAGAAGT	TCCGATTAA	ATTTTGGCCA	CAGGAATCTG	240
75	TCCGACAGAT	GACCATGTGA	TAAAGGAAC	AATGGTGTCC	AAGTTTCCAG	TGATTGTGGG	300
	ACATGAGGCA	ACTGGGATTG	TAGAGAGCAT	TGGAGAAGGA	GTGACTACAG	TGAAACCAGG	360
	TGACAAAGTC	ATCCCTCTCT	TTCTGCCACA	ATGTAGAGAA	TGCAATGCTT	GTCGCAACCC	420
	AGATGGCAAC	CTTTGCATTA	GGAGCGATAT	TACTGGTCGT	GGAGTACTGG	CTGATGGCAC	480
	CACCAATTT	ACATGCAAGG	GCAACACAGT	ACACCACTTC	ATGAACACCA	GTACATTTC	540
80	CGAGTACACA	CTGGTGGAAT	AATCTTCTGT	TGCTAAGATT	GATGATGCAG	CTCCTCCTGA	600
	GAAAGTCTGT	TTAATTGGCT	GTGGGTTTTC	CACTGGATAT	GGCGCTGCTG	TTAAACTG	660
	CAAGGTCAAA	CCTGGTTCCA	CTTGGCTCGT	CTTTGGCCTG	GGAGGAGTTG	GCCTGTGAGT	720
	CATCATGGGC	TGTAAGTCAG	CTGGTGCAAT	TAGGATCATT	GGGATTGACC	TCAACAAGA	780
	CAAAATTTAG	AAGGCCATGG	CTGTAGGTGC	CACTGAGTGT	ATCAGTCCCA	AGGACTCTAC	840
85	CAAAACCCAT	AGTAGAGTGC	TGTCAGAAAT	GACAGGCAAC	AACGTGGGAT	ACACCTTTGA	900
	AGTTATTGGG	CATCTTGAAA	CCATGATTGA	TGCCCTGGCA	TCCTGCCACA	TGAACATG	960
	GACCAGCSTG	GTTGTAGGAG	TTCCTCCATC	AGCCAAGATG	CTCACCTATG	ACCCGATGTT	1020

GCTCTTCACT GGACGCACAT GGAAGGGATG TGTCTTTGGA GGTTTGAAAA GCAGAGATGA 1080
 TGTCCCAAAA CTAGTGACTG AGTTCCTGGC AAAGAAATTT GACCTGGACC AGTTGATAAC 1140
 TCATGTTTTA CCATTTAAAA AAATCAGTGA AGGATTTGAG CTGCTCAATT CAGGACAAAG 1200
 CATTGGAACG GTCCTGACGT TTTGAGATCC AAAGTGGCAG GAGGTCTGTG TTGTTCATGGT 1260
 5 GAACTGGAGT TTCTCTTGTG AGAGTCCCT CATCTGAAAT CATGTATCTG TCTCACAAAT 1320
 ACAAGCATAA GTAGAAGATT TGTGGAAGAC ATAGAACCCT TATAAAGAAT TATTAACCTT 1380
 TATAAACATT TAAAGTCTTG TGAGCACCTG GGAATTAGTA TAATAACAAT GTTAATATTT 1440
 TTGAATTTACA TTTTGTAAAG CTATAATTGT ATCTTTTAAG AAAACATACA CTTGGATTTC 1500
 10 TATGTTGAAA TGGAGATTTT TAAGAGTTT AACCAGCTGC TGCAGATATA TAACTCAAAA 1560
 CAGATATAGC GTATAAGAT ATAGTAAATG CATCTCCCAG AGTAATATTC ACTTAACACA 1620
 TTGAAACTAT TATTTTTPAG ATTTGAATAT AAATGTATTT TTTAAACACT TGTATGAGT 1680
 TAACTGGAT TACATTTTGA AATCAGTTCA TTCCATGATG CATATTACTG GATTAGATTA 1740
 AGAAAGACAG AAAAGATTAA GGGACGGGCA CATTTTTCAA CGATTAAGAA TCATCATTAC 1800
 15 ATAACTGGT GAAACTGAAA AAGTATATCA TATGGGTACA CAAGGCTATT TGCCAGCATA 1860
 TATTAATATT TTAGAAAAATA TTCCTTTTGT AATACTGAAT ATAAACATAG AGCTAGAGTC 1920
 ATATTATCAT ACTTATCATA ATGTTCAATT TGATACAGTA GAATTGCAAG TCCCTAAGTC 1980
 CCTATTCAT GTGCTTAGTA GTGACTCCAT TTAATAAAAA GTGTTTTTAG TTTTAAACAA 2040
 CTAAACCG

Seq ID NO: 101 Protein sequence:
 Protein Accession #: NP_000664

1 11 21 31 41 51
 | | | | |
 25 MGTAGKVIK KAAVLWEQKQ PFSIEBIEVA PPKTKEVRK ILATGICRTD DHVIKGTMSV 60
 KFPVIVGHEA TGIVESIGEG VTTVKPGDKV IPLFLPQCRE CNACRNPDCN LCIRSDITGR 120
 GVLAGDTTRF TCKGKPVHFF MNTSTFTYET VVDESSVAKI DDAAPPEKVC LIGCGFSTGY 180
 GAAVKTGKVK PGSTCVVFLG GVGGLSVIMG CKSAGASRII GIDLNKDKFE KAMAVGATEC 240
 30 ISPKDSTKPI SEVLSEMTGN NVGYTFEVIH HLETMIDALA SCHMNYGTSV VVGVPSPAKM 300
 LTYDPMLEFT GRTWGCVCVF GLKSRDDVPK LVTEFLAKKF DLDQLITHVL PFKKISEGFE 360
 LLNSGQSIRT VLTFF

Seq ID NO: 102 DNA sequence
 Nucleic Acid Accession #: NM_006783.1
 Coding sequence: 1..786

1 11 21 31 41 51
 | | | | |
 40 ATGGATTGGG GGACGCTGCA CACTTTCATC GGGGGTGTCA ACAAACTCT CACCAGCATC 60
 GGAAGGTGT GGATCACAGT CATCTTAT TCCGAGTCA TGATCCTAGT GGTGGCTGCC 120
 CAGGAAGTGT GGGGTGACGA GCAAGAGGAC TTCGTCTGCA ACACACTGCA ACCGGGATGC 180
 AAAAAATGTG TCTATGACCA CTTTTTCCCG GTGTCCTGCA TCCGGCTGTG GGCCCTCCAG 240
 CTGATCTTCG TCTCCACCCC AGCGCTGCTG GTGGCCATGC ATGTGGCCTA CTACAGGCAC 300
 45 GAAACCACTC GCAAGTTCAG GCGAGGAGAG AAGAGGAATG ATTTCAAAGA CATAGAGGAC 360
 ATTAAGAGC ACAAGGTTCT GATAGAGGGG TCGCTGTGGT GGACGTACAC CAGCAGCATC 420
 TTTTCCGAA TCATCTTTGA AGCAGCCTTT ATGTATGTGT TTTACTTCTT TACAATGGG 480
 TACCACCTGC CTGGGTGTGT GAAATGTGGG ATTGACCCCT GCCCAACCT TGTGACTGTC 540
 TTTATTTCTA GGCACACAGA GAAGACCGTG TTTACCATTT TTATGATTTC TGCGTCTGTG 600
 50 ATTTGATGTC TGCTTAACGT GGCAGAGTTG TGCTACCTGC TGCTGAAAGT GTGTTTTAGG 660
 AGATCAAGA GAGCAGAC GCAAAAAAAT CACCCCAATC ATGCCCTAAA GGAGAGTAAG 720
 CAGAATGAAA TGAATGAGCT GATTTAGAT AGTGGTCAAA ATGCAATCAC AGGTTTCCCA 780
 AGCTAA

Seq ID NO: 103 Protein sequence:
 Protein Accession #: NP_006774.1

1 11 21 31 41 51
 | | | | |
 60 MDWGLTLTFI GGVNKHSTSI GKVVITVIFI FRVMILVVAA QEVWGDEQED FVCNTLQPGC 60
 KNCVYDHFPP VSHIRLWALQ LIPVSTPALL VAMHVAYYRH ETTRKFRRGE KRNDPKDIED 120
 IKKHKVRIEG SLWWTYSSSI FPRIIIEAAF MYVIFYLYNG YHLPWVLKCG IDPCPNLVDC 180
 FISRPTEKTV FTIFMISASV ICMLLNVAEL CYLLLVKCFR RSKRAQTQKN HPNHALKESK 240
 QNEMNELISD SQQNATITGFP S

Seq ID NO: 104 DNA sequence
 Nucleic Acid Accession #: NM_020411
 Coding sequence: 86-526

1 11 21 31 41 51
 | | | | |
 70 GGACCTGGGA AGGAGCATAG GACAGGGCAA GCGGGGATAA GGAGGGGCAC CACAGCCCTT 60
 AAGGCACGAG GGAACCTCAC TGCGCATGCT CCTTTGGTGC CCACCTCAGT GCGCATGTTT 120
 ACTGGGCGCT TCCCCATCGG CCCCTTCGCC AGTGTGGGGA ACGCCGCGGA GCTGTGAGCC 180
 75 GCGGACTCGG GTCCCTGAGG TCTGGATTCT TTCTCCGCTA CTGAGACACG GCGGACACAC 240
 ACAAAACACAG AACCACACAG CCACTCCAGT GAGCCAGTA ATGGAGAGCC CCAAAAAGAA 300
 GAACACGAGC CTGAAGTTCG GGATCTTACA CCTGGGCAGC AGACAGAAGA AGATCAGGAT 360
 ACAGCTGAGA TCCCACTGCG CGACATGGAA GGTGATCTGC AAGAGCTGCA TCAGTCAAAC 420
 ACCGGGGGATA AATCTGGATT TGGGTTCCGG CGTCAAGGTG AAGATAATAC CTAAAGAGGA 480
 80 AACTGTAA ATGCCAGAAG CAGGTGAAGA GCAACACAA GTTTAAATGA AGACAAGCTG 540
 AAACAACGCA AGCTGGTTTT ATATTAGATA TTTGACTTAA ACTATCTCAA TAAAGTTTTG 600
 CAGCTTTCAC CAAAAAATA AAAAAA

Seq ID NO: 105 Protein sequence:
 Protein Accession #: NP_065144.1

1 11 21 31 41 51

MLLWCPPQCA	CSLGVFSPAP	SPVWGTTRSC	EPATRVPEVW	ILSPLLRRHG	HTQTQNHITAS	60
PRSPVMESPK	KKNQQLKVG	LHLGSRQKKI	RIQLRSQCAT	WKVICKSCIS	QTPGINLDLG	120
SGVKVKIIPK	EEHCKMPEAG	EEQPQV				

Seq ID NO: 106 DNA sequence
Nucleic Acid Accession #: J04129
Coding sequence: 99-587

1	11	21	31	41	51	
CATCCCTCTG	GCTCCAGAGC	TCAGAGCCAC	CCACAGCCGC	AGCCATGCTG	TGCCTCCTGC	60
TCACCTTGGG	CGTGGCCCTG	GTCTGTGGTG	TCCCGGCCAT	GGACATCCCC	CAGACCAAGC	120
AGGACCTGGA	GCTCCCAAG	TTGGCAGGGA	CCTGGCACTC	CATGGCCATG	GCGACCAACA	180
ACATCTCCCT	CATGGCGACA	CTGAAGGCCC	CTCTGAGGGT	CCACATCACC	TCACTGTTGC	240
CCACCCCGA	GGACAACCTG	GAGATCGTTC	TGCACAGATG	GGAGAACAAC	AGCTGTGTTG	300
AGAAGAAGGT	CCTTGGAGAG	AAGACTGGGA	ATCCAAGAA	GTTCAAGATC	AACTATACGG	360
TGGCGAACGA	GGCCACGCTG	CTCGATACTG	ACTACGACAA	TTTCTGTGTT	CTCTGCCTAC	420
AGGACACCA	CACCCCATC	CAGAGCATGA	TGTGCCAGTA	CCTGGCCAGA	GTCTGTGTTG	480
AGGACGATGA	GATCATGCAG	GGATTTCATC	GGGCTTTCAG	GCCCCCTGCC	AGGCACCTAT	540
GGTACTTGCT	GGACTTGAAA	CAGATGGAA	AGCCGTGCCG	TTTCTAGCTC	ACCTCCGCCT	600
CCAGGAAGAC	CAGACTCCCA	CCCTTCCACA	CCTCCAGAGC	AGTGGGACTT	CCTCCTGCC	660
TTTCAAGAA	TAACCAAGC	TCAGAAGACG	ATGACGTGGT	CATCTGTGTC	GCCATCCCCT	720
TCCTGCTGCA	CACCTGCACC	ATTGCCATGG	GGAGGCTGCT	CCCTGGGGGG	AGAGTCTCTG	780
GCAGAGGTTA	TTAATAAACC	CTTGAGCAT	G			

Seq ID NO: 107 Protein sequence:
Protein Accession #: AAA60147

1	11	21	31	41	51	
MDIPQTKQDL	ELPKLAGTWH	SMAMATNNIS	LMATLKAPLR	VHITSLLPPT	EDNLEIVLHR	60
WENNSCVEKK	VLGEKTNPK	KFKINYTVAN	EATLLDIDYD	NFLFLCLQDT	TTPIQSMQC	120
YLARVLVEDD	EIMQGFRAF	RPLPRHLWYL	LDLQKMEEP	RF		

Seq ID NO: 108 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 48-794

1	11	21	31	41	51	
TCCCAGGCAG	CAGTTAGCCC	GCCGCCCCGC	TGTGTGTCCC	CAGAGCCATG	GAGAGAGCCA	60
GTCTGATCCA	GAAGGCCAAG	CTGGCAGAGC	AGGCCGAACG	CTATGAGGAC	ATGGCAGCCT	120
TCATGAAAGG	CGCCGTGGAG	AAGGGCAGAG	AGCTCTCCTG	CGAAGAGCGA	AACCTGCTCT	180
CAGTAGCCTA	TAAGAACGTG	TGGGCGGCC	AGAGGGCTGC	CTGGAGGGTG	CTGTCCAGTA	240
TTGAGCAGAA	AAGCAACGAG	GAGGGCTCGG	AGGAGAAGGG	GCCCCAGGGT	CGTGAGTACC	300
GGAGAAAGGT	GGAGACTGAG	CTCCAGGGCG	TGTGCGACAC	CGTGTGGGCG	CTGTGGGACA	360
GCCACCTCAT	CAAGGAGGCC	GGGACGCGCG	AGAGCCGGGT	CTTCTACCTG	AAGATGAAGG	420
GTGACTACTA	CCGCTACCTG	GCCGAGGTGG	CCACCGGTGA	CGACAAGAAG	CGCATATTG	480
ACTCAGCCCC	GTGAGCCTAC	CAGGAGGCCA	TGGACATCAG	CAAGAAGGAG	ATGCCGCCCA	540
CCAACCCCAT	CCGCTTGGGC	CTGGCCCTGA	ACTTTTCCGT	CTTCCACTAC	GAGATCGCCA	600
ACAGCCCGGA	GGAGGCCATC	TCTCTGGCCA	AGACCACTTT	CGACGAGGCC	ATGGCTGATC	660
TGCACACCTT	CAGCAGGAC	TCCTACAAAG	ACAGCACCTT	CATCATGCAG	CTGCTGCGAG	720
ACAACCTGAC	ACTGTGGACG	GCCGACAACG	CCGGGAAGA	GGGGGGCGAG	GCTCCCCAGG	780
AGCCCCAGAG	CTGAGTGTG	CCCGCCACCG	CCCCGCCCTG	CCCCCTCCAG	TCCCCACCC	840
TGCCGAGAGG	ACTAGTATGG	GGTGGGAGGC	CCACCCCTTC	TCCCCTAGGC	GCTGTCTCTG	900
CTCCAAGGGG	CTCCGTGGAG	AGGGACTGGC	AGAGCTGAGG	CCACCTGGGG	CTGGGGATCC	960
CACCTTCTTT	GCAGCTGTTG	AGCGCACCTA	ACCACTGGTC	ATGCCCCAC	CCCTGTCTCT	1020
CGCACCCGCT	TCCTCCGATC	CCAGGAGCCA	GGCTACTTCT	CCCCCTCTCT	TGCTCCCTCT	1080
CTGCCCTGCT	TGCTCTGTAT	CGTAGGAATT	GAGGAGTGTC	CGGCTTGTG	GCTGAGAACT	1140
GGACAGTGGC	AGGGGCTGGA	GATGGGTGTG	TGTGTGTGTG	TGTGTGTGTG	TGTGTGTGTG	1200
CGCGCGCGCC	AGTGCAAGAC	CGAGATTGAG	GAAAGCATG	TCTGCTGGGT	GTGACCATGT	1260
TTCTCTCTCA	TAAAGTTCCC	CTGTGACACT	C			

Seq ID NO: 109 Protein sequence:
Protein Accession #: NP_006133.1

1	11	21	31	41	51	
MERASLIQKA	KLAEQAERYE	DMAAFMKGAV	EKGEELSCEE	RNLLSVAYKN	VVGGQRAAWR	60
VLSSIEQKSN	EEGSEEEKPE	VREYREKVT	ELQGVCDTVL	GLLDSHLIKE	AGDAESRVFY	120
LKMKGDYRY	LAEVATGDDK	KRIIDSARSA	YQEAMDISKK	EMPPTNPIRL	GLALNFSVFH	180
YEIANSPPEA	ISLAKTTFDE	AMADLHLLSE	DSYKDSTLIM	QLLRDNLTLW	TADNAGEEGG	240
EAPQEPQS						

Seq ID NO: 110 DNA sequence
Nucleic Acid Accession #: NM_000695
Coding sequence: 407-1564

1	11	21	31	41	51	
CACGAGTTGG	TTTGGGAGCT	GCCAGTCTCC	TGGGAGGATC	GCAGTCAGCA	GAGCAGGGCT	60
GAGGCCTGGG	GGTAGGAGCA	GAGCCTGCGC	ATCTGGAGGC	AGCATGTCCA	AGAAAGGGAG	120
TGGAGGTGCA	CGGAAGGACC	CAGGGGAGCA	GCCACGCTG	GGGATGGACC	CCTTCGAGGA	180
CACACTGCGG	CGGCTGCGTG	AGGCCTTCAA	CTGAGGGCGC	ACGCGGCGCG	CCGAGTTCCG	240
GGCTGCGCAG	CTCCAGGGCC	TGGGCCACTT	CCTTCAAGAA	AACAAGCAGC	TTCTGCGCGA	300

5	CGTGCTGGCC	CAGGACCTGC	ATAAGCCAGC	TTTCGAGGCA	GACATATCTG	AGCTCATCCT	360
	TTGCCAGAAC	GAGGTTGACT	ACGCTCTCAA	GAACCTTCAG	GCCTGGATGA	AGGATGAACC	420
	ACGGTCCACG	AACCTGTTCA	TGAAGCTGGA	CTCGGTCTTC	ATCTGGAAGG	AACCTTTTGG	480
	CCTGGTCTCT	ATCATCGCAC	CCTGGAACCT	CCCATTTGAAC	CTGACCTCTG	TGCTCCTGGT	540
	GGGCACCTCT	CCCGCAGGGA	ATTGCGTGGT	GCTGAAGCCG	TCAGAAATCA	GCCAGGGCAC	600
	AGAGAAGGTC	CTGGCTGAGG	TGCTGCCCCA	GTACCTGGAC	CAGAGCTGCT	TTGCCGTGGT	660
	GCTGGGCGGA	CCCCAGGAGA	CAGGGCAGCT	GCTAGAGCAC	AAGTTGGACT	ACATCTTCTT	720
	CACAGGGAGC	CCTCGTGTGG	GCAAGATTGT	CATGACTGCT	GCCACCAAGC	ACCTGACGCC	780
10	TGTACCCCTG	GAGCTGGGGG	GCAAGAACC	CTGCTACGTG	GACGACAACT	GCGACCCCA	840
	GACCGTGGCC	AACCGCGTGG	CCTGGTTCTG	CTACTTCAAT	GCCGGCCAGA	CCTGCGTGGC	900
	CCCTGACTAC	GTCTGTGCA	GCCCCGAGAT	GCAGGAGAGG	CTGCTGCCCG	CCCTGCAGAG	960
	CACCATCACC	CGTTTCTATG	GCGACGACCC	CCAGAGCTCC	CCAAACCTGG	GCCGCATCAT	1020
	CAACCAGAAA	CAGTTCCAGC	GGCTGCGGGC	ATTGCTGGGC	TGCGGCCGCG	TGGCCATTGG	1080
15	GGGCCAGAGC	AACGAGAGCG	ATCGCTACAT	CGCCCCACG	GTGCTGGTGG	ACGTGCAGGA	1140
	GACGGAGCCT	GTGATGCAGG	AGGAGATCTT	CGGGCCCATC	CTGCCCATCG	TGAACGTGCA	1200
	GAGCGTGGAC	GAGGCCATCA	AGTTTCATCA	CCGGCAGGAG	AAGCCCCCTG	CCCTGTACGC	1260
	CTTCTCCAAC	AGCAGACAGG	TTGTGAACCA	GATGCTGGAG	CGGACCAACA	GCGGCAGCTT	1320
	TGGAGGCAAT	GAGGGCTTCA	CCTACATATC	TCTGCTGTCC	GTGCCATTCT	GGGGAGTCGG	1380
20	CCACAGTGGG	ATGGGCGCGT	ACCACGGCAA	GTTCACCTTC	GACACCTTCT	CCCACCAACG	1440
	CACCTGCCTG	CTCGCCCCCT	CGGGCCTGGA	GAAATTAAAG	GAGATCCGCT	ACCCACCCCTA	1500
	TACCGACTGG	AACACGAGC	TGTTACGCTG	GGGCATGGGC	TCCAGAGACT	GCACCTCTCT	1560
	GTGAGCGTCC	CACCCGCTCT	CAACGGGTCA	CACAGAGAAA	CCTGAGTCTA	GCCATGAGGG	1620
	GCTTATGCTC	CCAACTCACA	TTGTTCTCTC	AGACCGCAGG	CTCCCCCAGC	CTCAGGTTGC	1680
25	TGGAGCTGTG	ACATGACTGC	ATCCTGCGCT	CCAGGGCTGC	AAAGCAAGGT	CTTGCTTCTA	1740
	TCTGGGGGAC	GCTGCTCGAG	AGAGGCCGAG	AGGCCGAGA	ACATGCCAGG	TGTCTCTACT	1800
	CACCCCAACC	TCCCCAATTT	CAGCCCTTTG	CCCTCTCGGT	CAGGGTTGGC	CAGGCCCACT	1860
	CACAGGGGCA	GTGTCAACCT	GGAAATAACA	GTGCCCTGCC	TTCTTAGGGG	CATCAGCCCT	1920
	GAAAGGTTGA	GAGCGTGGAG	CCCTCCAGGC	CTTTGCTCTC	CCCTCTAGGC	ACACGCGCAC	1980
30	TTCCACCTCT	GCCCCATCCC	AACCTGACCA	GCACTGCCTC	CCCCAGGGAT	CCTCTCACAT	2040
	CCCACTCTGG	TCTCTGCACC	ACCCCTCTGG	TTCAACCCGC	ACCCTGCACT	CACCCACAGC	2100
	AGTCCATACC	ACTGGGAAAA	CTGGGGTTTG	CATCACTCCA	CTGCACAGTG	TTAGTGGGAC	2160
	CTGGGGGCAA	GTCCCTTGAC	TTCTCTGAGC	CTCAGTTTCC	TTATGTGAAA	GTGCTGGAAA	2220
	CCAAATGGGA	GTCACTTATG	CCAACTCTA	ATAAATGGGA	GTGGGGGGGG	CACATAGAAG	2280
35	CCCTCACACA	CACATGCCCG	TAACAGGATT	TATCACAAG	ACACGCTGCT	ATGTAAGACC	2340
	AGACACAGGG	CGTATGGAAA	AGCACGTCTT	CAAAGACTGT	AGTATTCCAG	ATGAGCTGCA	2400
	GATGCTTACC	TACCAACGGC	GTCTCCACCA	GAAACCATC	GCCAACTCCT	GCGATCAGCT	2460
	TGTGACTTAC	AAACCTTGT	TAAAGCTGC	TTACATGGAC	TTCTGTCTCT	TAAACGTTT	2520
40	CCCTTGGCTG	TGGCCCTCTG	TGTATGCTGC	GGATCCTTCC	AAGCACTCAT	AGCCCAAGATA	2580
	GGAATCTCT	GCTCTCCCA	AATAAATCCA	TCTGTTCT			

Seq ID NO: 111 Protein sequence:
Protein Accession #: NP_000686

45	1	11	21	31	41	51	
	MKDEPRSTNL	FMKLDVSFVI	KEPFLVLII	APWNYPLNLT	LVLLVGLPA	GNCVVLKPSE	60
	ISQGETKVL	EVLPQYLDQS	CFVVLGGPQ	ETGQLEHLK	DYIFFTGSPR	VGIKIVMTAAT	120
50	KHLTPVTLLE	GGKNPCVDD	NCDPQTVANR	VAWFVFNAG	QTCVADPYVL	CSPEMQERLL	180
	PLAQSTITRF	YGDPPQSSPN	LGRINQKQF	QRLRALLGCG	RVAIGGQSN	SDRYIAPTVL	240
	VDVQETEPVM	QEEIFGPILP	IVNVQSVDEA	IKFINRQEPK	LALYAFNSNR	QVNVQMLERT	300
	SSGSFGNNEG	FTYISLSSVP	FGGVGHSGMG	RYHGKFTFDT	FSHHRCTCLA	PSGLEKLKEI	360
	RYPPYTDWNQ	QLLRWGMGSQ	SCITLL				

Seq ID NO: 112 DNA sequence
Nucleic Acid Accession #: NM_004456
Coding sequence: 58-2298

60	1	11	21	31	41	51	
	GAATTCGGGG	CGACGCGCGG	GAACAACGCG	AGTCGGCGCG	CGGGACGAAG	AATAATCATG	60
	GGCCAGACTG	GGAAGAAATC	TGAGAAGGGA	CCAGTTTGT	GGCGGAAGCG	TGTAAATCA	120
	GAGTACATGC	GACTGAGACA	GCTCAAGAGG	TTGAGACGAG	CTGATGAAGT	AAAGAGTATG	180
65	TTTAGTTTCCA	ATCGTCAGAA	AATTTTGGAA	AGAACGGAAA	TCTTAAACCA	AGAATGGAAA	240
	CAGCGAAGGA	TACAGCCTGT	GCACATCCTG	ACTTCTGTGA	GCTCATGTGC	CGGGACTAGG	300
	GAGTGTTCGG	TGACCACTGA	CTTGGATTTT	CCAACACAAG	TCATCCCAT	AAAGACTCTG	360
	AATGCAAGTT	CTTCAGTACC	CATAATGTAT	TCTTGGTCTC	CCCTACAGCA	GAATTTTATG	420
	TGGGAAGATG	AAACTGTTTT	ACATAACATT	CCTTATATGG	GAGATGAAGT	TTTAGATCAG	480
70	GATGGTACTT	TCATTGAAGA	ACTAATAAAA	AATTATGATG	GGAAAGTACA	CGGGGATAGA	540
	GAATGTGGGT	TTATAAATGA	TGAAATTTT	GTGGAGTTGG	TGAATGCCCT	TGGTCAATAT	600
	AATGATGATG	ACGATGATGA	TGATGGAGAC	GATCCTGAAG	AAAGAGAAGA	AAAGCAGAAA	660
	GATCTGGAGG	ATCACCAGAG	TGATAAAGAA	AGCCGCCAC	CTCGGAAT	TCCTTCTGAT	720
	AAATTTTGG	AGGCCATTTT	CTCAATGTTT	CCAGATAAGG	GCACAGCAGA	AGAACTAAAG	780
75	GAAAAATATA	AAGAAGTACC	CGAACAGCAG	CTCCAGGCG	CATTCTCTCC	TGAATGTACC	840
	CCCAACATAG	ATGGACCAAA	TGCTAAATCT	GTTCAGAGAG	AGCAAGCTT	ACACTCCTTT	900
	CATACGCTTT	TCTGTAGGCG	ATGTTTTAAA	TATGACTGCT	TCCTACATCC	TTTTCATGCA	960
	ACACCCAACA	CTTATAAGCG	GAAGAACA	GAAACAGCTC	TAGACAACAA	ACCTTGTTGA	1020
	CCACAGTGT	ACCAGCATTT	GGAGGGAGCA	AAGGAGTTTG	CTGCTGCTCT	CACCGCTGAG	1080
80	CGGATAAAGA	CCCCACCAAA	ACGTCCAGGA	GGCCGCAGAA	GAGGACGGCT	TCCCAATAAC	1140
	AGTAGCAGCG	CCAGCAGCCC	CACCATTAAT	GTGCTGGAAT	CAAAGGATAC	AGACAGTGAT	1200
	AGGGAAGCAG	GGACTGAAAC	GGGGGAGAG	AACAATGATA	AAGAAGAAGA	AGAGAAGAAA	1260
	GATGAAACTT	CGAGCTCCTC	TGAAGCAAA	TCTCGGTGTC	AAACACCAAT	AAAGATGAAG	1320
	CCAAATATTG	AAAGCTCCTG	GAATGTGGAG	TGGAGTGGTG	CTGAAGCCTC	AATGTTTAGA	1380
	GTCTCTATTG	GCACTTACTA	TGCAAAATTC	TGTGCCATTG	CTAGGTTAAT	TGGGACCAAA	1440
85	ACATGTAGAC	AGGTGTATGA	GTTTAGAGTC	AAAGAATCTA	GCATCATAGC	TCCAGCTCCC	1500
	GCTGAGGATG	TGGATACTCC	TCCAAGGAAA	AAGAAGAGGA	AACACCGGTT	GTGGGCTGCA	1560
	CACGTGAGAA	AGATACAGCT	GAAAAAGGAC	GGCTCCTCTA	ACCATGTTTA	CAACTATCAA	1620

CCCTGTGATC ATCCACGGCA GCCTTGTGAC AGTTCGTGCC CTTGTGTGAT AGCACAAAAT 1680
 TTTTGTGAAA AGTTTTGTCA ATGTAGTTCA GAGTGTCAAA ACCGCTTTCC GGGATGCCGC 1740
 TGCAAAGCAC AGTGCACAC CAAGCAGTGC CCGTGCTACC TGGCTGTCCG AGAGTGTGAC 1800
 CCTGACCTCT GTCTTACTTG TGGAGCCGCT GACCATTTGG ACAGTAAAAA TGTGTCTCTG 1860
 AAGAACTGCA GTATTACGCG GGGCTCCAAA AAGCATCTAT TGCTGGCACC ATCTGACGTG 1920
 GCAGGCTGGG GGATTTTTAT CAAAGATCCT GTGCAGAAAA ATGAATTCAT CTCAGAATAC 1980
 TGTGGAGAGA TTATTCTCTA AGATGAAGCT GACAGAAGAG GGAAGTGTGA TGATAAATAC 2040
 ATGTGCAGCT TTCTGTTCAA CTTGAACAAAT GATTTTGTGG TGGATGCAAC CCGCAAGGGT 2100
 AACAAATTC GTTTTGCAAA TCATTGCGTA AATCCAAACT GCTATGCAAA AGTTATGATG 2160
 GTTAACGGTG ATCACAGGAT AGGTATTTTT GCCAAGAGAG CCATCCAGAC TGGCGAAGAG 2220
 CTGTTTGTGT ATTACAGATA CAGCCAGGCT GATGCCCTGA AGTATGTCG CATCGAAAGA 2280
 GAAATGGAAA TCCCTTGACA TCTGTACCT CCTCCCCCTC CTCTGAAACA GCTGCCTTAG 2340
 CTTCAGGAAC CTCGAGTACT GTGGGCAATT TAGAAAAAGA ACATGCAGTT TGAAATTCTG 2400
 AATTTGCAAA GTACTGTAAG AATAATTTAT AGTAATGAGT TTAATAATCA ACTTTTATT 2460
 GCCTTCTCAC CAGCTGCAAA GTGTTTGTGA CCAGTGAATT TTTGCAATAA TGCAGTATGG 2520
 TACATTTTTC AACTTTGAAT AAAGAATACT TGAACCTGAA AAAAAA AAAAAA

Seq ID NO: 113 Protein sequence:
 Protein Accession #: NP_004447

1 11 21 31 41 51
 MGQTGKKSEK GPVCRWRKVK SEYMRLRQLK RFRRADEVKS MFSSNRQKIL ERTEILNQEW 60
 KQRRIQPVHI LTSVSSLRGT RECSVSDLD FPTQVIPLKT LNAVASVPIM YSWSPLOQNF 120
 MVEDEVVLHN IPYMGDEVLD QDGTPIEELI KNYDGKVHGD RECGFINDEI FVELVNALGQ 180
 YNDDDDDDDDG DDPEEREKQ KDLEDHRDDK ESRPPRKFPK DKILEAISMM FPDKGTAEBL 240
 KEKYKELTEQ QLPGLPPEC TPNIDGPNK SVQREQSLHS FHTLFCRRCF KYDCFLHPFH 300
 ATPNTYKRKN TETALDNKPC GPQCYQHLEG AKEFAAALTA ERIKTPPKRP GRRRRGRLPN 360
 NSSRPSTPTI NVLESKDTDS DREAGTETGG ENNDKEEEK KDETSSSSEA NSRCQTPIM 420
 KPNIEPPENV EWSGAEASMF RVLIGTYIDN FCAIARLIGT KTCRQVYEFR VKESSIIAPA 480
 PAEDVDTPPR KKKRRHRHWA AHCRIQLKK DGSSNHVYNY QPCDHPRQPC DSSCPVIAQ 540
 NFCEKFCQCS SECQNRFPGC RCKAQCNKQ CPCYLAVREC DPDLCLTCGA ADHWDKSNVS 600
 CKNCISQRGS KKHLLAPSD VAGWGIFIKD PVQKNEFISE YCGEIIISQDE ADRRGKVYDK 660
 YMCSEFLNIN NDFVVDATRK GNKIRFANHS VNPNCYAKVM MVNGDHRIGI FAKRAIQTGE 720
 ELFDYRYSQ ADALKYVGIE REMEIP

Seq ID NO: 114 DNA sequence
 Nucleic Acid Accession #: NM_001827
 Coding sequence: 96-335

1 11 21 31 41 51
 AGTCTCCGGC GAGTTGTTGC CTGGGCTGGA CGTGGTTTGG TCTGCTGCGC CCGCTCTTCG 60
 CGCTCTCGTT TCATTTTCTG CAGCGCGCCA CGAGGATGGC CCACAAGCAG ATCTACTACT 120
 CGGACAAGTA CTTGACGAG CACTACGAGT ACCGGCATGT TATGTTACCC AGAGAACTTT 180
 CCAACAAGT ACCTAAACT CATCTGATGT CTGAAGAGGA GTGGAGGAGA CTTGGTGTCC 240
 AACAGAGTCT AGGCTGGGTT CATTACATGA TTCATGAGCC AGAACCACAT ATTCTTCTCT 300
 TTAGACGACC TCTTCCAAA GATCAACAAA AATGAAGTTT ATCTGGGGAT CGTCAAATCT 360
 TTTTCAAATT TAATGTATAT GTGTATATAA GGTAGTATTC AGTGAATACT TGAGAAATGT 420
 ACAAACTCTT CATCCATACC TGTGCATGAG CTGTATTCTT CACAGCAACA GAGCTCAGTT 480
 AAATGCAACT GCAAGTAGT TACTGTAAGA TGTTTAAGAT AAAAGTTCTT CCAGTCAGTT 540
 TTTCTTTAA GTGCTGTTT GAGTTTACTG AAACAGTTTA CTTTGTTCAT ATAAAGTTTG 600
 TATGTTGCAT TTAATAAAAA AAAAAA

Seq ID NO: 115 Protein sequence:
 Protein Accession #: NP_001818

1 11 21 31 41 51
 MAHKQIYYSD KYFDEHYEYR HVMLPRELSK QVPKTHLMSE EEWRLGVQO SLGWVHYMIH 60
 EPEPHILLFR RPLPKDQKQ

Seq ID NO: 116 DNA sequence
 Nucleic Acid Accession #: CAT cluster

1 11 21 31 41 51
 TCAGACCTCA TGAGTCACTT GGACTCTTGA GCCACCTCTG GGGGTGGAGT CTCTCTCTG 60
 GCATCTGGAC CCTTGGTGCT ATCGACGAAG CTGCGGTGGG GCTCTTAGCT GCTATGTGCA 120
 AGAGGTGTGT TCCAGGGAAA GCCCTATCT CTCTGCAGAG GTCAAGTGAA AGCGACGGCC 180
 GCAGCCAACA GAGTTCAAAA TGCAGGCTTG GAAAGTACAG GGGGCTCTGT GGAGGATGGG 240
 AAGGACTGAT CCACATTCCT ACCAGGAAGT TTAGCAGAAC CCCCCTGTGC CAACTGGACC 300
 CCTTGAAGG ACCTGGCTCA GGTGGACCA CTTCTTGAGA GGGAGGAGCT CTGGATTGTA 360
 TCAAGAATTC TTGCTGAGC ATGGTGCCTC ATGCCTATAA TACCAACACT TTGGGAGGCC 420
 AGTGTGGGAG GATCTCTTGA GCCCAGGAGT TCAAGACTAG CCTGGGCAAC ACAGAGAGAA 480
 CCCATCTCTA AATAATAAAT AATAATAAAA TAAAAAATTA GCAGGGCATG GTGGCATGTG 540
 CCTGTAGTTC CAGCTACCCA GGAGGCTGAG GCAAGAGGAT GGCTGGAGCC TGGGATGTTG 600
 AGGCTGCAAT GAACGTGTAT TACCCCACTG CACTCCAGCC TGGGCAAAAG AGCGAGAGAA 660
 CCTGTCTCAA ATAATAATAA TAATAATAAT CTTATTTTGG AGAATAAAGA GACCTCTGGA 720
 TTTGAGGTGC CATTTGGGTA GAAAGAAAAG ACGTTTACAC CGAGAAATAG TCTGTGTTGC 780
 CCTGAAGGAG CAGAGGGATG CATCGCTGGA GGTGACCTAC AGTTGAAGAA GACTCATTAT 840
 GACAGACCTT GTCCTTCTTC CTTGTGGAAA GTGTTTCTCT TGCTGCTACT GCTCATGAGA 900
 CTCTTCCCCC TCCCTGTCCC AGGGAACCAA AGGGCTTTCT ACCACACCTT TTCTTGCCCC 960
 CGCCTCCCA TGTCTGTGTG GCCTTGTGAC TCAGCAATTC TGTGTTGCTC CATTATCTTC 1020
 CAGCCGATA CAGAGTGAAT AGTTAACCACT ACTTAGGTCA AATAGGATCT AAATTTTGT 1080
 TCTGTCTCCG TGTAAAGAGG CCAGTGTTTG TGTGTTGCAA GCAGCCTTGG AATAGTAACT 1140

CTCTCATTT GTTTGGGATC TGGCCACCAA GTTCCAGAAT GATACACGGA TCAGTGCAGA 1200
 AGTTTCATCAG GCTCTCGGAC CTTAGGGCTG TTGGAGAAGG CTTACGCAGC AGAATCATG 1260
 GTGAAGGCTC GTGTTCTCCA TCCTCAACTT TCTTTGCTTC GATCATACAC AAGAATACAT 1320
 TTGGAGGGC AAAAAATGAA CACTGTGCTT CATTGCAGCC GTGTTTTGTG ACACAGATGC 1380
 ACAGTCTGCT GTGAAGACCT TCTCTCAAGT GGCATTTGGG AGTCCATGCC AGATCATGGT 1440
 GCTTCATGAG AGACTGACAG CTATCAGGGG TTGTGGCACT TAGTGAGGAC TCTCCTCCCC 1500
 CAGTGTGTGC TGATGACACA TACACACCTG ACAATAGCTT GAGTCTTCTC TGTTCCTTTT 1560
 ACTCTGTAGC CAACATACAC ATGATTAAAA ACCCTTTCTA AATATCTATC ATGGTTTCATC 1620
 CTTGTCCAAA TGCAGAGTCA GAGCTATTG TACTTCATTA TTATTCCAA GGCGAATAGT 1680
 TGGCTTTCTT TTTGCAAAAA TAATTAAAGT TTTTGTATGT TGCAAAAAAA AAAAAAAA 1740
 AAACAAAAAA

Seq ID NO: 117 DNA sequence
 Nucleic Acid Accession #: BC012178.1
 Coding sequence: 204-2285

1 11 21 31 41 51
 CTCTCTCTCC GCGGCGCTGG GGCCCGCGCT CCGCTGCTGT TGCTCCATTC GCGCTTTTC 60
 TGGCGGCTGG CTCCTCTCCG CTGCGGGCTG CTCTCGACC AGGCTCCTT CTCAACCTCA 120
 GCCCGCGGCG CCGACCCCTC CCGCCCGCTC TCGTACTGTC CCGCTCACCG 180
 CCGCGGCTCC GGCCCTGGCC CCGATGGCTC TGTGCAACGG AGACTCCAAG CTGGAGAAATG 240
 CTGGAGGAGA CCTTAAGGAT GGCCACCACC ACTATGAAGG AGCTGTTGTC ATCTGGATG 300
 CTGGTGTCTA GTACGGGAAA GTCATAGACC GAAGAGTGAG GGAAGTGTTC GTGCAGTCTG 360
 AAATTTTCCC CTGGAACCA CCAGCATTG CTATAAAGGA ACAAGGATTC CGTGCTATTA 420
 TCATCTCTGG AGGACCTAAT TCTGTGTATG CTGAAGATGC TCCCTGGTTT GATCCAGCAA 480
 TATTTCACTAT TGGCAAGCCT GTTCTTGGA TTTGCTATGG TATGCAGATG ATGAATAAGG 540
 TATTTGGAGG TACTGTGCAC AAAAAAAGTG TCAGAGAAGA TGGAGTTTTC AACATTAGTG 600
 TGGATAATAC ATGTTTCATTA TTCAGGGGCC TTCAGAAGGA AGAAGTTGTT TTGCTTACAC 660
 ATGGAGATAG TGTAGACAAA GTAGCTGATG GATTCAAGGT TGTGGCACGT TCTGGAAACA 720
 TAGTAGCAGG CATAGCAAAAT GAATCTAAAA AGTTATATGG AGCACAGTTC CACCTGAAG 780
 TTGGCTTAC AGAAAATGGA AAAGTAATAC TGAAGAATTT CCTTTATGAT ATAGCTGGAT 840
 GCAGTGGAA CTTACCCGTG CAGAACAGAG AACTTGAGTG TATTCGAGAG ATCAAAGAGA 900
 GAGTAGGCAC GTCAAAAGTT TTGGTTTAC TCAGTGGTGG AGTAGACTCA ACAGTTTGTA 960
 CAGCTTTGCT AAATCGTGCT TTGAACCAAG AACAAGTCAT TGCTGTGCAC ATTGATAATG 1020
 GCTTTATGAG AAAACGAGAA AGCCAGTCTG TTGAAGAGGC CCTCAAAAAG CTTGGAATTC 1080
 AGGTCAAAGT GATAAATGCT GCTCATTCTT TCTACAATGG AACAAACACC CTACCAATAT 1140
 CAGATGAAGA TAGAACCCTA CGGAAAAGAA TTAGCAAAAC GTTAAATATG ACCACAAATC 1200
 CTGAAGAGAA AAGAAAAATC ATTGGGGATA CTTTGTGTTA GATTGCCAAT GAAGTAATG 1260
 GAGAAATGAA CTTGAAACCA GAGGAGGTTT TCCTTGCCCA AGGTACTTTA CGGCTGATC 1320
 TAATTGAAAG TGCAATCCCT GTTGCAAGTG GCAAAGCTGA ACTCATCAA ACCCATCACA 1380
 ATGACACAGA GCTCATCAGA AAGTTGAGAG AGGAGGGAAA AGTAATAGAA CCTCTGAAAG 1440
 ATTTTCATAA AGATGAAGTG AGAATTTTGG GCAGAGAACT TGGACTTCCA GAAGAGTTAG 1500
 TTTCCAGGCA TCCATTTCCA GGTCTGGGCC TGGCAATCAG AGTAATATGT GCTGAAGAAC 1560
 CTTATATTGG TAAGGACTTT CCTGAAACCA ACAATATTTT GAAAATAGTA GCTGATTTT 1620
 CTGCAAGTGT TAAAAGCCA CATACCCTAT TACAGAGAGT CAAAGCCTGC ACAACAGAAG 1680
 AGGATCAGGA GAAGCTGATG CAAATTACCA GTCTGCATTC ACTGAATGCC TTCTTGCTGC 1740
 CAATTAAAC TGTAGGTGTG CAGGGTGACT GTCGTTCTTA CAGTTACGTG TGTGGAATCT 1800
 CCAGTAAAGA TGAACCTGAC TGGGAATCAC TTATTTTCT GGCTAGGCTT ATACCTCGCA 1860
 TGTGTACAAA GCTTAACAGA GTTGTATATA TATTTGGCCC ACCAGTTAAA GAACCTCCTA 1920
 CAGATGTTAC TCCCCTTTTC TTGACAACAG GGGTGCTCAG TACTTTACGC CAAGCTGATT 1980
 TTGAGGCCCA TAACATTTCT AGGGAGTCTG GGTATGCTGG GAAAATCAGC CAGATGCCGG 2040
 TGATTTGAC ACCATTACAT TTTGATCGGG ACCCACTTCA AAAGCAGCCT TCATGCCAGA 2100
 GATCTGTGTT TATTCGAACC TTTATTACTA GTGACTTCAT GACTGGTATA CCTGCAACAC 2160
 CTGGCAATGA GATCCCTGTA GAGGTGGTAT TAAAGATGGT CACTGAGATT AAGAAGATTC 2220
 CTGGTATTT TCGAATTATG TATGACTTAA CATCAAAGCC CCCAGGAATC ACTGAGTGGG 2280
 AGTAATAAAC TTCTTGTCTT ATTAATAA

Seq ID NO: 118 Protein sequence:
 Protein Accession #: AAH12178.1

1 11 21 31 41 51
 MALCNGDSKL ENAGGDLKDG HHYEGAVVI LDAGAQYGVK IDRRVRELFV QSEIFPLETP 60
 AFAIKEQGRF AIIISGGPNS VYAEDAPWFD PAIFTIGKPV LGICYGMQMM NKVFGGTVHK 120
 KSVREDGVFN ISVDNTCSLF RGLQKEEVVL LTHGDSVDKV ADGFKVVARV GNIVAGIANE 180
 SKKLYGAQFH PEVGLTENGK VILKNFLYDI AGCSGFTTVQ NRELECI REI KERVGTSKVL 240
 VLLSGGVDS TCTALLNRAL NQEQVIAVHI DNGFMRKRES QSV EALKKL GIQVKVINAA 300
 HSFYNGTTTL PISDEDRTPR KRISKTLNMT TSPEEKRKII GDTFVKIANE VIGEMNLKPE 360
 EVFLAQGTLR PDLIESASLV ASGKAELIKT HHNDTELIRK LREBKVIEP LKDFHKDEV 420
 ILGRELGLPE ELVSRHPPFG PGLAIRVICA EEPYICKDFP ETNNILKIVA DFSASVKKPH 480
 TLLQVRKACT TEEDQELMQ ITSLSLNAF LLPIKTVGVQ GDCRSYSYVC GISSKDEPDW 540
 ESLIFLARLI PRMCHNVNVR VYIFGPPVKE PPTDVTPTFL TTGVLSTLRQ ADPEAHNLLR 600
 ESGYAGKISQ MPVILTPLHF DRDPLQKQPS CQRSVIRTFT ITSDFMTGIP ATPGNEIPVE 660
 VVLKRMVTEIK KIPGLSRIMY DLTSKPPGTT EWE

Seq ID NO: 119 DNA sequence
 Nucleic Acid Accession #: NM_006500.1
 Coding sequence: 27..1967

1 11 21 31 41 51
 ACTTGCGCTCT CGCCCTCCGG CCAAGCATGG GGCTTCCAG GCTGGTCTGC GCCTTCTTGC 60
 TCGCCGCTCT CTGCTGCTGT CCTCGCTGCG CGGGTGTGCC CGAGAGAGCT GAGCAGCCTG 120
 CGCCTGAGCT GGTGGAGGTG GAAGTGGGCA GCACAGCCCT TCTGAAGTGC GGCCTCTCCC 180
 AGTCCCAAGG CAACCTCAGC CATGTGCACT GGTCTTCTGT CCACAAGGAG AAGCGGACGC 240

	TCATCTTCGG	TGTGGCGCAG	GGCCAGGGCC	AGAGCGAACC	TGGGGAGTAC	GAGCAGCGGC	300
	TCAGCTCCA	GGACAGAGGG	GCTACTCTGG	CCCTGACTCA	AGTCACCCCC	CAAGACGAGC	360
	GCATCTTCTT	GTGCCAGGGC	AAGCGCCCTC	GGTCCCAGGA	GTACCCGATC	CAGCTCCCGC	420
5	TCTACAAAGC	TCCGGAGGAG	CCAAACATCC	AGGTCAACCC	CCTGGGCATC	CCTGTGAACA	480
	GTAAGGAGCC	TGAGGAGGTC	GCTACCTGTG	TAGGGAGGAA	CGGGTACCCC	ATTCTCAAG	540
	TCATCTGGTA	CAAGAAATGGC	CGGCCCTCTGA	AGGAGGAGAA	GAACCGGGTC	CACATTCAGT	600
	CGTCCCAGAC	TGTGGAGTGC	AGTGGTTTGT	ACACCTTGCA	GAGTATTCTG	AAGGCACAGC	660
	TGGTTAAAGA	AGACAAAGAT	GCCAGTTTTT	ACTGTGAGCT	CAACTACCGG	CTGCCAGTGT	720
10	GGAAACCATAT	GAAGGAGTCC	AGGGGAAGTCA	CCGTCCCTGT	TTTCTACCCG	ACAGAAAAAG	780
	TGTGGCTGGA	AGTGGAGCCC	GTGGGAATGC	TGAAGGAAGG	GGACCGCGTG	GAAATCAGGT	840
	GTTTGGCTGA	TGGCAACCTT	CCACCACACT	TCAGCATCAG	CAAGCAGAAC	CCCAGCACCA	900
	GGGAGGCAGA	GGAAAGAGACA	ACCAACGACA	ACGGGGTCCCT	GGTGTGGAG	CCTGCCCGGA	960
	AGGAACACAG	TGGGCGCTAT	GAATGTCAAG	CCTGGAACCT	GGACACCATG	ATATCGCTGC	1020
	TGAGTGAAAC	ACAGGAACAT	CTGGTGAACCT	ATGTGTCTGA	CGTCCGAGTG	AGTCCCGCAG	1080
15	CCCCTGAGAG	ACAGGAAGGC	AGCAGCCTCA	CCCTGACCTG	TGAGGCAGAG	AGTAGCCAGG	1140
	ACCTCGAGTT	CCAGTGGCTG	AGAGAAGAGA	CAGACCAGGT	GCTGGAAAGG	GGGCTGTGTC	1200
	TTCAGTTGCA	TGACCTGAAA	CGGGAGGCAG	GAGGCGGCTA	TCGCTGCGTG	CGCTCTGTGC	1260
	CCAGCATACC	CGCCCTGAAC	CGCACACAGC	TGGTCAAGCT	GGCCATTTTT	GGCCCCCTTT	1320
20	GGATGGCATT	CAAGGAGAGG	AAGGTGTGGG	TGAAAGAGAA	TATGGTGTG	AATCTGTCTT	1380
	GTGAAGCGTC	AGGGGACCCC	CGGCCACCA	TCTCTGGAA	CGTCAACGGC	ACGGCAAGTG	1440
	AACAAGACCA	AGATCCACAG	CGAGTCTTGA	GCACCTTGAA	TGTCTCTGTG	ACCCCGGAGC	1500
	TGTTGGAGAC	AGGTGTTGAA	TGCACGGCCT	CCAACGACCT	GGGCAAAAAC	ACCAGCATCC	1560
	TCTTCTGGA	GCTGGTCAAT	TTAACCAACC	TCACACCAGA	CTCCAACACA	ACCACTGGCC	1620
25	TCAGCACTTC	CACCTGCCAGT	CCTCATACCA	GAGCCAACAG	CACCTCCACA	GAGAGAAAGC	1680
	TGCCGGAGCC	GGAGAGCCGG	GGCGTGGTCA	TCGTGGCTGT	GATTGTGTGC	ATCCTGGTCC	1740
	TGGCCGTGCT	GGGCGCTGTC	CTCTATTTC	TCTATAAGAA	GGGCAAGCTG	CCGTGCAGGC	1800
	GCTCAGGGAA	GCAGGAGATC	ACGCTGCCCC	CGTCTCGTAA	GACCGAACTT	GTAGTTGAAG	1860
	TTAAGTCAAG	TAAGCTCCCA	GAAGAGATGG	GCCTCCTGCA	GGGCAGCAGC	GGTGACAAGA	1920
30	GGGCTCCGGG	AGACCAGGGA	GAGAAATACA	TCGATCTGAG	GCATTAGCCC	CGAATCACTT	1980
	CAGCTCCCTT	CCCTGCCTGG	ACCATTCCCA	GCTCCCTGCT	CACCTTCTCT	TCAGCCAAAG	2040
	CCTCCAAAGG	GACTAGAGAG	AAGCCTCCTG	CTCCCTCAC	CTGCACACCC	CCTTTCAGAG	2100
	GGCCACTGGG	TTAGGACCTG	AGGACCTCAC	TTGGCCCTGC	AAGCCGCTTT	TCAGGGACCA	2160
	GTCCACCACC	ATCTCTCTCA	CGTTGAGTGA	AGCTCATCCC	AAGCAAGGAG	CCCCAGTCTC	2220
35	CCGAGCGGGT	AGGAGAGTTT	CTTGCAGAAC	GTGTTTTTTC	TTTACACACA	TTATGGCTGT	2280
	AAATACCTGG	CTCCTGCCAG	CAGCTGAGCT	GGGTAGCCTC	TCTGAGCTGG	TTTCTTGCCC	2340
	CAAAAGGCTG	CTTCCACCAT	CCAGGTGCAC	CACCTGAAGT	AGGACACACC	GGAGCCAGGC	2400
	GCCTGCTCAT	GTTGAAGTGC	GCTGTTTACA	CCCGCTCCGG	AGAGCACCCC	AGCGGCATCC	2460
	AGAAGCAGCT	GCAGTGTTCG	TGCCACCACC	CTCCTGCTCG	CCTCTTCAAA	GTCTCTGTG	2520
40	ACATTTTTTC	TTTGGTCAGA	AGCCAGGAAC	TGGTGTCAAT	CCTTAAAGAA	TACGTGCCGG	2580
	GGCCAGGTGT	GGTGGCTCAC	GCCTGTAATC	CCAGCACTTT	GGGAGGCCGA	GGCGGGCGGA	2640
	TCACAAAGTC	AGGAGAGAGC	CATCCTGGCT	AACACGGTGA	AACCTGTCT	CTACTAAAAA	2700
	TACAAAAAAA	AATTAGCTAG	GGTAGTGGT	TGGCACCTAT	AGTCCCAGCT	ACTCGGAAGG	2760
	CTGAAGCAGG	AGAATGTTAT	GAATCCAGGA	GGTGGAGCTT	GCAGTGAGCC	GAGACCGTGC	2820
45	CACCTGCATC	CAGCCTGGGC	AACACAGCGA	GACTCCGTCT	CGAGGAAAAA	AAAAGAAAAG	2880
	ACGCGTACCT	CGGGTGAGGA	AGCTGGGCGC	TGTTTTTCGAG	TTCAAGTGAA	TTAGCTCAA	2940
	TCCCGTGTGT	CACCTGTCTC	CATAGCCCTC	TTGATGGATC	ACGTAAAACT	GAAAGGCAGC	3000
	GGGGAGCAGA	CAAAGATGAG	GTCTACACTG	TCCTTCATGG	GGATTAAAGC	TATGGTTATA	3060
	TTAGCACCAA	ACTTCTACAA	ACCAAGCTCA	GGGCCCCAAC	CCTAGAAGGG	CCCAATGAG	3120
50	AGAATGGTAT	TTAGGGATGG	AAAAAGGGGC	CTGGCTAGAG	CTTCGGGTGT	GTGTGTCTGT	3180
	CTGTGTGTAT	GCATACATAT	GTGTGTATAT	ATGGTTTTGT	CAGGTGTGTA	AATTGGCAAA	3240
	TTGTTTCTTT	TATATATGTA	TGTATATATA	TATATGAAAA	TATATATATA	TATGAAAAAT	3300
	AAAGCTTAAT	TGTCCCGAAA	AATCATACAT	TGCTTTTTTA	TTCTACATGG	GTACCACAGG	3360
	AACCTGGGGG	CCTGTGAAAC	TACAACCAAA	AGGCACACAA	AACCGTTTCC	AGTTGGCAGC	3420
55	AGAGATCAGG	GGTTACCTCT	GCTTCTGAGC	AAATGGCTCA	AGCTCTACCA	GAGCAGACAG	3480
	CTACCCTACT	TTTCAGCAGC	AAAACGTCCC	GTATGACGCA	GCACGAAGGG	CCTGGCAGGC	3540
	TGTTAGCAGG	AGCTATGTCC	CTTCTATATG	TTTCCGTCCA	CTT		

Seq ID NO: 120 Protein sequence:
Protein Accession #: NP_006491.1

	1	11	21	31	41	51	
65	MGLPRLVCAF	LLAACCCCPR	VAGVPGEAEQ	PAPELVEVEV	GSTALLKCGI	SQSQGNLSHV	60
	DWFSVHKEKR	TLIFRVRQGG	GQSEPGGEYEQ	RLSLQDRGAT	LALTQVTPQD	ERIFLCCQKR	120
	PRSQEYRIQL	RVKYKPEEEN	IQVNPLGIPV	NSKEPEEVAT	CVGRNGYPIPI	QVIWYKNGRP	180
	LKEEKNRVHI	QSSQTVESSG	LYTLQSLILKA	QLVKEDKDAQ	FYCELNYRLP	SGNHMKESRE	240
70	VTVPVFPYTE	KWLEVEPVG	MLKEGDRVEI	RCLADGNPPP	HFSISKQNPFS	TREAEETTN	300
	DNGVLVLEPA	RKEHSGRYEC	QAWNLDTMIS	LLSEPQELLV	NYVSDVRVSP	AAPERQEGSS	360
	LTLTCEAESS	QDLFQWLRE	ETDQVLERGP	VLQLHDLKRE	AGGGYRCVAS	VPSIPGLNRT	420
	QLVKLAIFGP	PWMAFKERKV	WVKENMVLNL	SCEASGHPRP	TISWNVNGTA	SEQDQDPQRV	480
	LSTLNVLVTP	ELLETVGECT	ASNDLGKNTS	ILFLELVNLT	TLTPDSNTTT	GLSTSTASPH	540
75	TRANSTSTER	KLPEPESRGV	VIVAVIVCIL	VLAVLGAVLY	FLYKKGKLEPC	RRSGKQBEITL	600
	PPSRKTELTV	EVKSKDLPEE	MGLLQSSGSD	KRAPGDQGEK	YIDLRLH		

Seq ID NO: 121 DNA sequence
Nucleic Acid Accession #: NM_018306
Coding sequence: 60-671

	1	11	21	31	41	51	
80	ATAGTCTACA	CAGAGCTCCC	CTTGCTGCCC	AGACAAGCTG	AAGGACCACA	GGAAAAGCCA	60
	TGGAGACTTC	AGCATCCTCC	TCCAGCCTCC	AGGACAACAG	TCAAGTCCAC	AGAGAAACAG	120
85	AAGATGTAGA	CTATGGAGAG	ACAGATTTCC	ACAAGCAAGA	CGGGAAGGCT	GGACTCTTTT	180
	CCCAAGAACCA	ATATGAGAGA	AACAAGTCTT	CTTCTCCTCC	CTTCTCTTCC	TCCTCATCCT	240
	CCTCATCTTC	TTCATCCTCC	TCCTCCTCAG	GTCCTGGGCA	TGGGGAGCCT	GACGTTTTGA	300

5
10
15
20

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AGGATGAGCT TCAACTCTAT GGAGATGCTC CTGGAGAGGT GGTACCCCTCT GGGGAATCAG 360
GACTCCGAAG GAGAGGCTCT GACCCAGCAA GTGGAGAAGT GGAGGCCTCT CAGTTAAGAA 420
GACTGAATAT AAAGAAAGAT GATGAGTTTT TCCATTTCGT CCTCCTGTGC TTGCCATCG 480
GGGCCCTTGCT GGTGTGTTAT CACTATTACG CAGACTGGTT CATGTCCTCT GGGGTCGGCC 540
TGCTCACCTT CGCTCCCTG GAAACCGTTG GCATCTACTT CGGACTAGTG TACCGTATCC 600
ACAGCGTCCT CCAAGGCTTC ATCCCTCTCT TCCAGAAGTT TAGGCTGACA GGGTTCAGGA 660
AGACTGACTG AGGCCACTTC CAGGTGGGCA GCAGAGGCAG GCCCAGTGT GACCACCACT 720
GCGACCCCTG AGCCCAACAAG GGCAGAGCAG CATCTGAGA GACGCACAGG AGACCAAGCC 780
AGACCAATAA ACAGAAACACT TTTCTTCCA TGTGCTCTGA ATGTTGGCAC CAGCCCGGGC 840
AGGGGCATCT CATTTGGGCA GTACTGCTGT GCAACCCAGC TGCAAGGATG GAAGGCAGAG 900
GGTGGGTGTG GGGCCTGAGG CTTACAGTA CCTGGACCAG CAGGAAGATT CTGGGAGGTC 960
ACTGCTCTCA GAGGACAGCA AGGGACCTTG AGCTCTGCAA GCTGTGATCT GTCTGGGTTT 1020
ATGGTTTTTC TCAAATCCCA GGCTATCTGC ATGCGCTCTC AGGTGCTACC GAGCCATCCT 1080
GGGAGAGATG GATGGTCCAC TGCTTTGAGG CAGGGAGCCA TCGGGCTGGG GCCCTTGGT 1140
GAACCTGATG CAGGTAAGAT GCTGAGGACT AAAACCATTT TTTTTCACC CAAAAAATAA 1200
GGCAGGAAAA TGATCATCAG AAACATAAAT GCAGCCAGGC ATGGGGGCTC ACGACTGTAA 1260
TCCTCGCACT TTGGGAGGCT CAGGCTAAGG GTCGCTTGAA GCTGAGAGTT CAAGACCAAC 1320
CTGGGCAACA TAGTGAGACC CCCATCTCTA CAATTTTTTT TTAATGACCA AATGTGGCGG 1380
TACATACCTG TACATACCTG CGGTTCCAGC TACTCAAGAG GCTGAGGCAG GAGGACTGCT 1440
TGAGCCCAGG AGTTTCAGGGC TGCAGTGAGG TACGATCAAG CCACTGCACT CCAGCCTGGG 1500
CGACAGAGCA AGATCGTTTC TCTAAATT

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25 Seq ID NO: 122 Protein sequence:
Protein Accession #: NP_060776

30

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1 11 21 31 41 51
| | | | |
METSASSSQP QDSQVHRET EDVDYGETDF HKQDGKAGLF SQEQYERNKS SSSSFSSSSS 60
SSSSSSSSSS GPCHGEPDVL KDELLQLYGDA PGEVVPSEGS GLRRRGSDPA SGEVEASQLR 120
RLNIKKDDEF FHFVLLCFAI GALLVCYHYD ADWFMSLGVG LLTFASLETV GIYFGLVYRI 180
HSLVQGFPL FQKFRLLTGR KTD

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35 Seq ID NO: 123 DNA sequence
Nucleic Acid Accession #: BC022542
Coding sequence: 243..896

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55
60
65
70

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1 11 21 31 41 51
| | | | |
ACTTGGTCCC AGCCGATAAA TCTGGGGCAG CGCGCGGTAG GAGCTGCGGG CGGCCAGGCC 60
CCTTCCTGCG TCCGCACTCG GCGCCGCGCG CCCCTCTCGG GCGTCCGGCT TCCGGCGTCC 120
TGGCGGCTCG GGTGGCGGCG GTTCGGGCGG CCGCCTGGCT GCTCCTCGGG CGCGCGACGG 180
GGCTCAGCGG CGGGCCCGCC ACGGCCTTCA CCGCCGCGCG CTCTGACGCC GGCATAAGGG 240
CCATGTGTTT TGAATATTAT TTAGGGCAAG AAGTTTGTAA AGATGGTTTC CACAGAGACC 300
TTTAAATCAA AGTGAAGTTT GGGGAAAGCA TTGAGGACTT GCACACGTGC CGTCTCTTAA 360
TTAAACAGGA CATTCCTGCA GGACTTTATG TGGATCCGTA TGAGTTGGCT TCATTACGAG 420
AGAGAAACAT AACAGAGGCA GTGATGTTT CAGAAAATTT TGATATAGAG GCCCTAACT 480
ATTTGTCCAA GGAGTCTGAA GTTCTCATTT ATGCCAGACG AGATTACAG TGCATTGACT 540
GTTTTCAGC CTTTTTGCCT GTGCACTGCC GCTATCATCG GCCGCACAGT GAAGATGGAG 600
AAGCCTCGAT TGTGGTCAAT AACCCAGATT TGTGATGTT TTGTGACCAA GAGTTCCCGA 660
TTTTGAAATG CTGGGCTCAC TCAGAAAGTG CAGCCCTTG TGCTTTGGAT AATGAGGATA 720
TATGCCAATG GAACAAGATG AAGTATAAAT CAGTATATAA GAATGTGATT CTACAAGTTC 780
CAGTGGGACT GACTGTACAT ACCTCTCTAG TATGTTCTGT GACTCTGCTC ATTACAATCC 840
TGTGCTCTAC ATTGACTCCT GTAGCAGTTT TCAAATATGG CCATTTTCTC CTATAAGTTT 900
TATGTAGTTA AATGCTTCTT AGAAACCTAA ATAAGATCTA TTAATTTCTG ACGAGAGGTG 960
TTCTTCTAGA ATTAATTACT TTTATCTTTT GTCTTCATTT GTGGCCAAA TTAGTGTTC 1020
TAGAGGAAAT TTGGGATCAT TCTCAGCTAA TTCCAAAATG TAGTGCTCTA TTGCATGGAT 1080
CCTTGGTAAT CCTCAAGCAT CAGATGCCAT AAGGGGAAAC TTAATTTCTG TAAATTAATG 1140
TTTATTTTGT GAGAAGTGAC TTTATCTTCA TTTGGGGTAG AAAAATTATT TCTTTATGTA 1200
GTAGAGACAA ATTATTCTCA TTTTGCAAGT ACTTTCATTT TAAGCTACAA ATTGAGAAAA 1260
CCGTTATAAA TAAGAAATAA ATAGGCCAGG CACAGTGGCT CACACCTGTA ATCCAGCAC 1320
TTTGGGAGGC CAGAGTGGGC GGAATCACCAG AGGTCAAGAG TTTGAGACCA GCTTGGTGAA 1380
ACCCTGTCTC TACTAAAAAT ACAAAAGTTA GCTGGGGCTG GTGGTGGGCA TCTGTAGTCC 1440
CAGCTAATTG GAAGGGTGAG GCGGGAGGAT CGCTTGAACC TGGGAGGCGG AGGTTCCAGA 1500
GAGCCAAGAT CGCACCCTG CACTACAGCC TGGGCGACAG AACGAGACCC TGCTCCAAA 1560
GGAAAAACAA AAAAGAAGAA TAAAATAATT TGGATGAAAA TCATGTTTAT TTAATAAGTA 1620
ATGTCATGAG ACTATTAAAG ATGTGCCAGA GTTCAATGA AAATCATTAA AGTAGGACAG 1680
CTAAGAAATT AATATTAATA TAAAATTAT TGATAATCTT AAATTATTGA TTATTCCTTA 1740
ACGCACTCCA TTCTCTTTT ACATTTTATC ATGTTTCTTT TGAATATATG AATTGGCAAA 1800
GGACTTGATG AAAGTGAATA CTAAGATTTG GTACAGAGTA TGTACGGAAG ACAACTCAGA 1860
TTGCCATTTT AAATAAGATT GTACATGAAC AAAAAAAAAA AAAAAA

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75 Seq ID NO: 124 Protein sequence:
Protein Accession #: AAH22542

80

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1 11 21 31 41 51
| | | | |
MCSBIILRQE VLKDFGFRDL LIKVKFGESI EDLHTCRLLI QDIPAGLYV DPYELASLRE 60
RNITEAVMVS ENFDIEAPNY LSKSEVLIY ARRDSCIDC FQAFPLVHCR YHRPHSEDE 120
ASIVVNNPDL LMFCDQAGSR RMIRFRFDSF DKTIEFPILK CWAHSEVAAP CALENEDICQ 180
WNKMKYKSVY KNVLQVPVG LTVHTSLVCS VTLLITLLCS KKKKK

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85 Seq ID NO: 125 DNA sequence
Nucleic Acid Accession #: NM_004994.1
Coding sequence: 20..2143

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1      11      21      31      41      51
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AGACACCTCT GGCCTCACCA TGAGCCTCTG GCAGCCCTTG GTCCTGGTGC TCCTGGTGCT 60
5 GGGCTGCTGC TTTGCTGCCC CCAGACAGCG CCAGTCCACC CTGTGCTCTT TCCTGGAGGA 120
CCTGAGAACG AATCTCACCG ACAGGCAGCT GGCAGAGGAA TACCTGTACC GCTATGTTTA 180
CACTCGGGTG GCAGAGATGC GTGGAGAGTC GAAATCTCTG GGGCCTGCGC TGCTGCTTCT 240
CCAGAAGCAA CTGTCCCTGC CCGAGACCGG TGAGCTGGAT AGGCCACGC TGAAGGCCAT 300
GCCAAGCCCA CGGTGCGGGG TCCCAGACCT GGCAGATTTC CAAACCTTTG AGGGCGACCT 360
CAAGTGGCACC CACCACAACA TCACCTATTG GATCCAAAAC TACTCGGAAG ACTTGCCGCG 420
10 GCGGTTGATT GACGACGCCT TTGCCGCGC CTTCGCACTG TGGAGCGCGG TGACGCCGCT 480
CACCTTCACT CGCGTGATCA GCCGGGACGC AGACATCGTC ATCCAGTTTG GTGTGCGGGA 540
GCACGGAGAC GGGTATCCCT TCGACGGGAA GGACGGGCTC CTGGCACACG CCTTTCCTCC 600
TGGCCCCGGC ATTACGGGAG ACGCCCATTT CGACGATGAC GAGTTGTGGT CCTGGGCAA 660
GGGCGTCTGT GTTCCAACCT GGTTTGGAAG CGCAGATGGC GCGGCCTGCC ACTTCCCTCT 720
15 CATCTTCGAG GGCCTCTCCT ACTCTGCCTG CACCACCGAC GGTGCTCCG ACGGCTTGCC 780
CTGGTGAGAG ACCACGGCCA ACTACGACAC CGACGACCGG TTTGGCTTCT GCCCCAGCGA 840
GAGACTCTAC ACCCGGAGAG GCAATGTGTA TGGGAAACCC TGCCAGTTTC CATTCATCTT 900
CCAAGGCCAA TCCCTACTCGC CCTGCACACG GGACGGTCGC TCCGACGGCT ACCGCTGGTG 960
CGCCACCACC GCCAACTACG ACCGGGACAA GCTCTTCGGC TTCTGCCCGA CCGAGCTGA 1020
20 CTCGACGGTG ATGGGGGGCA ACTCGGCGGG GGAGCTGTGC GTCTTCCCTT TCACTTTCCT 1080
GGGTAAGGAG TACTCGACCT GTACCAAGCA GGGCCGCGGA GATGGGCGCC TCTGGTGCGC 1140
TACCACCTCG AACTTTGACA GCGACAAGAA GTGGGGCTTC TGCCCGGACC AAGGATACAG 1200
TTTGTTCCTC GTGGCGCGCG ATGAGTTCCG CCACGCGCTG GGCTTAGATC ATTCTCAGT 1260
25 GCGGAGGCG CTATGTACC CTATGTACC CTTCAGTGAG GGGCCCCCTT TGCATAAGGA 1320
CGACGTGAAT GGCATCCGGC ACCTCTATGG TCCTCGCCCT GAACCTGAGC CACGGCCTCC 1380
AACCACCAAC ACACCGCAGC CCGGCTTCC CCGACGGTTC TGCCCAACCG GACCCCCCAG 1440
TGTCACCCCC TCAGAGCGCC CCACAGCTGG CCCCACAGGT CCCCCCTCAG CTGGCCCCAC 1500
AGGTCCCCCC ACTGCTGGCC CTTCACGGC CACTACTGTG CCTTTGAGTC CGGTGGACGA 1560
TGCTGCAAC TCGACGCAT TCGACGCAT CGCGGAGATT GGGAAACGAG TGTATTGTGT 1620
30 CAAGGATGGG AAGTACTGGC GATTCTCTGA GGGCAGGGGG AGCCGGCCCG AGGGCCCTTT 1680
CCTTATCGCC GACAAGTGGC CCGCGCTGCC CCGCAAGCTG GACTCGTCTT TTGAGGAGCC 1740
GCTCTCCAAG AAGCTTTTCT TCTTCTCTGG GCGCCAGGTG TGGGTGTACA CAGGCGCGTC 1800
GGTGCTGGG CCGAGGGCGT TGGACAAGCT GGGCCTGGGA GCCGACGTGG CCCAGGTGAC 1860
CGGGGCCCTC CGGAGTGGCA GGGGGAAGAT GCTGCTGTTT AGCGGGCGGC GCCTCTGGAG 1920
35 GTTCGACGTG AAGGCGCAGA TGGTGGATCC CCGGAGCGCC AGCGAGGTGG ACCGGATGTT 1980
CCCCGGGGTG CCTTTGAGCA CGCACGACGT CTTCAGTAC CGAGAGAAAG CCTATTCTCT 2040
CCAGGACCGC TCTTACTGGC GCGTGAAGTT CCGGAGTGAG TTGAACGAGG TGGACCAAGT 2100
GGGTACGTG ACCTATGACA TCCTGCAGTG CCTTGAGGAC TAGGGCTCCC GTCTCTCTTT 2160
40 GCAGTGCCAT GTAAATCCCC ACTGGACCA ACCCTGGGGA AGGAGCCAGT TTGCCGGATA 2220
CAAACTGGTA TTCTGTTCTG GAGGAAAGGG AGGAGTGGAG GTGGGCTGGG CCTCTCTTTC 2280
TCACCTTGT TTTTGTGTGG AGTGTCTTA ATAACTTGG ATTCTCTAAC CTTT

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Seq ID NO: 126 Protein sequence:
Protein Accession #: NP_004985.1

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1      11      21      31      41      51
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5 RGESKSLGPA LLLLQKQLSL PETGELDSAT LKAMRTPRCG VPDLGRFQTF EGDWKHHHN 120
ITWYIQNSE LDPRAVIDDA FARAFALWSA VTPLTFTRVY SRDADIVIQF GVAEHGDGYP 180
FDGKDGLLAH AFPPGPIQGG DAHPDDDELW SLGKGVVVT RFGNADGAAC HFPFIFEGRS 240
YSACTTDGRS DGLPWCSTTA NYDTDDRFGF CPSERLYTRD GNADGKPCQF PFIFQGSYS 300
ACTTDRSDG YRWCAATTANY DRDKLFGFCP TRADSTVMGG NSAGELCVFF FTPLGKEYST 360
CTSEGRGDGR LWCATTNFD SDKKWGFCDP QGYSLFLVAA HEFGHALGLD HSSVPEALMY 420
55 PMYRFTGPP LHKDDVNGIR HLYGPRPEPE PRPPTTTTPQ PTAPPTVCPT GPPTVHPSE 480
PTAGTGPPTS AGPTGPPTAG PSTATTVPLS PVDDACNVNI FDAIAEIGNQ LYLKDKGYW 540
RFSEGRGSRP QGFPLIADKW PALPRKLDV FEEPLSKLFF FFSGRQVWVY TGASVLGPRR 600
LDKLGLGADV AQVTGALRSR RGKMLLFSGR RLWRFDVKAQ MVDPRSASEV DRMFPGVPLD 660
60 THDVFYREK AYFCQDRFYW RVSSRSELNQ VDQGVYTYD ILQCPED

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Seq ID NO: 127 DNA sequence
Nucleic Acid Accession #: NM_004181
Coding sequence: 32-670

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1      11      21      31      41      51
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5 GGTGCGCGGC CAGTGGCGCT TCGTGGACGT GCTGGGGCTG GAAGAGGAGT CTCTGGGCTC 120
GGTGCCAGCG CCTGCTGCGT CGCTGCTGCT GCTGTTTCCC CTCACGGCCC AGCATGAGAA 180
CTTCAGGAAA AAGCAGATTG AAGAGCTGAA GGGACAAGAA GTTAGTCTTA AAGTGTACTT 240
CATGAAGCAG ACCATTGGGA ATTCCTGTGG CACAATCGGA CTTATTACG CAGTGGCCAA 300
TAATCAAGAC AAACCTGGAT TTGAGGATGG ATCAGTCTTG AACAGTTTC TTTCTGAAAC 360
AGAGAAATG TCCCTGAAG ACAGAGCAAA ATGCTTTGAA AAGAATGAGG CCATACAGGC 420
AGCCCATGAT GCCGTGGCAC AGGAAGGCCA ATGTCGGGTA GATGACAAGG TGAATTTCCA 480
75 TTTTATTCTG TTTAACAACG TGGATGGCCA CCTCTATGAA CTGTATGAC GAATGCCTTT 540
TCCGGTGAAC CATGGCGCCA GTTCAGAGGA CACCCTGCTG AAGGACGCTG CCAAGGTGTG 600
CAGAGAATTC ACCGAGCGTG AGCAAGGAGA AGTCCGCTTC TCTGCCGTGG CTCTCTGCAA 660
GGCAGCCTAA TGCTCTGTGG GAGGGACTTT GCTGATTTC CCTCTTCCCT TCAACATGAA 720
AATATATACC CCCCATGGAG TCTAAAATGC TTCAGTACTT GTGAAACACA GCTGTTCTTC 780
80 TGTCTGCGAG ACACGCCTTC CCCTCAGCCA CACCCAGGCA CTTAAGCACA AGCAGAGTGC 840
ACAGCTGTCC ACTGGGCAT TGTGGTGTGA GCTTCAGATG GTGAAGCATT CTCCCCAGTG 900
TATGCTTGT ATTCCGATATC TAACGCTTTA AATGGCTACT TTGGTTTCTG TCTGTAAAGT 960
AAGACCTTGG ATGTGGTTAT GTTGCTCTAA AGAATAAATT TTGCTGATAG TAGC

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Seq ID NO: 128 Protein sequence:
Protein Accession #: NP_004172

1	11	21	31	41	51	
MLNKLVSRLG	VAGQWRFDV	LGLEESLGS	VPAPACALLL	LFPLTAQHEN	FRKKQIEELK	60
GQEVSPKVYF	MKQTIGNSCG	TIGLIHAVAN	NQDKLGFEDG	SVLKQFLSET	EKMSPEDRAK	120
CFEKNEAIPA	AHDAVAQEGG	CRVDDKVNFI	FILFNNVDGH	LYELDGRMPF	PVNHGASSED	180
TLKDAAKVC	REFTEREQGE	VRFSAVALCK	AA			

Seq ID NO: 129 DNA sequence
Nucleic Acid Accession #: NM_000213
Coding sequence: 127-5385

1	11	21	31	41	51	
CGCCCGCGCG	CTGCAGCCCC	ATCTCCTAGC	GGCAGCCCCG	GCGCGGAGGG	AGCGAGTCCG	60
CCCCGAGGTA	GGTCCAGGAC	GGGCGCACAG	CAGCAGCCGA	GGCTGGCCCG	GAGAGGGAGG	120
AAGAGGATGG	CAGGGCCACG	CCCCAGCCCA	TGGGCCAGGC	TGCTCCTGGC	AGCCTTGATC	180
AGCGTCAGCC	TCTCTGGGAC	CTTGCCAAAC	CGCTGCAAGA	AGGCCCCAGT	GAAGAGCTGC	240
ACGGAGTGTG	TCCGTGTGGA	TAAGGACTGC	GCCTACTGCA	CAGACGAGAT	GTTTCAGGGAC	300
CGGCGCTGCA	ACACCCAGGC	GGAGCTGCTG	GCCGCGGGCT	GCCAGCGGGA	GAGCATCGTG	360
GTCTATGGAGA	GCAGCTTCCA	AATCACAGAG	GAGACCCAGA	TTGACACCAC	CCTGCGGCGC	420
AGCCAGATGT	CCCCCAAGG	CCTGCGGGTC	CGTCTGCGGC	CCGGTGAGGA	GCGGCATTTT	480
GAGCTGGAGG	TGTTTGAGCC	ACTGGAGAGC	CCCGTGGACC	TGTACATCCT	CATGGACTTC	540
TCCAACCTCCA	TGTCCGATGA	TCTGGACAAC	CTCAAGAAGA	TGGGGCAGAA	CCTGGCTCGG	600
GTCTTGAGCC	AGCTCACCAG	CGACTACACT	ATTGGATTTC	GCAAGTTTGT	GGACAAAGTC	660
AGCGTCCCAG	AGACGGACAT	GAGGCTTGAG	AAGCTGAAGG	AGCCCTGGCC	CAACAGTGAC	720
CCCCCTTCT	CCTTCAAGAA	CGTCATCAGC	CTGACAGAAG	ATGTGGATGA	GTTCCGGAAAT	780
AAACTGCAGG	GAGAGCGGAT	CTCAGGCAAC	CTGGATGCTC	CTGAGGCGCG	CTTCGATGCC	840
ATCCTGCAGA	CAGCTGTGTG	CACGAGGGAC	ATTGGCTGGC	GCCCGGACAG	CACCCACCTG	900
CTGCTCTTCT	CCACCGAGTG	AGCCTTCAC	TATGAGGCTG	ATGGCGCCAA	CGTGCTGGCT	960
GGCATCATGA	GCCGCAACGA	TGAACGGTGC	CACCTGGACA	CCACGGGACG	CTACACCCAG	1020
TACAGGACAC	AGGACTACCC	GTCCGTGCCC	ACCCTGGTGC	GCCTGCTCGC	CAAGCACAAAC	1080
ATCATCCCCA	TCTTTGTGCT	CACCAACTAC	TCCTATAGCT	ACTACGAGAA	GCTTCACACC	1140
TATTTCCCTG	TCTCCTCACT	GGGGGTGCTG	CAGGAGGACT	CGTCCAACAT	CGTGGAGCTG	1200
CTGGAGGAGG	CCTTCAATCG	GATCCGCTCC	AACCTGGACA	TCCGGGCCCT	AGACAGCCCC	1260
CGAGGCCCTT	GGACAGAGGT	CACCTCCAAG	ATGTTCCAGA	AGACGAGGAC	TGGGTCTCTT	1320
CACATCCCGG	GGGGGGAAGT	GGGTATATAC	CAGGTGCAGC	TGCGGGCCCT	TGAGCACGTG	1380
GATGGGACGC	ACGTGTGCGA	GCTGCCGGAG	GACCAAGAAG	GCAACATCCA	TCTGAAACCT	1440
TCCTTCTCCG	ACGGCCTCAA	GATGGACGCG	GGCATCATCT	GTGATGTGTG	CACCTGCGAG	1500
CTGCAAAAAG	AGGTGCGGTC	AGCTCGCTGC	AGCTTCAACG	GAGACTTCGT	GTGCGGACAG	1560
TGTGTGTGCA	GCGAGGGCTG	GAGTGGCCAG	ACCTGCAACT	GCTCCACCCG	CTCTCTGAGT	1620
GACATTACAG	CCTGCTCCG	GGAGGGCGAG	GACAAGCCGT	GCTCCGCGCC	TGGGGAGTGC	1680
CAGTGGGGGC	ACTGTGTGTG	CTACGGCGAA	GGCCGCTACG	AGGGTCAGTT	CTGCGAGTAT	1740
GACAACTTCC	AGTGTCCCG	CACCTCCGGG	TTCCTCTGCA	ATGACCGAGG	ACGCTGCTCC	1800
ATGGGCCAGT	GTGTGTGTGA	GCCTGGTTGG	ACAGGCCCAA	GCTGTGACTG	TCCCTCAGC	1860
AATGCCACCT	GCATCGACAG	CAATGGGGGC	ATCTGTAATG	GACGTGGCCA	CTGTGAGTGT	1920
GGCCGCTGCC	ACTGCCACCA	GCAGTCGCTC	TACACGGACA	CCATCTGCGA	GATCAACTAC	1980
TCGGCGATCC	ACCCGGGCTT	CTGCGAGGAC	CTACGCTCCT	GCGTGCAGTG	CCAGGCGTGG	2040
GGCACCGGCG	AGAAGAAAGG	GCGCACGTGT	GAGGAATGCA	ACTTCAAGGT	CAAGATGCTG	2100
GACGAGCTTA	AGAGAGCCGA	GGAGGTGGTG	GTGCGCTGCT	CCTTCCGGGA	CGAGGATGAC	2160
GACTGCACCT	ACAGCTACAC	CATGGAAGGT	GACGGCGCCC	CTGGGCCCAA	CAGCACTGTC	2220
CTGGTGCACA	AGAAGAAGCA	CTGCCCTCCG	GGCTCCTTCT	GGTGGCTCAT	CCCCCTGCTC	2280
CTCCTCCTCC	TGCCGCTCCT	GGCCCTGCTA	CTGCTGCTAT	GCTGGAAGTA	CTGTGCTGTC	2340
TGCAAGGCCCT	GCCTGGCCTT	TCTCCCGTGC	TGCAACCGAG	GTCAATGGT	GGGCTTTAAG	2400
GAAGACCCT	ACATGCTCGC	GGAGAACCTG	ATGGCCTCTG	ACCACTTGGA	CACGCCCATG	2460
CTGCGCAGCG	GGAACCTCAA	GGGCCGTGAC	GTGGTCCGCT	GGAAGGTCAC	CAACAACATG	2520
CAGCGGCCCTG	GCTTTGCCAC	TCATGCCCCT	AGCATCAACC	CCACAGAGCT	GGTGCCCTAC	2580
GGGCTGTCTT	TGCGCCTGGC	CCGCCTTTGC	ACCGAGAAC	TGCTGAAGCC	TGACACTCGG	2640
GAGTGGCGCC	AGCTGCGGCA	GGAGGTGGAG	GAGAACCTGA	ACGAGGTCTA	CAGGCAGATC	2700
TCCGGTGTAC	ACAAGCTCCA	GCAGACCAAG	TTCGGGCAGC	AGCCCAATGC	CGGGAAAAAG	2760
CAAGACCACA	CCATTGTGGA	CACAGTGTCT	ATGGCGCCCC	GCTCGGCCAA	GCCGGCCCTG	2820
CTGAAGCTTA	CAGAGAAGCA	GGTGGAAACG	AGGGCCTTCC	ACGACCTCAA	GGTGGCCCCC	2880
GGCTACTACA	CCCTCACTGC	AGAACGAGAC	GCCCGGGGCA	TGGTGGAGTT	CCAGGAGGGC	2940
GTGGAGCTGG	TGGAGCTACG	GGTGCCCTTC	TTTATCCGGC	CTGAGGATGA	CGACGAGAAG	3000
CAGCTGCTGG	TGGAGGCCAT	CGACGTGCCC	GCAGGCACTG	CCACCCTCGG	CCGCCGCTCG	3060
GTAAACATCA	CCATCATCAA	GGAGCAAGCC	AGAGACGTGG	TGTCTCTTGA	GCAGCTGAG	3120
TTCTCGTCA	CCCGCGGGGA	CCAGGTGGCC	CGCATCCCTG	TCATCCGGCG	TGTCTCGGAC	3180
GGCGGGAAGT	CCCAGTCTC	CTACGCAACA	CAGGATGGCA	CCGCGCAGGG	CAACCGGGAC	3240
TACATCCCCG	TGGAGGGTGA	GCTGCTGTTC	CAGCCTGGGG	AGGCCTGGAA	AGAGCTGCAG	3300
GTGAAGCTCC	TGGAGCTGCA	AGAAGTTGAC	TCCCTCCTGC	GGGGCCGCCA	GGTCCGCCGT	3360
TTCCACGTCC	AGCTCAGCAA	CCCTAAGTTT	GGGGCCCAAC	TGGGCCAGCC	CCACTCCACC	3420
ACCATCATCA	TCAGGGACCC	AGATGAACCTG	GACCGGAGCT	TCAAGAGTCA	GATGTTGTCA	3480
TCACAGCCAC	CCCCTCACGG	CGACCTGGGC	GCCCCGCAGA	ACCCCAATGC	TAAGGCCGCT	3540
GGGTCCAGGA	AGATCCATT	CAACTGGCTG	CCCCCTTCTG	GCAAGCCAAT	GGGGTACAGG	3600
GTAAAGTACT	GGATTTCAGG	TGACTCCGAA	TCCGAAGCCC	ACCTGCTCGA	CAGCAAGGTC	3660
CCCTCAGTGG	AGCTCACCAC	CCTGTACCCG	TATTGCGACT	ATGAGATGAA	GGTGTGCGCC	3720
TACGGGGCTC	AGGGCGAGGG	ACCCTACAGC	TCCCTGGTGT	CCTGCCGCAC	CCACCAGGAA	3780
GTGCCAGCG	AGCCAGGGCG	TCTGGCCTTC	AATGTGCTCT	CCTCCACGGT	GACCCAGCTG	3840
AGCTGGGCTG	AGCCGGCTGA	GACCAACGGT	GAGATCACAG	CCTACGAGGT	CTGCTATGGC	3900
CTGGTCAACG	ATGACAACCG	ACCTATTGGG	CCCATGAAGA	AAGTGTGCTG	TGACAACCTC	3960
AAGAACCAGG	TGCTGCTTAT	TGAGAACCTT	CGGGAGTCCC	AGCCCTACCG	CTACACGCTG	4020
AAGGCGCGCA	ACGGGGCCCG	CTGGGGCCCT	GAGCGGGAGG	CCATCATCAA	CCTGGCCACC	4080
CAGCCCAAGA	GGCCCATGTC	CATCCCCATC	ATCCCTGACA	TCCCTATCGT	GGACGCCGAC	4140
AGCGGGGAGG	ATACGACAG	CTTCTTATG	TACAGCGATG	ACGTTTACAG	CTCTCCATCG	4200
GGCAGCCAGA	GGCCAGCGT	CTCCGATGAC	ACTGAGCACC	TGGTGAATGG	CCGGATGGAC	4260
TTTGCTTCC	CGGGCAGCAC	CAACTCCCTG	CACAGGATGA	CCACGACCAG	TGCTGCTGCC	4320
TATGGCACCC	ACCTGAGCCC	ACACGTGCCC	CACCGCGTGC	TAAGCACATC	CTCCACCTTC	4380

ACACGGGACT ACAACTCACT GACCCGCTCA GAACACTCAC ACTCGACCAC ACTGCCGAGG 4440
 GACTACTCCA CCTTCACCTC CGTCTCCTCC CACGACTCTC GCCTGACTGC TGGTGTGCC 4500
 GACACGCCCA CCCGCTTGGT GTTCTCTGCC CTGGGGCCCA CATCTCTCAG AGTGAGCTGG 4560
 CAGGAGCCGC GGTGCGAGCG GCCGCTGCAG GGCTACAGTG TGGAGTACCA GCTGCTGAAC 4620
 GGCGGTGAGC TGCATCGGCT CAACATCCCC AACCTGCCCC AGACCTCGGT GGTGGTGGAA 4680
 GACCTCTCTG CCAACCACTC CTACGTGTTC CGCGTGCGGG CCCAGAGCCA GGAAGGCTGG 4740
 GGCCGAGAGC GTGAGGGTGT CATACCACTT GAATCCAGG TGCACCCGCA GAGCCACTG 4800
 TGTCCCTGCG CAGGCTCCGC CTTCACTTTG AGCACTCCCA GTGCCCCAGG CCCGCTGGTG 4860
 TTCACTGCCC TGAGCCCAAG CTCGCTGCAG CTGAGCTGGG AGCGGCCACG GAGGCCCAAT 4920
 GGGGATATCG TCGCTACTCT GGTGACCTGT GAGATGGCCC AAGGAGGAGG GCCAGCCACC 4980
 GCATTCCGGG TGGATGGAGA CAGCCCCGAG AGCCGGCTGA CCGTGCCGGG CCTCAGCGAG 5040
 AACGTGCCCT ACAAGTTCAA GGTGCAGGCC AGGACCACCT AGGGCTTCGG GCCAGAGCGC 5100
 GAGGGCATCA TCACCATAGA GTCCCAAGAT GGAGGACCCT TCCCGCAGCT GGGCAGCCGT 5160
 GCCGGGCTCT TCCAGCACCC GCTGCAAAAG GAGTACAGCA GCATCACCAC CACCACACCC 5220
 AGCGCCACCG AGCCCTTCTT AGTGGATGGG CCGACCCCTG GGGCCAGCA CCTGGAGGCA 5280
 GGCGGCTCCC TCACCCGGCA TGTGACCCAG GAGTTTGTGA GCCGGACACT GACCACCAGC 5340
 GGAACCCCTA GCACCCACAT GGACCAACAG TTCTTCCAAA CTTGACCCCA CCTGCCCCA 5400
 CCCCAGCCAT GTCCCTAGAG GCGTCTCTCC GACTCCTCTC CCGGAGCCTC CTCAGCTACT 5460
 CCATCCTTGC ACCCTGCGG GCCCAGCCCA CCCGCATGCA CAGAGCAGGG GCTAGGTGTC 5520
 TCCTGGGAGG CATGAAGGGG GCAAGGTCCG TCCTCTGTGG GCCCAAACCT ATTTGTAACC 5580
 AAAGAGCTGG GAGCAGACA AGGACCCAGC CTTTGTCTG CACTTAATAA ATGTTTGTG 5640
 ACTG

Seq ID NO: 130 Protein sequence:
 Protein Accession #: NP_000204

1 11 21 31 41 51
 MAGPRPSPA RLLAALISV SLSGTLANRC KKAPVKSCTE CVRVKDCAY CTDEMFRDRR 60
 CNTQAEELAA GCQRESIVVM BSSFQITEET QIDTTLRRSQ MSPQGLRVRL RPEERHFEL 120
 EVFEPLESPV DLYILMDFSN SMSDDLNLK KMGQNLARVL SOLTSDYITG FGKFPVDKVS 180
 PQTMRPPEKL KEPWNSDPP FSFKNVILST EDVDEFNRKL QGERISGNLD APEGGFDAI 240
 QTAVCTRDIG WRPDSTHLLV FSTESAFHYE ADGANVLAGE MSRNDERCHL DTTGTYTQYR 300
 TDQYPSVPTL VRLAKHNI PIFAVTNYSY SYYEKLHTYF PVSSGLVLQE DSSNIVELLE 360
 EAFNRIRSNL DIRALDSPRG LRTEVTSKMF QKTRTGSPHI RRGEVGIYQV QLRALHVDG 420
 THVQPLPEDQ KGNHILKPSF SDGLKMDAGI ICDVCTCELQ KEVRSARCSF NGDFVCGQCV 480
 CSEGWGQTC NCSTGSLSDI QPCLREGEDK PCSGRGECQC GHCVCYGBGR YEGQFCEYDN 540
 FQCPRTSGFL CNDRGRCMSG QCVCEPGWTG PSCDCPLSNA TCIDSNGGIC NGRGHCECGR 600
 CHCHQQLSYT DTICEINYSY IHPGLCEDLR SCVQCQAWGT GEKKGRTCEE CNFKVKMVD 660
 LKRAEEVVVR CSFDEDDDC TYSYTMEDGD APGPNSTVLV HKKDKCPPGS FWLIPLLLL 720
 LLPLALLLLL LCWKYCACCK ACLALLPCCN RGHMVGFKED HYMLRENLM SDHLDTPLMR 780
 SGNLKGRODV RWKVTNNMQR PGFATHAASI NPTELVPYGL SLRLARLCTE NLLKPDTR 840
 AQLRQEVEEN LNEVYRQISG VHKLQQTFR QPNAGKKQD HTIVDTVLMA PRSAKPALLK 900
 LTEXQVEQRA FHDLLKVAPEY YTLTADQDAR GMVEFQEGVE LVDVVRVPLFI RPEDDDKQL 960
 LVEALDVPAQ TATLGRRLVN ITIIEQOARD VVSFEQPEFS VSRGDQVARI PVIRRVLDGG 1020
 KSQVSYRTQD GTAGNDRYI PVEGELLFQP GEAWKELQVK LLELQEVDSL LRGRQVRRFH 1080
 VQLSNPKFGA HLGQPHSTTI IIRDPDELDR SFTSMLSSQ PPPHGDLAG QNPNAKAAGS 1140
 RKIHFNWLP SGKPMGYRVK YWIQDSESE AHLDSKVPS VELTNLYPYC DYEMKVCAYG 1200
 AQGEGPYSSL VSCRTHQVEP SEPGRFAFNV VSSVTQLSW AEPATNGEII TAYEVGYGLV 1260
 NDDNRPIGEM KKVLDNPKN RMLLIENLRE SQPYRYTVKA RAGAGWGP ER EAIINLATQP 1320
 KRPMISIPI DIPIVDAQSG EDYDSFLMYS DDVLRSPSGS QRPVSDDTE HLVNGRMDFA 1380
 FPGSTNSLHR MTTTSLAAYG THLSPHVPHR VLSTSTLSTR DYNLSLRSEH SHSTTLPRDY 1440
 STLTSVSSHD SRLTAGVBDT PTRLVFSALG PTLRVSQWE PRCEPRLQGY SVEYQLLNGG 1500
 ELHLRLNPNP QGTAVVVFVR LPHNSYVFRV RAQSQEGWGR EREGVITIES QVHPQSPLC 1560
 LFGSAFTLST PSAPGPLVFT ALSPDSLQLS WERPRRPNGD IVGYLVTCM AQGGGPATF 1620
 RVDGDSPEER LTVPLSENV PYKFKVQART TEGFPGPERE IITIESQDGG PFPQLGSRAG 1680
 LFQHLQSEY SSIHTHTSA TEPFLVDGPT LGAQHLEAG SLTRHVTQEF VSRLTTSST 1740
 LSTHMDQQFF QT

Seq ID NO: 131 DNA sequence
 Nucleic Acid Accession #: BC004372
 Coding sequence: 132..2231

1 11 21 31 41 51
 CCTCGTGCCG CGGACCCAG CCTCTGCCAG GTTCGGTCCG CCATCCTCGT CCCGCTCTCC 60
 GCCGGCCCTT GCCCGCGGCC CAGGGATCCT CCAGCTCCTT TCGCCCGCGC CCTCCGTTCC 120
 CTCGGGACAC CATGGACAAG TTTTGGTGGC ACGCAGCCTG GGGACTCTGC CTCGTGCCGC 180
 TGAGCCTGGC GCAGATCGAT TTGAATATAA CCTGCCGCTT TGCAGGTGTA TTCCACGTGG 240
 AGAAAAATGG TCGCTACAGC ATCTCTCGGA CGGAGGCCGC TGACCTCTGC AAGGCTTTCA 300
 ATAGCACCTT GCCCACAATG GCCCAGATGG AGAAAGCTCT GAGCATCGGA TTTGAGACCT 360
 GCAGGTATGG GTTCATAGAA GGGCATGTGG TGATTCCCGG GATCCACCCC AACTCCATCT 420
 GTGCAGCAAA CAACACAGGG GTGTACATCC TCACATCCAA CACCTCCAG TATGACACAT 480
 ATTGCTTCAA TGCTTCAGCT CCACCTGAAG AAGATTGTAC ATCAGTCACA GACCTGCCCA 540
 ATGCCTTTGA TGGACCAATT ACCATAACTA TTGTTAACCG TGATGGCACC CGCTATGTCC 600
 AGAAAGGAGA ATACAGAAGC AATCCTGAAG ACATCTACCC CAGCAACCTT ACTGATGATG 660
 ACGTGAGCAG CGGCTCCTCC AGTGAAGGGA GCAGCACTTC AGGAGGTATC ATCTTTTACA 720
 CCTTTCTTAC TGTACACCCC ATCCAGACG AAGACAGTCC CTGGATCACC GACAGCACAG 780
 ACAGAATCCC TGCTACCACT ACGTCTTCAA ATACCATCTC AGCAGGCTGG GAGCCAAATG 840
 AAGAAAATGA ATATGAAAGA GACAGACACC TCAGTTTTTC TGGATCAGGC ATTGATGATG 900
 ATGAAGATT TATCTCCAGC ACCATTTCAA CCACACACG GGCTTTTAC CACACAAAAC 960
 AGAACCAAGA CTGACCCAG TGGAACCCAA GCCATTCAA TCCGGAAGTG CTACTTCAGA 1020
 CAACCACAAG GATGACTAGT GTAGACAGAA ATGGCACCAC TGCTTATGAA GGAACCTGGA 1080
 ACCCAGAAGC ACACCTCCCT CTCATTACCC ATGAGCATCA TGAGGAAGAA GAGACCCAC 1140
 ATTCTACAAG CACAATCCAG GCAACTCCTA GTAGTACAAC GGAAGAAACA GCTACCCAGA 1200
 AGGAACAGTG GTTTGGCAAC AGATGGCATG AGGGATATCG CCAACACCC AGAGAAAGACT 1260

CCCATTCCGAC AACAGGGGACA GCTGCAGCCT CAGCTCATAC CAGCCATCCA ATGCAAGGAA 1320
 GGACAACACC AAGCCCAGAG GACAGTTTCTT GGACTGATTT CTTCAACCCA ATCTCACACC 1380
 CCATGGGACG AGGTCATCAA GCAGGAAGAA GGATGGATAT GGACTCCAGT CATAGTACAA 1440
 CGCTTCAGCC TACTGCAAAAT CCAAAACACAG GTTTGGTGGG AGATTTGGAC AGGACAGGAC 1500
 CTCTTTCAAT GACAACGCAG CAGAGTAATT CTCAGAGCTT CTCTACATCA CATGAAGGCT 1560
 TGGAGAAGA TAAAGACCAT CCAACAACCTT CTACTCTGAC ATCAAGCAAT AGGAATGATG 1620
 TCACAGGTGG AAGAAGAGAC CCAATCATTT CTGAAGGCTC AACTACTTTA CTGAAGGTT 1680
 ATACCTCTCA TTACCCACAC ACGAAGGAAA GCAGGACCTT CATCCCAGTG ACCTCAGCTA 1740
 AGACTGGGTC CTTTGGAGTT ACTGCAGTTA CTGTTGGAGA TTCCAACCTCT AATGTCAATC 1800
 GTTCTTATC AGGAGACCAA GACACATTCC ACCCCAGTGG GGGGTCCCCT ACCACTCATG 1860
 GATCTGAATC AGATGGACAC TCACATGGGA GTCAAGAAGG TGGAGCAAAC ACAACCTCTG 1920
 GTCCTATAAG GACACCCCAA ATTCCAGAAT GGCTGATCAT CTTGGCATCC CTCTTGGCCT 1980
 TGGCTTTGAT TCTTGCAGTT TGCATTGCAG TCAACAGTCG AAGAAGGTGT GGGCAGAAGA 2040
 AAAAGCTAGT GATCAACAGT GGCAATGGAG CTGTGGAGGA CAGAAAGCCA AGTGGACTCA 2100
 ACGAGAGGC CAGCAAGTCT CAGGAAATGG TGCATTTGGT GAACAAGGAG TCGTCAGAAA 2160
 CTCCAGACCA GTTTATGACA GCTGATGAGA CAAGGAACCT GCAGAATGTG GACATGAAGA 2220
 TTGGGGTGTG ACACCTACAC CATTATCTTG GAAAGAAACA ACCGTTGGAA ACATAACCAT 2280
 TACAGGGAGC TGGGACACTT AACAGATGCA ATGTGCTACT GATTGTTTCA TTGCGAATCT 2340
 TTTTTCATCAT AAAATTTTCT ACTCTTAAAA AAAAAA AAAAAA

Seq ID NO: 132 Protein sequence:
 Protein Accession #: AAH04372

1 11 21 31 41 51
 MDKFWWHAAM GLCLVPLSLA QIDLNITCRF AGVFHVEKNG RYSISRTEAA DLCKAFNSTL 60
 PTMAQMEKAL SIGPETYCRYG FIEGHVVIPR IHPNSICAA NTGVYILTSN TSQYDTYCFN 120
 ASAPPEEDCT SVTDLNPAFD GPITITIVNR DGTRYVQKGE YRTNPEDIYP SNPTDDDVSS 180
 GSSSSRSSTS GGYIFYTFTST VHPIDEDSP WITDSTRIP ATSTSSNTIS AGWEPNEENE 240
 DERDRHLSFS GSGIDDEDF ISSTISTTPR AFDHTKQND WTQWNP SHSN PEVLLQTTR 300
 MTDVDRNGTT AYEGNWNPEA HPPLIHHEHH EEEETPHSTS TIQATPSSTT EETATQKEQW 360
 FGNRWHEGYR QTPREDSRST TGTAASAHT SHPMQGRITP SPEDSSWTF FNPISHPMGR 420
 GHQAGRRMDM DSSHSTTLQP TANPNTGLVE DLDRTGPLSM TTQSNSQSF STSHEGLEED 480
 KDHPSTTSLT SSNRNDVTGG RRDPNHSEGS TTLLEGYTS YPHTKESRTF IPVTSAKTGS 540
 FGVTAVTVDG SNSNVNRLS GDQTFHPSG GSHTHGSES DGHSHGSEQE GANTTSGPIR 600
 TPQIPEWLI LALLALALI LAVCIAVNSR RRCGQKKLV INSGNGAVED RKPSGLNGEA 660
 SKSQEMVHLV NKESSETPDQ FMTADETRNL QNVDMKIGV

Seq ID NO: 133 DNA sequence
 Nucleic Acid Accession #: NM_002882
 Coding sequence: 150-755

1 11 21 31 41 51
 CGAGGTTCCG GTCGTGGGGC GGAGGGAAGA GCGGGCGGGC GGGAGGCGCC GGCGCCAGAC 60
 GCGGAGGGAA GGAGCTACGA GTAGCCGCCG AGAGGCCCGC GAGCCAGCGA CGACCCAGCC 120
 AGCCGAGCCG CCGCCGCCGC CGCGCCGCCA TGGCGGCCGC CAAGGCACT CATGAGGACC 180
 ATGATACTTC CACTGAGAAT ACAGACGAGT CCAACCATGA CCCTCAGITT GAGCCAATAG 240
 TTTCTCTTCC TGAGCAAGAA ATTAATAACAC TGAAGAAGA TGAAGAGGAA CTTTTTAAAA 300
 TCGCGGCAAA ACTGTTCGGA TTTGCTCTG AGAACGATCT CCCAGAAATG AAGGAGCGAG 360
 GCACTGTGTA CGTCAAGCTC CTGAAGCACA AGGAGAAAGG GGCCATCCGC CTCCTCATGC 420
 GGAGGGACAA GACCTGAAG ATCTGTGCCA ACCACTACAT CACGCCGATG ATGGAGCTGA 480
 AGCCCAACGC AGGTAGCGAC CGTGCCTGGG TCTGGAACAC CCACGCTGAC TTCGCCGACG 540
 AGTGGCCCAA GCCAGAGCTG CTGGCCATCC GCTTCTTGAA TGCTGAGAAAT GCACAGAAAT 600
 TCAAAACAAA GTTTGAAGAA TGCAGGAAAG AGATCGAAGA GAGAGAAAG AAGCAGGAT 660
 CAGGCAAAAA TGATCATGCC GAAAAAGTGG CGGAAAAGCT AGAAGCTCTC TCGGTGAAGG 720
 AGGAGACCAA GGAGGATGCT GAGGAGAAGC AATAAATCGT CTTATTTTAT TTTCTTTTCC 780
 TCTCTTTCTT TTTCTTTT TAAAAAATTT TACCTTGCCC CTCTTTTTCG GTTGTGTTTT 840
 ATTCTTTTAT TTTTACAAGG GACGTTATAT AAAGAACTGA ACTC

Seq ID NO: 134 Protein sequence:
 Protein Accession #: NP_002873

1 11 21 31 41 51
 MAAAKDTHED HDTSTENTDE SNHDPQFEPI VSLPEQEIKT LEEDEEELFK MRAKLFRFAS 60
 ENDLPEWKER GTGDVKKLKH KEKGAIKLLM RRDKTLKICA NHYITPMEL KPNAGSDRAW 120
 VWNTHADFAD ECPKPELLAI RFLNAENAQK FKTKFEECRK EIEEREKKAG SGKNDHAEKV 180
 AEKLEALSVK EETKEDAEK Q

Seq ID NO: 135 DNA sequence
 Nucleic Acid Accession #: NM_000077.2
 Coding sequence: 277-742

1 11 21 31 41 51
 CCCAACCTGG GCGCACTTCA GGTGTGCCAC ATTGCTTAAG TGCTCGGAGT TAATAGCACC 60
 TCCTCCGAGC ACTCGCTCAC GGCCTCCCTT TGCTTGGAAA GATACCGCGG TCCCTCCAGA 120
 GGATTGAGG GACAGGGTCG GAGGGGGCTC TTCGCCAGC ACCGGAGGAA GAAAGAGGAG 180
 GGGCTGGCTG GTCACCAAGG GGTGGGGCGG ACCGCGTGC CTGCGCGGCT GCGGAGAGGG 240
 GGAGAGCAGG CAGCGGGCGG CGGGGAGCAG CATGAGCCG GCGGCGGGGA GCAGCATGGA 300
 GCCTTCGGCT GACTGCTTGG CCACGGCCGC GGCCTGGGGT CGGGTAGAGG AGGTGCGGGC 360
 GCTGCTGGAG GCGGGGGCGC TGCCCAACGC ACCGAATAGT TACGCTCGGA GGCCGATCCA 420
 GGTATGATG ATGGGCAGCG CCCGAGTGGC GGAGCTGCTG CTGCTCCACG GCGCGGAGCC 480

CAACTGCGCC GACCCCGCCA CTCTCACCCG ACCCGTGAC GACGCTGCCC GGGAGGGCTT 540
 CTTGGACACG CTGGTGGTGC TGCACCGGGC CGGGGCGCGG CTGGACGTGC GCGATGCCTG 600
 GGGCCGTCTG CCCGTGGACC TGGCTGAGGA GCTGGGCCAT CGCATGTTCG CACGGTACCT 660
 GCGCGCGGCT GCGGGGGGCA CCAGAGGCAG TAACCATGCC CGCATAGATG CCGCGGAAGG 720
 TCCCTCAGAC ATCCCCGATT GAAAGAACCA GAGAGGCTCT GAGAAACCTC GGGAAACTTA 780
 GATCATCAGT CACCGAAGGT CCTACAGGGC CACAACTGCC CCCGCCACAA CCCACCCCGC 840
 TTTTCGTAGT TTTTATTTAGA AAATAGAGCT TTTAAATATG TCCTGCCTTT TAACGTAGAT 900
 ATATGCCTTC CCCCACTACC GTAAATGTCC ATTTATATCA TTTTATATAT ATTCTTATAA 960
 AAATGTAAAA AAGAAAAACA CCGCTTCTGC CTTTCTACTG TGTGGAGATT TTCTGGAGTG 1020
 AGCACTCAGC CCTTAAGCGC ACATTCATGT GGGCATTCTT TGCAGCCTC GCAGCCTCCG 1080
 GAAGCTGTGC ACTTCATGAC AAGCATTTTG TGAAC TAGGG AAGCTCAGGG GGGTTACTGG 1140
 CTTCTCTTGA GTCACACTGC TAGCAATAGG CAGAACCAAA GCTCAATAA AAATAAAAAA 1200
 ATTTTCATTTC ATTCACTC

Seq ID NO: 136 Protein sequence:
 Protein Accession #: NP_000068.1

1 11 21 31 41 51
 | | | | | |
 MEPAAGSSME PSADWLATAA ARGRVEEVRA LLEAGALPNA PNSYGRRIPIQ VMMGMSARVA 60
 ELLLLHGAEP NCADPATLTR PVHDAAREGF LDTLVVLHRA GARLDVRDAW GRLPVDLAE 120
 LGHRDVARYL RAAAGGTRGS NHARIDAAREG PSDIPD

Seq ID NO: 137 DNA sequence
 Nucleic Acid Accession #: NM_058196.1
 Coding sequence: 104-421

1 11 21 31 41 51
 | | | | | |
 TGTGTGGGGG TCTGCTTGCC GGTGAGGGGG CTCTACACAA GCTTCCTTTC CGTCATGCCG 60
 GCCCCACCCC TGGCTCTGAC CATTCTGTTC TCTCTGGCAG GTCATGATGA TGGGCAGCGC 120
 CCGAGTGGCG GAGCTGCTGC TGCTCCACGG CGCGGAGCCC AACTGCGCCG ACCCCGCCAC 180
 TCTCACCCGA CCCGTGCACG ACGCTGCCCG GGAGGGCTTC CTGGACACGC TGGTGGTGCT 240
 GCACCGGGCC GGGGCGCGGC TGGACGTGCG CGATGCCCTGG GGGCGTCTGC CCGTGGACCT 300
 GGCTGAGGAG CTGGGCCATC GCGATGTGCG ACGGTACCTG CGCGCGGCTG CGGGGGGCAC 360
 CAGAGGCAGT AACCATGCCC GCATAGATGC CGCGGAAGGT CCCTCAGACA TCCCCGATTG 420
 AAAGAACCAG AGAGGCTCTG AGAAACCTCG GGAAACTTAG ATCATCAGTC ACCGAAGGTC 480
 CTACAGGGCC ACAACTGCCC CCGCCACAAC CCACCCCGCT TTCGTAGTTT TCATTTAGAA 540
 AATAGAGCTT TTAATAATGT CCTGCCTTTT AACGTAGATA TAAGCCTTCC CCCACTACCG 600
 TAAATGTCCA TTTATATCAT TTTTATATAA TTCTTATAAA AATGTAAAAA AGAAAAACAC 660
 CGCTTCTGCC TTTTCACTGT GTTGGAGTTT TCTGGAGTGA GCACCTACGC CCTAAGCGCA 720
 CATTTCATGT GGCATTTCTT GCGAGCCTCG CAGCCTCCGG AAGCTGTGCA CTTTCATGCA 780
 AGCATTTTGT GAACCTAGGA AGCTCAGGGG GGTACTAGGC TTCTCTTGGT TCACACTGCT 840
 AGCAATGGC AGAACCAAG CTCAAATAAA AATAAATAA TTTTCATTCA TTCACTC

Seq ID NO: 138 Protein sequence:
 Protein Accession #: NP_478103.1

1 11 21 31 41 51
 | | | | | |
 MMMGMSARVAE LLLLHGAEPN CADPATLTRP VHDAAREGFL DTLVVLHRAG ARLDVRDAWG 60
 RLPVDLAEEL GHRDVARYLR AAAGGTRGSN HARIDAAREG SDIPD

Seq ID NO: 139 DNA sequence
 Nucleic Acid Accession #: NM_058197.1
 Coding sequence: 272-684

1 11 21 31 41 51
 | | | | | |
 CCCAACCTGG GCGCACTTCA GGTGTGCCAC ATTGCTAAG TGCTCGGAGT TAATAGCACC 60
 TCCTCCGAGC ACTCGCTCAC GCGGTCCCCT TGCTTGGAAG GATACCGCGG TCCCTCCAGA 120
 GGATTTGAGG GACAGGGTCG GAGGGGGCTC TTCCGCCAGC ACCGGAGGAA GAAAGAGGAG 180
 GGGCTGGCTG GTCAACAGAG GGTGGGGCGG ACCCGTGCCT CTGCGCGGCT GCGGAGAGGG 240
 GGAGAGCAGC CAGCGGGCGG CGGGGAGCAG CATGGAGCCG GCGGCGGGGA GCAGCATGGA 300
 GCCGCGGGCG GGGAGCAGCA TGGAGCCTTC GGCTGACTGG CTGGCCACGG CCGCGGCCCG 360
 GGGTCGGGTA GAGGAGGTGC GGGCGCTGCT GGAGGCGGGG GCGCTGCCCA ACGCACCGAA 420
 TAGTTACGGT CGGAGGCCGA TCCAGGTGGG TAGAAGGTCT GCAGCGGGAG CAGGGGATGG 480
 CGGGCGACTC TGGAGGACGA AGTTTGCAGG GGAATTGGAA TCAGGTAGCG CTTTCGATTCT 540
 CCGGAAAAAG GGGAGGCTTC CTGGGGAGTT TTCAGAAGGG GTTTGTAATC ACAGACCTCC 600
 TCCTGGCGAC GCCCTGGGGG CTTGGGAAAC CAAGGAAGAG GAATGAGGAG CCACGCGCGT 660
 ACAGATCTCT CGAATGCTGA GAAGATCTGA AGGGGGGAAC ATATTGTAT TAGATGGAAG 720
 TCATGATGAT GGGCAGCGCC CGAGTGGCGG AGCTGCTGCT GCTCCACGGC GCGGAGCCCA 780
 ACTGCGCCGA CCCCGCCACT CTCACCGGAC CCGTGCACGA CGCTGCCCGG GAGGGCTTCC 840
 TGGACACGCT GGTGTGCTG CACCGGGCCG GGGCGCGGCT GGACGTGCGC GATGCTGGG 900
 GCCGTCTGCC CGTGGACCTG GCTGAGGAGC TGGGCCATCG CGATGTGCGA CGGTACCTGC 960
 GCGCGGCTGC GGGGGGCACC AGAGGCAGTA ACCATGCCCG CATAGATGCC GCGGAAGGTC 1020
 CCTCAGACAT CCCCGATTGA AAGAACCAGA GAGGCTCTGA GAAACCTCGG GAACTTAGAT 1080
 CATCAGTCAC CGAAGGTCTC ACAGGGCCAC AACTGCCCCC GCCACAACCC ACCCCGCTTT 1140
 CGTAGTTTTC ATTTAGAAAA TAGAGCTTTT AAAAAATGCC TGCCCTTTTA CGTAGATATA 1200
 TGCCCTCCCC CACTACCGTA AATGTCCATT TATATCATTT TTTATATATT CTTATAAAAA 1260
 TGTAAAAAAG AAAAAACCG CTCTGCTCTT TTCCTGTGT TGGAGTTTTC TGGAGTGAGC 1320
 ACTCACGCCC TAAGCGCACA TTCATGTGGG CATTTCTTGC GAGCCTCGCA GCCTCCGGAA 1380
 GCTGTGACTC TCATGACAA GATTTTGTGA ACTAGGGAAG CTCAGGGGGG TTACTGGCTT 1440
 CTCTTGAGTC ACACCTGCTAG CAAATGGCAG AACCAAGACT CAAATAAAAA TAAATAAATT 1500

Seq ID NO: 140 Protein sequence:
Protein Accession #: NP_478104.1

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1      11      21      31      41      51
|      |      |      |      |      |
MEPAAGSSME PAAGSSMEPS ADWLATAAAR GRVEEVRALL EAGALPNAPN SYGRRPIQVG 60
RRSAAGAGDG GRLWRKTFAG ELESQSASIL RKKGRLLPGEF SEGVCNHRFP PGDALGAWET 120
KEEE

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Seq ID NO: 141 DNA sequence
Nucleic Acid Accession #: NM_058195.1
Coding sequence: 163-684

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1      11      21      31      41      51
|      |      |      |      |      |
CCTCCCTACG GCGCGCTCCG GCAGCCCTTC CCGCGTGC GC AGGGCTCAGA GCCGTTCGGA 60
GATCTTGGAG GTCCGGGTGG GAGTGGGGGT GGGGTGGGGG TGGGGGTGAA GGTGGGGGGC 120
GGGCGCGCTC AGGGAAGCGG GGTGCGCGCC TCGGGGCGCG AGATGGGCAG GGGGCGGTGC 180
GTGGGTCCCA GTCTGCAGTT AAGGGGGCAG GAGTGGCGCT GCTCACCTCT GGTGCCAAAG 240
GGCGGCGCAG CGGCTGCCGA GCTCGGCCCT GGAGGCGGCG AGAACATGGT GCGCAGGTTC 300
TTGGTGACCC TCCGATTTCG GCGCGCGTGC GGCCCGCCGC GAGTGAGGGT TTTCGTGGTT 360
CACATCCCGC GGCTCACGGG GGAGTGGGCA GCGCCAGGGG CGCCCGCCGC TGTGGCCCTC 420
GTGCTGATGC TACTGAGGAG CCAGCGTCTA GGGCAGCAGC CGCTTCTTAG AAGACCAGGT 480
CATGATGATG GGCAGCGCCC GAGTGGCGGA GCTGCTGCTG CTCCACGGCG CGGAGCCCAA 540
CTGCGCCGAC CCCGCCATCT TCACCCGACC CGTGACGAC GCTGCCCGGG AGGGCTTCTC 600
GGACACGCTG GTGGTGCTGC ACCGGGCCGG GCGCGCGGCT GACGTGCGCG ATGCTTGGGG 660
CCGTCTGCCG GTGGACCTGG CTGAGGAGCT GGGCCATCGC GATGTGCGAC GGTACCTGCG 720
CGCGGCTGCG GGGGGCACCA GAGGCAGTAA CCATGCCCGC ATAGATGCCG CGGAAGGTCC 780
CTCAGACATC CCCGATTGAA AGAACAGAG AGGCTCTGAG AAACCTCGGG AAAGTTAGAT 840
CATCAGTCAC CGAAGGTCTC ACAGGGCCAC AACTGCCCCC GCCACAACCC ACCCGCTTTT 900
CGTAGTTTTT ATTTAGAAAA TAGAGCTTTT AAAAATGTCC TGCCCTTTTAA CGTAGATATA 960
TGCCCTTCCC CACTACCGTA AATGTCCATT TATATCATTT TTTATATATT CTTATAAAAA 1020
TGTAATAAAG AAAAACACCG CTCTGCCTT TTCACGTGTG TGGAGTTTTC TGGAGTGAGC 1080
ACTCAGCCCC TAAGCGCACA TTCATGTGGG CATTTCTTGC GAGCCTCGCA GCCTCCGGAA 1140
GCTGTGCACT TCATGACAAG CATTTTGTGA ACTAGGGAAG CTCAGGGGGG TTACTGGCTT 1200
CTCTTGAGTC ACACGTCTAG CAAATGGCAG AACCAAAGCT CAAATAAAAA TAAAAAATT 1260
TTCATTCATT CACTC

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Seq ID NO: 142 Protein sequence:
Protein Accession #: NP_478102.1

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1      11      21      31      41      51
|      |      |      |      |      |
MGRGRVCVPS LQLRGQEWRC SPLVPKGGAA AELGPGGGE NMVRRFLVTL RIRRACGPPR 60
VRVFFVHPR LTGEWAAPGA PAAVALVLM LRSQRLGQQP LPRRPGHDDG QRP SGAAAAA 120
PRRGAQLRRP RHSHPTARR CPGLPGHAG GAAPGRGAAG RARCLGPSAR GPG

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Seq ID NO: 143 DNA sequence
Nucleic Acid Accession #: NM_018131
Coding sequence: 412..1107

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1      11      21      31      41      51
|      |      |      |      |      |
GAAATTGCAC ACTTAAAGAC ATCAGTGGAT GAAATCACAA GTGGGAAAGG AAAGCTGACT 60
GATAAAGAGA GACAGAGACT TTTGGAGAAA ATTCGAGTCC TTGAGGCTGA GAAGGAGAAG 120
AATGCTTATC AACTCACAGA GAAGGACAAA GAAATACAGC GACTGAGAGA CCAACTGAAG 180
GCCAGATATA GTACTACCGC ATTGCTTGAA CAGCTGGAAG AGACAACGAG AGAAGGAGAA 240
AGGAGGGAGC AGGTGTTGAA AGCCTTATCT GAAGAGAAAG ACGTATTGAA ACAACAGTTG 300
TCTGCTGCAA CCTCAGCAAT TGCTGAACCT GAAAGCAAAA CCAATACACT CCGTTTATCA 360
CAGACTGTGG CTCCAAACTG CTTCAACTCA TCAATAAATA ATATTATGA AATGGAATA 420
CAGCTGAAAG ATGCTCTGGA GAAAAATCAG CAGTGGCTCG TGTATGATCA GCAGCGGGAA 480
GTCTATGTAA AAGGACTTTT AGCAAGATC TTTGAGTTGG AAAAGAAAAA GGAAACAGCT 540
GCTCATTCAC TCCCACAGCA GACAAAAAAG CCTGAATCAG AAGGTATCT TCAAGAAGAG 600
AAGCAGAAAT GTTACAACGA TCTCTTGGCA AGTGCAAAA AAGATCTTGA GGTGAAACGA 660
CAAAACATAA CTCAGCTGAG TTTTGAACCT AGTGAATTC GAAGAAAAATA TGAAGAAACC 720
CAAAAGAAG TTCACAATTT AAATCAGCTG TTGTATTAC AAAGAAGGGC AGATGTGCAA 780
CATCTGGAAG ATGATAGGCA TAAAACAGAG AAGATACAAA AACTCAGGGA AGAGAATGAT 840
ATTGCTAGGG GAAAACCTGA AGAAGAGAAG AAGAGATCCG AAGAGCTCTT ATCTCAGGTC 900
CAGTCTCTTT ACACATCTCT GCTAAGCAG CAAGAAGAAC AAACAAGGGT AGCTCTGTG 960
GAACAACAGA TGCAGGCATG TACTTTAGAC TTTGAAAAATG AAAAAGTCCG CCGTCAACAT 1020
GTGCAGCATC AATTGCATGT AATTCTTAAG GAGCTCCGAA AAGCAAGAAA AAATAACACA 1080
GTTGGAATCC TTGAAACAGC TTCATGAGTT TGCCATCACA GAGCCATTAG TCACTTTCCA 1140
AGGAGAGACT GAAAACAGAG AAAAAGTTGC CGCCTCACCA AAAAGTCCCA CTGCTGCACT 1200
CAATGGAAGC CTGGTGAATG GTCCCAAGTG CAATATACAG TATCCAGCCA CTGAGCATCG 1260
CGATCTGCTT GTCCATGTGG AATACTGTTT AAAGTAGCAA AATAAGTATT TGTTTTGATA 1320
TTAAAAGATT CAATACTGTA TTTTCTGTTA GCTTGTGGGC ATTTTGAATT ATATATTTCA 1380
CATTTTGCAT AAAAAGTGCCT ATCTACCTTT GACACTCCAG CATGCTAGTG AATCATGTAT 1440
CTTTTAGGCT GGTGTGCATT TCTCTGGCA GTGATACCTC CCTGACATGG TTCATCATCA 1500
GGCTGCAATG ACAGATGTG GTGAGCAGCG TCTACTGAGA TACTAACATT TTGACTGTCT 1560
AAAATACTTG GTGAGGAAAA GATAGCTCAG GTTATTGCTA ATGGGTAAAT GCACCAGCAA 1620
GCCAAATATT TTATGTTTTCG GGGGTTTGA AAAATCAAAG ATAATTAACC AAGGATCTTA 1680
ACTGTGTTCC CATTTTTTAT CCAAGCACTT AGAAAACCTA CAATCTTAAT TTTGATGTCC 1740
ATTGTTAAGA GGTGGTGATA GATACTATTT TTTTTCATA TTGTATAGCG GTTATTAGAA 1800

```


AAGTTGGGGA TTTTCTTGAT CTTTATTGCT GCTTACCATT GAAACTTAAC CCAGCTGTGT 1860
 TCCCAACTC TGGTCTGCGC ACGAAACAGT ATCTGTTTGA GGCATAATCT TAAGTGGCCA 1920
 CACACAATGT TTTCTCTTAT GTTATCTGGC AGTAACTGTA ACTTGAATTA CATTAGCACA 1980
 TTCTGCTTAG CTAAATTTGT TAAAATAAAC TTTAATAAAC CCATGTAGCC CTCTCATTTG 2040
 ATTGACAGTA TTTTAGTTAT TTTTGGCATT CTAAAGCTG GGCATGTAA TGATCAGATC 2100
 TTTGTTTGTG TGAAACAGGT TTTTATATACA TGCTTTTGT AAACCAAAA CTTTAAAT 2160
 TCTTCAGGT TTTCAACATG CTTACCACTG GGCTACTGTA AATGAGAAAA GAATAAAAT 2220
 ATTTAATGTT TT

Seq ID NO: 144 Protein sequence:
 Protein Accession #: NP_060601

1 11 21 31 41 51
 | | | | |
 MEIQLKDALE KNQQLVYDQ QREVYVKGLL AKIFELEKKT ETAHSLFPQQ TKKPESEGYL 60
 QBEKQKCYND LLASAKKDL EBRQTITQLS FELSEFRRKY EBTQKEVHNL NQLLYSQRRR 120
 DVQHLEDDRH KTEKIQLKRE ENDIARGKLE EEKKRSEELL SQVQSLYTSI LKQEQEQTTRV 180
 ALLEQQMQAC TLDFFENEKLD RQHVQQLHV ILKELRKARK NNTVGILETA S

Seq ID NO: 145 DNA sequence
 Nucleic Acid Accession #: NM_001168
 Coding sequence: 50..478

1 11 21 31 41 51
 | | | | |
 CCGCCAGATT TGAATCGCGG GACCCGTTGG CAGAGGTGGC GCGCGCGGCA TGGGTGCCCC 60
 GACGTGCCCC CTGCGCTGCG AGCCCTTTCT CAAGGACCAC CGCATCTCTA CATTCAAGAA 120
 CTGGCCCTTC TTGGAGGGCT GCGCCTGCAC CCCGAGCGG ATGGCCGAGG CTGGCTTCAT 180
 CCACTGCCCC ACTGAGAACG AGCCAGACTT GGCCCACTGT TTCTTCTGCT TCAAGGAGCT 240
 GGAAAGGCTGG GAGCCAGATG ACGACCCCAT AGAGGAACAT AAAAAGCATT CGTCCGGTTG 300
 CGCTTTCCTT TCTGTCAAGA AGCAGTTTGA AGAATTAACC CTGTGTGAAT TTTTGAAACT 360
 GGACAGAGAA AGAGCCAAGA ACAAATTCG AAAGGAAACC AACATAAGA AGAAGAAATT 420
 TGAGGAAACT GCGAAGAAAG TGCGCCGTGC CATCGAGCAG CTGGCTGCCA TGGATTGAGG 480
 CCTCTGGCGG GAGCTGCCCT GTCCAGAGT GGCTGCACCA CTTCAGGGT TTATTCCTGT 540
 GTGCCACCA GCTTCTCTGT GCGCCCTTAG CAATGTCTTA GGAAAGGAGA TCAACATTTT 600
 CAAATTAGAT GTTCAACTG TGCTCCTGTT TTGTCTTGAA AGTGGCACCA GAGGTGCTTC 660
 TGCCGTGTGA GCGGGTGCTG CTGGTAACAG TGGCTGCTTC TCTCTCTCTC TCTCTTTTTT 720
 GGGGGCTCAT TTTTCTGTGT TTGATTCCTG GGCTTACCAG GTGAGAAAGT AGGGAGGAAG 780
 AAGGCAGTGT CCCTTTTGTCT AGAGCTGACA GCTTTGTTCG CGTGGGCAGA GCCTTCCACA 840
 GTGAATGTGT CTGGACCTCA TGTGTGTAG GCTGTACAG TCCTGAGTGT GGACTTGGCA 900
 GGTGCTGTGT GAATCTGAGC TGCAGGTTCC TTATCTGTCA CACCTGTGCC TCCTCAGAGG 960
 ACAGTTTTTT TGTGTGTGTG TTTTGTGTG TTTTGTGTG TTTTGTGTG TTTTGTGTG 1020
 GTGATGAGAG AATGGAGACA GAGTCCCTGG CTCTCTACT GTTTAACAAC ATGGCTTTCT 1080
 TATTTTGTGT GAATGTGTAA TTCACAGAAT AGCACAACT ACAATTAAAA CTAAGCACAA 1140
 AGCCATTCTA AGTCATTGGG GAAACGGGGT GAACTTCAGG TGGATGAGGA GACAGAATAG 1200
 AGTGATAGGA AGCGCTGTGC AGATACTCCT TTGCGCACTG CTGTGTGATT AGACAGGCC 1260
 AGTGAGCCGC GGGGCACATG CTGGCCGCTC CTCCCTCAGA AAAAGGCAGT GGCCCTAAATC 1320
 CTTTTTAAAT GACTTGGCTC GATGTGTGTG GGGACTGGCT GGGCTGTGC AGGCCGTGTG 1380
 TCTGTGAGG CAACCTTAC ATCTGTACAG TTCTCCACAC GGGGGAGAGA CGCAGTCCGC 1440
 CCAGTCCCCC GCTTCTTTTG GAGGCAGCAG CTCCCGCAGG GCTGAAGTCT GGCGTAAGAT 1500
 GATGGAATTG ATTCGCCCTC CTCCCTGTCA TAGAGCTGCA GGGTGGATTG TTACAGCTTC 1560
 GCTGGAAACC TCTGGAGGTC ATCTCGGCTG TTCCTGAGAA ATAAAAAGCC TGTCAATTC

Seq ID NO: 146 Protein sequence:
 Protein Accession #: NP_001159

1 11 21 31 41 51
 | | | | |
 MGAPTLPPAW QPFLKDHRI TFKNWPFLG CACTPERMAE AGFIHCPTEN EPDLAQCFPC 60
 FKELEGWEPD DDPIEBHKH SSGCAFLSVK KQFBEELTGE FLKLDREKAK NKIAKETNNK 120
 KKEFBETAK VRRATBQLAA MD

Seq ID NO: 147 DNA sequence
 Nucleic Acid Accession #: NM_014176.1
 Coding sequence: 127-720

1 11 21 31 41 51
 | | | | |
 GCGCGCAGCG CTGGTACCCC GTTGGTCCGC GCGTTGCTGC GTTGTGAGGG GTGTGAGCTC 60
 AGTGATATCC AGGCAGCTCT TAGTGTGGAG CAGTGAACCTG TGTGTGGTTC CTCTACTTGT 120
 GGGATCATGC AGAGAGCTTC ACGTCTGAAG AGAGAGCTGC ACATGTTAGC CACAGAGCCA 180
 CCCCCAGGCA TCACATGTTG GCAAGATAAA GACCAATATG ATGACCTGCG AGCTCAATA 240
 TTAGGTGGAG CCAACACACC TTATGAGAAA GGTGTTTTTA AGCTAGAAGT TATCATTCCT 300
 GAGAGGTACC CATTGTAACC TCCTCAGATC CGATTCTCTA CTCCAATTAT TCATCCAAAC 360
 ATTGAATCTG TGGGAAGGAT TTGTCTGGAT GTTCTCAAA TGGCCACCAA AGGTGCTTGG 420
 AGACCATCCC TCAACATCGC AACTGTGTTG ACCTCTATTC AGCTGCTCAT GTGAGAACCC 480
 AACCTGATG ACCCGCTCAT GGCTGACATA TCCTCAGAA TTAATATATA TAAGCCAGCC 540
 TTCTCAAGA ATGCCAGACA GTGGACAGAG AAGCATGCAA GACAGAAACA AAAGGCTGAT 600
 GAGGAAGAGA TGCTTGATTA TCTACAGAG GCTGGTGACT CCAGAGTACA CAACTCAACA 660
 CAGAAAGGA AGGCCAGTCA GCTAGTAGGC ATAGAAAAGA AATTCATCC TGATGTTTAG 720
 GGGACTTGTG CTGGTGTATC TTAGTTAATG TGTCTTTTGC CAAGGTGATC TAAGTTGCCT 780
 ACCTTGAATT TTTTGTAAAT TATATTGAT GACATAATTT TTGTGTAGTT TATTATCTT 840
 GTACATATGT ATTTTGAAT CTTTAAACC TGAAAAATAA ATAGTCATTT AATGTTGAAA 900

AAAAAAAAA AAAAAAAAAA AAAAAAAAAA

Seq ID NO: 148 Protein sequence:
Protein Accession #: NP_054895.1

1	11	21	31	41	51	
MQRASRLKRE	LHMLATEPPF	GITCWQDKDQ	MDDLRAQILG	GANTPYEKG	FKLEVIIPER	60
YFPEPQIRF	LTPHYHPNID	SAGRICLDVL	KLPPKGAWRP	SLNIATVLTS	IQLLMSEPNP	120
DDPLMADISS	EFKYNKPAPL	KNARQWTEKH	ARQKQKADEE	EMLDNLPEAG	DSRVHNSTQK	180
RKASQLVIGIE	KKFHPDV					

Seq ID NO: 149 DNA sequence
Nucleic Acid Accession #: NM_003812
Coding sequence: 224-2722

1	11	21	31	41	51	
TCCTCTGCGT	CCCGCCCCGG	GAGTGGCTGC	GAGGCTAGGC	GAGCCGGGAA	AGGGGGCGCC	60
GCCCAGCCCC	GAGCCCCGGG	CCCCGTGCCC	CGAGCCCGGA	GCCCCCTGCC	CGCGGCGGCA	120
CCATGCGCGC	CGAGCCGGGC	TGACCGGCTC	CGCCCGCGGC	CGCCCGCGAG	CTAGCCCGGC	180
GCTCTGCGCG	GCCACACGGA	GCGGCGCCCG	GGAGCTATGA	GCCATGAAGC	CGCCCGGCGC	240
CAGCTCGCGG	CAGCCGCCCC	TGGCGGGCTG	CAGCCTTGCC	GGCGCTTCCT	GCGGCCCCCA	300
ACGCGGCCCC	GCCGGCTCGG	TGCCTGCGAG	CGCCCGGGCC	CGCACGCGCG	CCTGCGCGCT	360
GCCTCTCGCT	CTTCTCCTGC	TGCCTCCGCT	CGCCCGCTCG	TCCCGGCCCC	GCGCCTGGGG	420
GGCTGCTGGG	CCGAGCGCTC	CGCATTGGAA	TGAAACTGCA	GAAAAAATT	TGGGAGTCCT	480
GGCAGATGAA	GACAATACAT	TGCAACAGAA	TAGCAGCAGT	AATATCAGTT	ACAGCAATGC	540
AATGCAGAAA	GAAATCACAC	TGCCTTCAAG	ACTCATATAT	TACATCAACC	AAGACTCGGA	600
AAGCCCTTAT	CACGTTCTTG	ACACAAAGGC	AAGACACCCG	CAAAAACRTA	ATAAGGCTGT	660
CCATCTGGCC	CAGGCAAGCT	TCCAGATTGA	AGCCTTCGGC	TCCAAATTCA	TTCTTGACCT	720
CATACTGAAC	AATGTTTGT	TGCTTCTGA	TTATGTGGAG	ATTCACACG	AAAATGGGAA	780
ACCACAGTAC	TCTAAGGGTG	GAGAGCACTG	TTACTACCAT	GGAAGCATCA	GAGGCGTCAA	840
AGACTCCAAG	GTGGCTCTGT	CAACCTGCAA	TGGACTTCAT	GGCATGTTTG	AAGATGATAC	900
CTTCGTGTAT	ATGATAGAGC	CACATAGAGC	GGTTTATGAT	GAGAAAAGCA	CAGGTCGACC	960
ACATATAATC	CAGAAAACCT	TGGCAGGACA	GTATTCTAAG	CAAATGAAGA	ATCTCACTAT	1020
GGAAAGAGGT	GACCAAGTGC	CCTTTCTCTC	TGAATTACAG	TGGTTGAAAA	GAAGGAAGAG	1080
AGCAGTGAAT	TCGCGGGTGA	GTATATTGTA	AGAAATGAAA	TATTTGGAAC	TTATGATTGT	1140
TAATGATCAC	AAAACGTATA	AGAAGCATCG	CTCTTCTCAT	GCACATACCA	ACAACCTTGC	1200
AAAGTCCGTG	GTCAACCTTG	TGGATTCTAT	TTACAAGGAG	CAGCTCAACA	CCAGGGTTGT	1260
CCTGGTGGCT	GTAGAGACCT	GGACTGAGAA	GGATCAGATT	GACATCACCA	CCAACCTTGT	1320
GCAGATGCTC	CATGAGTTCT	CAAAATACCG	GCAGCGCAT	AAGCAGCATG	CTGATGCTGT	1380
GCACCTCATC	TCGCGGGTGA	CATTTCACCT	TAAGAGAAGC	AGTCTGAGTT	ACTTTGGAGG	1440
TGCTGTCTCT	CGCACAGAG	GAGTTGGTGT	GAATGAGTAT	GGTCTTCCAA	TGGCAGTGGC	1500
ACAAGTATTA	TCGCAGAGCC	TGGCTCAAAA	CCTTGGAAAT	CAATGGGAAC	CTTCTAGCAG	1560
AAAGCCAAAA	TGTACTGCA	CAGAATCCTG	GGGTGGCTGC	ATCATGGAGG	AAACAGGGGT	1620
GTCCCATCTC	CGAAAATTTT	CAAAAGTCAG	CATTTTGGAG	TATAGAGACT	TTTACAGAG	1680
AGGAGGTGGA	GCCTGCCTTT	TCAACAGGCC	AACAAAGCTA	TTTGAGCCCA	CGGAATGTGG	1740
AAATGGATAC	GTGGAAGCTG	GGGAGGAGTG	TGATTGTGGT	TTTCTATGTT	AATGCTATGG	1800
ATTATGCTGT	AAGAAATGTT	CCCTCTCCAA	CGGGGCTCAC	TGCAGCGACG	GGCCCTGCTG	1860
TAACAATACC	CATGTCTTTT	TTACAGCCAC	AGGGTATGAA	TGCCGGGATG	CTGTGAACGA	1920
GTGTGATATT	ACTGAATATT	GTACTGGAGA	CTCTGGTCAG	TGCCCCACAA	ATCTTCATAA	1980
GCAAGACGGA	TATGCATGCA	ATCAAAATCA	GGGCCGCTGC	TACAAATGGC	AGTGAAGAG	2040
CAGAGACAAC	CAGTGTCACT	ACATCTGGGG	AACAAAGGCT	GCAGGGTCTG	ACAAGTTCTG	2100
CTATGAAAAG	CTGAATACAG	AAGGCACTGA	GAAGGGAAAC	TGCGGGAAGG	ATGGAGACCG	2160
GTGGATTCTG	TCAGCAAAAC	ATGATGTGTT	CTGTGGATTG	TTACTCTGTA	CCAATCTTAC	2220
TCGAGCTCCA	CGTATTGGTC	AACTTCAGGG	TGAGATCATT	CCAATCTCCT	TCTACCATCA	2280
AGGCCGGGTG	ATTGACTGCA	GTGGTGCCCA	TGTAGTTTGA	GATGATGATA	CGGATGTGGG	2340
CTATGTAGAA	GATGGAGCCG	CATGTGGCCC	GTCTATGATG	TGTTTAGATC	GGAAAGTCCT	2400
ACAAATTCAA	GCCTTAAATA	TGAGCAGCTG	TCCACTCGAT	TCCAAGGGTA	AAGTCTGTTC	2460
GGGCCATGGG	GTGTGTAGTA	ATGAAGCCAC	CTGCATTGTT	GATTTTCACT	GGGCAGGGAC	2520
AGATTGCGAGT	ATCCGGGATC	CAGTTAGGAA	CCTTCACCCC	CCCAAGGATG	AAGGACCCAA	2580
GGGTCTTAGT	GCCACCAATG	TCATAATAGG	CTCCATCGCT	GGTGCCATCC	TGGTAGCAGC	2640
TATTGTCTCT	GGGGGCACAG	GCTGGGGATT	TAAAAATGTC	AAGAAGAGAA	GGTTCGATCC	2700
TACTCAGCAA	GGCCCCATCT	GAATCAGCTG	CGCTGGATGG	ACACCGCCTT	GCACTGTTGG	2760
ATTCTGGGTA	TGACATACTC	GCAGCAGTGT	TACTGGAAC	ATTAAGTTTG	TAAACAAAAC	2820
CTTTGGGTGG	TAATGACTAC	GGAGCTAAAG	TTGGGGTGAC	AAGGATGGGG	TAAAGAAAAA	2880
CTGTCTCTTT	TGGAATAAT	GTCAAAGAAC	ACCTTTCACC	ACCTGTCAGT	AAACGGGGGA	2940
GGGGGCAAAA	GACCATGCTA	TAAAAAGAAC	TGTTCCAGAA	TCTTTTTTTT	TCCCTAATGG	3000
ACGAAGGAAC	AACACACATA	CAAAAATTAA	ATGCAATAAA	GGAATCATT	AAAA	

Seq ID NO: 150 Protein sequence:
Protein Accession #: NP_003803

1	11	21	31	41	51	
MKPPGSSSRQ	PPLAGCSLAG	ASCGPQRGPA	GSVPASAPAR	TPPCRLLLV	LLLPPLAASS	60
RPRAGAAAP	SAPHWNETAE	KNLGLVADED	NTLQONSSSN	ISYSNAMQKE	ITLPSRLIYY	120
INQDSESPYH	VLDTKARHQ	KHNKAVHLAQ	ASFQIEAFGS	KFILDILNL	GLLSSDYVEI	180
HYENGKPYQS	KGGEHCYYHG	SIRGVKDSKV	ALSTCNGLHG	MFEDDTFVYM	IEPLELVHDE	240
KSTGRPHIIQ	KTLAQQYSKQ	MKNLTMERGD	QWFFLSELQW	LKRRKRAVNP	SRGIFEEMKY	300
LELMIVNDHK	TYKKHRSSHA	HTNNFAKSVV	NLVDSTYKQ	LNTRVVLVAV	ETWTEKDQID	360
ITNPNVQMLH	EFKSKYRQRIK	QHADAHLIS	RVTFFHYKRS	LSYFVGVCSS	TRGVGVNEYG	420
LPMVAQVLIS	QSLAQNLIQ	WEPSSRKPKC	DCTESWGGCI	MEETGVSHSR	KFSKCSILEY	480
RDFLQRGGGA	LCFNRPTKLF	EPTECGNGYV	EAGEECDGCF	HVECYGLCK	KCSLSNGAHC	540
SDGPCCNNTS	CLFQPRGYEC	RDAVNECDIT	EYCTGDSGQC	PPNLHKQDGY	ACNQNGRCY	600
NGECKTRDNQ	CQYIWGTAKA	GSDKFCYEKL	NTEGTEKGNC	GKDGDRWIC	SKHDVFCGFL	660

LCTNLTRAPR IGQLQGEIIP TSFYHQGRVI DCSGAHVLD DTDVGVYVED GTPCGPSMMC 720
 LDRKCLQIQ A LMSSCPLDS KGKVCSGHGV CSNEATCICD FTWAGTDCSI RDPVRNLHPP 780
 KDEGPKGPSA TNLIGSIAG AILVAAIVLG GTGWGFKNVK KRRFDPTQQG PI

Seq ID NO: 151 DNA sequence
 Nucleic Acid Accession #: NM_023915
 Coding sequence: 250-1326

1 11 21 31 41 51
 10 GGCACGAGGG TTTCGTTTTC ATGCTTTACC AGAAAATCCA CTTCCTGCC GACCTTAGTT 60
 TCAAAGCTTA TTCTTAATTA GAGACAAGAA ACCTGTTTCA ACTTGAAGAC ACCGTATGAG 120
 GTGAATGGAC AGCCAGCCAC CACAATGAAA GAAATCAAAC CAGGAATAAC CTATGCTGAA 180
 15 CCCACGCCTC AATCGTCCCC AAGTGTTCCT TGACACGCAT CTTTGCTTAC AGTGCATCAC 240
 AACTGAAGAA TGGGGTTCAA CTTGACGCTT GCAAAATTAC CAAATAACGA GCTGCACGGC 300
 CAAGAGAGTC ACAATTACAG CAACAGGAGC GACGGGCCAG GAAAGAACAC CACCTTCAC 360
 AATGAATTG ACACAATTGT CTTGCCGGTG CTTTATCTCA TTATATTGT GGCAAGCATC 420
 TTGCTGAATG GTTTAGCAGT GTGGATCTTC TTCCACATTA GGAATAAAAC CAGCTTCATA 480
 20 TTCTATCTCA AAAACATAGT GGTTCGAGAC CTCATAATGA CGCTGACATT TCCATTTGCA 540
 ATAGTCCATG ATGCAGGATT TGGACCTTGG TACTTCAAGT TTATTCTCTG CAGATACACT 600
 TCAGTTTTGT TTTATGCAAA CATGTATACT TCCATCGTGT TCCTTGGGCT GATAAGCACT 660
 GATCGCTATC TGAAGGTGCT CAAGCCATT GGGGACTCTC GGATGTACAG CATAACCTTC 720
 ACGAAGGTTT TATCTGTTTG TGTTTGGGTG ATCATGGCTG TTTTGTCTTT GCCAAACATC 780
 25 ATCCTGACAA ATGGTCAGCC AACAGAGGAC AATATCCATG ACTGCTCAA ACTTAAAGT 840
 CCTTTGGGGG TCAATGGGA TACGGCAGTC ACCTATGTGA ACAGCTGCTT GTTTGTGGCC 900
 GTGCTGGTGA TCTGTATCGG ATGTTACATA GCCATATCCA GGTACATCCA CAAATCCAGC 960
 AGGCAATTCA TAAGTCAGTC AAGCCGAAAG CGAAAACATA ACCAGAGCAT CAGGGTTGTT 1020
 GTGGCTGTGT TTTTACCTG CTTTCTACCA TATCACTTGT GCAGAATTCC TTTTACTTTT 1080
 30 AGTCACTTAG ACAGGCTTTT AGATGAATCT GCACAAAAA TCCTATATTA CTGCAAGAA 1140
 ATTACACTTT TCTTGTCTGC GTGTAATGTT TGCCCTGGATC CAATAATTTA CTTTTCATG 1200
 TGTAGTTCAT TTTCAAGAAG GCTGTTCAA AAATCAAATA TCAGAACCAG GAGTGAAAGC 1260
 ATCAGATCAC TGCAAGTGT GAGAAGATCG GAAGTTCGCA TATATTATGA TTACACTGAT 1320
 GTGTAGGCCT TTTATTGTTT GTTGAATCG ATATGTACAA AGTGTAATAA AATGTTTCTT 1380
 35 TTCATTATCC TTAATAAAAA AA

Seq ID NO: 152 Protein sequence:
 Protein Accession #: NP_076404

1 11 21 31 41 51
 40 MGFNLTAKL PNNELHQES HNSGNRSDGP GKNTTLHNEF DTIVLPVLYL IIFVASILLN 60
 GLAVWIFFHI RNKTSFIFYL KNIVVADLIM TLTFPFRIVH DAGFGFWYFK FILCRYTSVL 120
 45 FYANMYTSIV FLGLISIDRY LKVVVKPFQDS RMYSTITTKV LSVCVVWIMA VLSLPNIILT 180
 NQOPTEDNIH DCSKLSPLG VKWHTAVTVV NSCLFVAVLV ILIGCYIAIS RYIHKSSRQF 240
 ISQSSRKRKH NQSIKRVVAV FFTCFLPYHL CRIPFTFSLH DRLLDESAQK ILYYCKEITL 300
 FLSACNVCLD PIIFYFMCRS FSRRLPKKSN IRTRESIRS LQSVRRSEVR IYYDYTDV

Seq ID NO: 153 DNA sequence
 Nucleic Acid Accession #: D80008.1
 Coding sequence: 149-739

1 11 21 31 41 51
 55 GTTCGGCGCC AAAGCGCGGA GCGGAGGCCG AGGCGAGAGC CTGGCGCTGT AGGACTAGAA 60
 CGAAAGGAGT GAGGCGCCGA GAGCCCAGAT ACCATTTTGG CGTGAGAGCT GGTGGTTGGC 120
 AAGGCGCGCG GAGTGGGAAG CGTCCGCCAT GTTCTGCGAA AAAGCCATGG AACTGATCCG 180
 CGAGCTGCAT CGCGCGCCCG AAGGGCAACT GCCTGCCTTC AACGAGGATG GACTCAGACA 240
 60 AGTTCGTGGAG GAGATGAAAG CTTTGTATGA AAAAAACCAG TCTGATGTGA ATGAAGCAAA 300
 GTCAGGTGGA CGAAGTGATT TGATACCAAC TATCAAAATT CGACACTGTT CTCTGTTAAG 360
 AAATCGACGC TGCACGTGAG CATACCTGTA TGACCGCTTG TCTCGGATCA GAGCACTCAG 420
 ATGGGAATAT GGTAGCGTCT TGCCAAATGC ATTACGATT CACATGGCTG CTGAAGAAAT 480
 GGAGTGGTTT AATAATTATA AAAGATCTCT TGCTACTTAT ATGAGGTCAC TGGGAGGAGA 540
 65 TGAAGGTTTG GACATTACAC AGGATATGAA ACCACCAAAA AGCCTATATA TTGAAGTCCG 600
 GTGTCTAAAA GACTATGGAG AATTTGAAGT TGATGATGGC ACTTCAGTCC TATTAATAAA 660
 AAATAGCCAG CACTTTTTCAT CTCGATGGAA ATGTGAGCAG CTGATCAGAC AAGGAGTCCT 720
 GGAGCACATC CTGTCTATGAC CATGCCGCGA GGCACCTCCA GGCTTCACTC AACTCATGGA 780
 CTCCTCTGTA CTCACCTCTC CCACCACTCC CTTACCTCC CTCTTTGATT TTAGAAGCTA 840
 70 TAGACATTGT TTAAGATAAC TAAGATAACT TGGCTAAGAA GTATAATTG CTAACATATA 900
 AGGACTTTCT TTTTAAATG TTGTACACTA TTCTTCTTAC TCTTTTGGG TTTTGGTTTT 960
 GTTTTGTAGA GACTGTCTCA CTATGTTGCC CAAGCTGGTC TCAAACTCCT GGCCTCAAGC 1020
 AGTCTCTCCA CCTTAGCTTC TCAAAGTGTT GAGATCACAG GCGTGAGCCA CTGCACCCGG 1080
 CCCCTACTCC TTTTCTAAT AAGCTGTATC TGTAAATCACA GCATTCTTAC AGTTGTTTACA 1140
 75 GTGTGTTTTT TAAATGAAA TAAACATGGT TACATTGAA TCTCTTAAAT AAGCAGTCAC 1200
 TTGGCTGGAC AGGAAGAAGG TAGATCCTGT GTGTCTTGT TTCTGGTCAT GTGTATTGTA 1260
 CAAGCTAGAG AGCTGAATTT CTGAGATACA CATTTTCAA TCACATGCAA GTGAAGATGA 1320
 TGGTCTGTAG AAATTTTCAG TATATATAAT GTTTAATGAC ATACTAATTT ATCATCTGGC 1380
 TATTTGGGAA GGAAGGACAC ACATGGATT TGCACATTT CACCATGGTG GCTGGTGTGG 1440
 80 CTTGTGGCTA TGGGTGATC ACCAGTATCA CCACCTTGGG AGGGGACAGT GAAATTTGGG 1500
 CTAGAGAAGG AACTTTGTAC AGTTTTCCTT GAGATTGAGA TTGACTGAAA AGTCACATGA 1560
 AGAGTTGATT GTCTTTTAA TGGTATGTTT AAACAGCTGA CATTTTAAAT TTTGATGAAA 1620
 TCCAGTTTAT TCGTTTGTTC TTTTATGCTT TGGGTGTTGC ATCCGAGAAA TCTTTTCCCA 1680
 TCCCAAGATC ACAATTTTTT TTCCTTTTTC CTCTAGAAG TGTATAAAT TTAAGCTTTA 1740
 TACTTTGGTC TATGACCCGT TTTTTTTTTT GTTTTGTGTT GTTTTTCCTG TTGTTTCTTT 1800
 85 GTTTTGAGAT GGATGCTTGT TCTGTCAACC AGGCTGGGGT GCAGTGGCGT GACTCTGGCT 1860
 CACTGCAATC TCTATCCCCT GGGTTCAGT GATTCTCTTG TCTCAGCCTC CCAAGTAGCT 1920
 GGGATTACAG GCACAGGCCG CCACGCTCGG CTAATTTTTG TATTTTATGT AGAGACAGAG 1980

TTTTACCATG TTGGCCAGGC TGGTTTCAAA CTCCTGACCT CAAGTGACCC ACCTTGGCCT 2040
 CCCAAGTTT TGGGATTACA AGTGTGGGCC ACCGCGGCCA GCCTATGATC CATTTTGAAT 2100
 GAATTTTTTA TATGGTGCAA GGTGTCAATC CACCTTCACT TTTTCTTGGG AATATAGATA 2160
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 TTTGTTAAAA AGTAGTTTGC AATGTATATG TGGGTTTATT TCAGGACTCT GTTTTGTTC 2280
 ATTGACCTGT TTTTCTCTCC TGAATGCCAA TACCATATTT GTATGTAGTG TATGTAATTT 2340
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 TTTGTAGAGA TGGGTTTCA CCGTGTGGC CAGGCTGTGT TGAACCTCTG AGCTAAAGCA 2460
 ATACACTTGC CTCGTCTCTC CCATGTGCTG GGATTACAGG CGTGAGCCTT GGTGCTGGCC 2520
 CAGTGTACCA CATTCTTTT TGAGATTTGT TTTGGCTATG TTAAGTCTTT TGCTTTTGAT 2580
 GTGAAATTTG GGAACAGGCA GGGTGTGGTG GCTTATGCCT GTAATCCTAG AACTTTGGGA 2640
 GGCCTAGATG GGTGGATCAC TTGAGCTCAG GAGTTCAGA CCAGCCCGGG CCTATGGCAA 2700
 AACTCCGTCT CTACAAAAAA TAGAAAAAAT TAGCCAGGTG TGGTGGTGCA TGCCTGTAGT 2760
 CACAGTTACA CGGACAGGCT AGGTGGGAGG ATCACTTGAA CCCCAGAGGT CAAGACTGCA 2820
 GTGAGCTGAG ATCACACCA TGTACTCCAG CCTGGGTGAC AAAGTGAGAC TCTATCTCAA 2880
 AAAGAAATTA GGATCAATTT GTCAATTTCT ACAACAACAA CAACAAAAAC CCCTGTTGGG 2940
 CACCTTGATT GAGATTGCAAT TGAATTTATA TAAAACTGTT GGGAGAATTG ACATCTTAAT 3000
 AATATTGAGT CTCTGGCCT ATAAACAAGG TCTGTCTTCC TAGGTATTAA TGTTTGTCT 3060
 TCTATTTCTC TTAATAATCT TTTGTAGTTT TCAGTGTACA GGTCTACCAT GTCAGCATT 3120
 CATAGTTTGG ATGCTAAATG GTATTTTAAA ATTTCAAATT CTAACCACTT GTTGCTAGTA 3180
 AATAGAAATA CAATTGATGT TGAACCTTGA TCCTTCAGCC TTGCTAAACT GTGAGTTCTC 3240
 ATGGTGTTTT TGTAAATTAC ATCAACAGTC ATGTGTTCTA TGAATAAAGA GTTTTACTCC 3300
 TTC

Seq ID NO: 154 Protein sequence:
 Protein Accession #: BAA11503.1

1 11 21 31 41 51
 MFCEKAMELI RELHRAPEGO LPAFNEGLR QVLEEMKALY EQNQSDVNEA KSGGRSDLIP 60
 TIKFRHCSLL RNRRCTVAYL YDRLLRIRAL RWEYGSVLPN ALRFHMAAEE MEWFNNYKRS 120
 LATYMRSLGG DEGLDITQDM KPPKSLYIEV RCLKDYGEFE VDDGTSVLLK KNSQHFLPRW 180
 KCEQLIRQGV LEHILS

Seq ID NO: 155 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 149-709

1 11 21 31 41 51
 GTTCGGCGCC AAAGCGCGGA GCGGAGGCCG AGGCGAGAGC CTGGCGCTGT AGGACTAGAA 60
 CGAAAGGAGT GAGGCGCCGA GAGCCAGAT ACCATTTTGG CGTGAGAGCT GGTGGTTGGC 120
 AAGGCGCGCG GAGTGGGAAG CGTCCGCCAT GTTCTGCGAA AAAGCCATGG AACTGATCCG 180
 CGAGCTGCAT CGCGCGCCCG AAGGGCAACT GCCTGCCTTC AACGAGGATG GACTCAGACA 240
 AGTTCTGGAG GAGATGAAAG CTTTGTATGA ACAAACACAG TCTGTATGTA ATGAAGCAAA 300
 GTCAGGTGGA CGAAGTGATT TGATACCAAC TATCAAATTT CGACACTGTT CTCTGTTAAG 360
 AAATCGACGC TGCACGTGTG CATACCTGTA TGACCGCTTG CTTCGGATCA GAGCACTCAG 420
 ATGGGAATAT GGTAGCGTCT TGCCAAATGC ATTACGATTT CACATGGCTG CTGAAGAAAT 480
 GGAGTGGTTT AATAATTATA AAAGATCTCT TGCTACTTAT ATGAGGTGAC TGGGAGGAGA 540
 TGAAGGTTTG GACATTACAC AGGATATGAA ACCACCAAAA AGCCTATATA TTGAAGCTGG 600
 ATGCAGTGGC GCGATCTCGG CTCAACCTGC AACCTCCACC TCCCAGGTTT ACCTCAACTG 660
 CAACCTCCAC CTCCCAGGTC CGGTGCTTAA AAGACTATGG AGAATTTGAA GTTGATGATG 720
 GCACCTCAGT CCTATTAAAA AAAAATAGCC AGCACTTTTT ACCTCGATGG AAATGTGAGC 780
 AGCTGATCAG ACAAGGAGTC CTGGAGCACA TCCTGTCTAT ACCATGCGCC GAGGCACTTC 840
 CAGGCTTAC TCAACTCTAT GACTCCTCTG TACTCACTCT CTCCCACTCT CCTTCACCT 900
 CCCTCTTTGA TTTTAGAAGC TATAGACATT GTTTAAGATA ACTAAGAATA CTTGGCTAAG 960
 AAGTATAATT TGCTAACTAT TAAGGACTTT CTTTTTTTAA TGTGTGACAC TATCTCTCCT 1020
 ACTCTTTTTT GGTTTTGGTT TTGTTTGTGA GAGACTGTCT CACTATGTTG CCAAGCTGG 1080
 TCTCAAATCT CTGGCTCAA GCAGTCTCTC CACCTTAGCT TCTCAAAGTG TTGAGATCAC 1140
 AGGCGTGAGC CACTGCACCC GGCCCTACT CCTTTTTCTA ATAAGCTGTA TCTGTAATCA 1200
 CAGCATTCCT ACAGTTCTTA CAGTGTGTTT TTTAAATGAA AGTAAACATG GTTACATTGG 1260
 AATCTCTTAA ATAAGCAGTC ACTTGGCTGG ACAGGAAGAA GGTAGATCCT GTGTGTCTTG 1320
 TTTTCTGTGC ATGCTGTATT TACAAGCTAG AGAGCTGAAT TTCTGAGATA CACATTTTCA 1380
 AATCACATGC AAGTGAAGAT GATGGTCTGT AGAAATTTTC AGTATATATA ATGTTAATG 1440
 ACATACTAAT TTATCATCTG GCTATTGGG AAGGAAGGAC ACACATGGAT TTTGCACATT 1500
 TCCACCATTG TGGCTGGTGT GGCTTGTGGC TATGGGGTGA TCACCAAGTAT CACCACCTTG 1560
 GAAGGGGACA GTGAAATTGG GGCTAGAGAA GGAACCTTGT ACAGTTTTCC CTGAGATTCA 1620
 GATTGACTGA AAAGTCACAT GAAGAGTTGA TTGTCTTTTA ATGGTATGTT TTAACAGCT 1680
 GACATTTTAA ATTTTGATGA AATCCAGTTT ATTCGTTTGT TCTTTTATGC TTTGGGTGTT 1740
 GCATCCGAGA AATCTTTTCC CATCCCAAGA TCACAATTTT TTTTCTTTT TACTTCTAGA 1800
 AGTGTATAA TTTTAAGCTT TATACCTTGG TCTATGACCC GTTTTTTTT TTGTTTGTGTT 1860
 TTGTTTTTTC GTTTGTTTCT TTGTTTGTAG ATGGAGTCTT GTTCTGTAC CCAGGCTGGG 1920
 GTGCAGTGGC GTGATCTTGG CTCACTGCAA TCTCTATCCC CTGGGTTCAA GTGATTCTCT 1980
 TGTCTCAGCC TCCCAAGTAG CTGGGATTAC AGGCACAGGC CGCCACGCCT GGCTAATTTT 2040
 TGTATTTTAA GTAGAGACAG AGTTTACCA TGTGGCCAG GCTGGTTTCA AACTCCTGAC 2100
 CTCAAGTGAC CCACCTTGGC CTCCCAAAGT TTTGGGATTA CAAGTGTGGG CCACCGCGGC 2160
 CAGCCTATGA TCCATTTTGA ATGAATTTT TATATGGTGC AAGGTGTCAA TCCACCTTCA 2220
 CTTTTTCTTG GGAATATAGA TATCCAGCTG TTTCACTACC ATTTTGTGAA AGGACTGCCC 2280
 TTTGCTCTAT CACCTTTGCA TTTTGTGTTA AAAGTAGTTG TCAATGTATA TGTGGGTTTA 2340
 TTTCAAGGACT CTGTTTGTGT CCATTGACCT GTTTTCTCT CCTGAATGCC AATACCATTAT 2400
 TTGTATGTAG TGTATGTAAT TTTCTAATAA TTCTTGAAAC AGATAGTATT AATGTGTCAT 2460
 ATTTTGTCTG TGTGTTGTAT TTTTGTAGA GATGGGGTTT CACCGTGTG GCCAGGCTGT 2520
 GTTGAACCTC TGAGCTAAAG CAATACACTT GCCTCGTCTT CCCCATGTGC TGGGATTACA 2580
 GGCCTGAGCC TTGGTGCTGG CCCAGTGTAC CACATTTCTT TTTGAGATT GTTTTGGCTA 2640
 TGTTAAGTCC TTTGCTTTTG ATGTGAAAT TGGGAACAGG CAGGGTGTGG TGGCTTATGC 2700
 CTGTAATCCT AGAACTTTGG GAGGCCTAGA TGGGTGGATC ACTTGAGCTC AGGAGTTCCA 2760
 GACCAGCCCG GGCCTATGGC AAAACTCCGT CTCTACAAAA AATAGAAAAA ATTAGCCAGG 2820

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TGTGGTGGTG	CATGCCTGTA	GTCACAGTTA	CACGGCAGGC	TGAGGTGGGA	GGATCACTTG	2880
AACCCCGAG	GTCAGACTG	CAGTGAGCTG	AGATCACACC	ACTGTACTCC	AGCCTGGGTG	2940
ACAAAGTGAG	ACTCTATCTC	AAAAAGAAAT	TAGGATCAAT	TTGTCAATTT	CTACAACAAC	3000
AACAAACAAA	ACCCCTGTTG	GGCACCTTGA	TTGAGATTGC	ATTGAATTTA	TATAAAACTG	3060
TTGGGAGAAT	TGACATCTTA	ATAATATTGA	GTCCTCTGGC	CTATAAACAA	GGTCTGTCTT	3120
CCTAGGTATT	AATGTTTTGT	CTTCTATTTC	TCTTAATAAT	CTTTTGTAGT	TTTCAGTGTA	3180
CAGGTCTACC	ATGTGAGAT	TTCATAGTTT	TGATGCTAAA	TGGTATTTTA	AAATTTCAAA	3240
TTCTAACAC	TTGTTGCTAG	TAAATAGAAA	TACAATTGAT	GTTGAACCTG	TATCCTTCAG	3300
CCTTGCTAAA	CTGTGAGTTC	TCATGGTGTT	TTTGTAATTT	ACATCAACAG	TCATGTGTTC	3360
TATGAATAAA	GAGTTTTACT	CCTTC				

Seq ID NO: 156 Protein sequence:
Protein Accession #: Eos sequence

15
20

1	11	21	31	41	51	
MFCEKAMELI	RELHRAPEQG	LPAFNEGLR	QVLEEMKALY	EQNQSDVNEA	KSGGRSDLIP	60
TIKFRHCSLL	RNRRCCTVAYL	YDRLLRIRAL	RWEYGSVLBN	ALRFHMAAEE	MEWFNNYKRS	120
LATYMRSLGG	DEGLDITQDM	KPPKSLYIEA	GCSGSAISQP	ATSTSQVHLN	CNLHLPGPVS	180
KRLWRI						

Seq ID NO: 157 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 148-621

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1	11	21	31	41	51	
TTCGGCGCCA	AAGCGCGGAG	CGGAGGCCGA	GGCGAGAGCC	TGGCGCTGTA	GGACTAGAAC	60
GAAAGGAGTG	AGGCCGCCGAG	AGCCGAGATA	CCATTTTGGC	GTGAGAGCTG	GTGGTTGGCA	120
AGGCCGCGGG	AGTGGGAAGC	GTCCGCCCATG	TTCTGCGAAA	AAGCCATGGA	ACTGATCCGC	180
GAGCTGCATC	GCGCGCCCGA	AGGGCAACTG	CCTGCCTTCA	ACGAGGATGG	ACTCAGACAA	240
GTTCTGGAGG	AGATGAAAGC	TTTGTATGAA	CAAAACCAGT	CTGATGTGAA	TGAAGCAAAG	300
TCAGGTGGAC	GAAGTGATT	GATACCAACT	ATCAAATTTT	GACACTGTTC	TCTGTTAAGA	360
AATCGACGCT	GCACGTGAGC	ATACCTGTAT	GACCGCTTGC	TTCCGATCAG	AGCACTCAGA	420
TGGGAATATG	GTAGCGTCTT	GCCAAATGCA	TTACGATTTC	ACATGGCTGC	TGAAGAAGTC	480
CGGTGCTTAA	AAGACTATGG	AGAATTTGAA	GTTGATGATG	GCACCTTCAGT	CCTATTAAAA	540
AAAAATAGCC	AGCACTTTT	ACCTCGATGG	AAATGTGAGC	AGCTGATCAG	ACAAGGAGTC	600
CTGGAGCACA	TCTGTCTATG	ACCATGCGCC	GAGGCACTTC	CAGGCTTCAC	TCAACTCATG	660
GACTCCTCTG	TACTCACTCT	CTCCACCACT	CCCTTCACCT	CCCTCTTTGA	TTTTAGAAGC	720
TATAGACATT	GTTTAAGATA	ACTAAGAATA	CTTGGCTAAG	AAGTATAATT	TGCTAACTAT	780
TAAGGACTTT	CTTTTTTTAA	TGTTGTACAC	TATTCTTCCT	ACTCTTTTTT	GGTTTTGGTT	840
TTGTTTTGTA	GAGACTGTCT	CACATGTTG	CCCAAGCTGG	TCTCAAACTC	CTGGCCTCAA	900
GCAGTCTCC	CACCTTAGCT	TCTCAAAGTG	TTGAGATCAC	AGGCGTGAGC	CACCTGCACCC	960
GGCCCCACT	CCTTTTTCTA	ATAAGCTGTA	TCTGTAATCA	CAGCATTCCCT	ACAGTTGTTA	1020
CAGTGTGTTT	TTTAATGAA	AGTAAACATG	GTTACATTG	AATCTCTTAA	ATAAGCAGTC	1080
ACTTGGCTGG	ACAGGAAGAA	GGTAGATCCT	GTGTGTCTTG	TTTTCTGGTC	ATGTGTATTG	1140
TACAAGCTAG	AGAGCTGAAT	TTCTGAGATA	CACATTTTCA	AATCACATGC	AAGTGAAGAT	1200
GATGGTCTGT	AGAAATTTTC	AGTATATATA	ATGTTTAATG	ACATACTAAT	TTATCATCTG	1260
GCTATTTGGG	AAGGAAGGAC	ACACATGGAT	TTTGACATT	TCCACCATTG	TGGCTGGTGT	1320
GGCTTGTGGC	TATGGGGTGA	TCACCAGTAT	CACCACCTTG	GAAGGGGACA	GTGAAATTGG	1380
GGCTAGAGAA	GGAACTTTGT	ACAGTTTCC	CTGAGATTCA	GATTGACTGA	AAAGTCACAT	1440
GAAGAGTTGA	TTGCTTTTAA	ATGGTATGTT	TTAAACAGCT	GACATTTTAA	ATTTTGATGA	1500
AATCCAGTTT	ATTCTGTTGT	TCTTTTATGC	TTTGGGTGTT	GCATCCGAGA	AATCTTTTCC	1560
CATCCCAAGA	TCACAATTTT	TTTTCTTTT	TACTTCTAGA	AGTGTATATA	TTTTAAGCTT	1620
TATACTTTGG	TCTATGACCC	GTTTTTTTTT	TTGTTTGTG	TTGTTTTTTC	GTTTGTCTCT	1680
TTGTTTTGAG	ATGGAGTCTT	GTTCTGTCTC	CCAGGCTGGG	GTGCACTGGC	GTGATCTTGG	1740
CTCAGTGCAA	TCTCTATCCC	CTGGGTTCAA	GTGATTCTCT	TGTCTCAGCC	TCCCAAGTAG	1800
CTGGGATTAC	AGGCACAGCC	CGCCACGCCT	GGCTAATTTT	TGTATTTTAA	GTAGAGACAG	1860
AGTTTTACCA	TGTTGGCCAG	GCTGGTTTCA	AACTCCTGAC	CTCAAGTGAC	CCACCTTGGC	1920
CTCCCAAAGT	TTTGGGATTA	CAAGTGTGGG	CCACCGCGGC	CAGCCTATGA	TCCATTTTGA	1980
ATGAATTTTT	TATATGGTGC	AAGGTGTCAA	TCCACCTTCA	CTTTTCTTTG	GGAAATATAGA	2040
TATCCAGCTG	TTTCACTAGC	ATTTTGTGAA	AGGACTGCCC	TTTGCTCTAT	CACCTTTGCA	2100
TTTTTGTATA	AAAGTAGTTG	TCAAATGTATA	TGTGGGTTTA	TTTCAGGACT	CTGTTTGTGT	2160
CCATTGACCT	GTTTTTCTCT	CCTGAATGCC	AATACCATAT	TTGTATGTAG	TGTATGTAAT	2220
TTTCTAATAA	TTCTTGAAAC	AGATAGTATT	AATGTGTCAAT	ATTTTGTCTG	TTGTTTGTAT	2280
TTTTTGTAGA	GATGGGGTTT	CACCGTGTG	GCCAGGCTGT	GTTGAACTCC	TGAGCTAAAG	2340
CAATACACTT	GCCTCGTCTT	CCCCATGTGC	TGGGATTACA	GGCGTGAGCC	TTGGTGCTGG	2400
CCCAGTGATC	CACATTTCTT	TTTGAGATT	GTTTTGGCTA	TGTTAAGTCC	TTTGCTTTTG	2460
ATGTGAAATT	TGGGAACAGG	CAGGGTGTGG	TGGCTTATGC	CTGTAATCCT	AGAACTTTGG	2520
GAGGCTTAGA	TGGGTGGATC	ACTTGAGCTC	AGGAGTTCCA	GACCAGCCCG	GGCCTATGGC	2580
AAAACCTCCG	CTCTACAAAA	AATAGAAAAA	ATTAGCCAGG	TGTGGTGGTG	CATGCCTGTA	2640
GTCACAGTTA	CACGGCAGGC	TGAGGTGGGA	GGATCACTTG	AACCCAGAG	GTCAAGACTG	2700
CAGTGAGCTG	AGATCACACC	ACTGTACTCC	AGCCTGGGTG	ACAAAGTGAG	ACTCTATCTC	2760
AAAAAGAAAT	TAGGATCAAT	TTGTCAATTT	CTACAACAAC	AACAACAAAA	ACCCCTGTTG	2820
GGCACTTGA	TTGAGATTGC	ATTGAATTTA	TATAAAACTG	TTGGGAGAA	TGACATCTTA	2880
ATAATATTGA	GTCTTCTGGC	CTATAAACAA	GGTCTGTCTT	CCTAGGTATT	AATGTTTTGT	2940
CTTCTAATTC	TCTTAATAAT	CTTTTGTAGT	TTTCAGTGTA	CAGGTCTACC	ATGTCAGCAT	3000
TTCTAGTTT	TGATGCTAAA	TGGTATTTTA	AAATTTCAAA	TTCTAACCAA	TTGTTGCTAG	3060
TAAATAGAAA	TACAATTGAT	GTTGAACCTG	TATCCTTCAG	CCTTGCTAAA	CTGTGAGTTC	3120
TCATGGTGTT	TTTGTAATTT	ACATCAACAG	TCATGTGTTC	TATGAATAAA	GAGTTTTACT	3180
CCTTC						

Seq ID NO: 158 Protein sequence:
Protein Accession #: Eos sequence

85

1	11	21	31	41	51

MFCEKAMELI RELHRAPEGO LPAFNEDGLR QVLEEMKALY EQNQSDVNEA KSGGRSDLIP 60
 TIKFRHCSLL RNRRCTVAYL YDRLLRIRAL RWEYGSVLPN ALRFHMAAEE VRCLKDYGEF 120
 EVDDGTSVLL KNSQHFLLR WKCEQLIRQG VLEHILS

5

Seq ID NO: 159 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 149-229

10 1 11 21 31 41 51
 | | | | | |
 GTTCGGCGCC AAAGCGCGGA GCGGAGGCCG AGGCGAGAGC CTGGCGCTGT AGGACTAGAA 60
 CGAAAGGAGT GAGGCGCCGA GAGCCCGAGT ACCATTTTGG CGTGAGAGCT GGTGGTTGGC 120
 AAGGCCGCGG GAGTGGGAAG CGTCCGCCAT GTTCTGCGAA AAAGCCATGG AACTGATCCG 180
 CGAGCTGCAT CGCGCGCCCG AAGGGCAACT GCCTGCCTTC AACAAATTAG TGGGTGTGGT 240
 15 GGCACACACC TGTAGTCCCA GCAACTTAGG AGGCTGAAGT GAGAGGATTG CATGGCTCCA 300
 GGAAGTTGAA ACTGCAGTGA ACTGTGGTCA CGCTATTACA CTCCAGCCTG GGTGACAGAC 360
 TGAATCCCTG TCTCAAAAG GAAAAGGAGG ATGGACTCAG ACAAGTTCTG GAGGAGATGA 420
 AAGCTTTGTA TGAACAAAC CAGTCTGATG TGTCTCTGT TAAGAAATCG ACGCTGCACT 480
 GTAGCATACC TGTATGACCG CTTGCTTCGG ATCAGAGCAC TCAGATGG

20

Seq ID NO: 160 Protein sequence:
 Protein Accession #: Eos sequence

25 1 11 21 31 41 51
 | | | | | |
 ATGTTCTGCG AAAAAGCCAT GGAAGTATG CGCGAGCTGC ATCGCGCGCC CGAAGGGCAA 60
 CTGCTGCTCT TCAACAATTA G

30

Seq ID NO: 161 DNA sequence
 Nucleic Acid Accession #: U10694
 Coding sequence: 1333-2280

35 1 11 21 31 41 51
 | | | | | |
 GGATCCGGCC GGATCTCAGG GAGGTGAGGA CTTTGTCTCT AGAGGGTGTG TGTGGACAAA 60
 ACAGGGAGGC CTGTGTTCG ACAGACACAG TGGTCCCAGG ATTGAGAGC AGTCCAGGTG 120
 AGGAACCTAA GGGAGGATCG AGGGTACCTC CAGGCCAGAG AAACCTCTCAG ATCAAGAGAG 180
 TTTGCCCTGC CCCTACTGTC ACCCCAGAGA GCGCGGGCAG GGCTGTCTGC TGAGGTCCCT 240
 40 CTTTATCTCT GGGATCACTG GTGTGCGGGA GGGCTGGCCT TGGTCTGAGG GGGCTGCACT 300
 CACGTCAGCA GAGGGAGGGT CCGAGGCCCT GCCAGGAGTC CAGGTGCAGA CTGAGGGGAC 360
 CCCACTCACC AAACACAGAG GACCTAGCCC CACCTGCCCC CTGTGTCTCAG CTGAGGGGAG 420
 CCGCTGGGTG GATGGACTCC CCTCACTTCC TCTTCAGGTG TCTCTTGAG ATAGGGCTTC 480
 AGGTCAACAG AGGGAGGGTT CCAGACCCCTG CAGGCATCAA GATGAGGACC AGGCAGTATC 540
 CTCACCCAG GACACATGGA CCCCATTGAA TTAGACATC TCTTACTGTA CTTCCGAGGA 600
 45 AAACCTGGGC AGGTGTGGGC AGATGTTGGT TGGGGCATGT CCTTCTGTTC CATATCAGGG 660
 ATGTGAGCTC CTGATCTGAG AGACTCTCAG GCAAGTAGAG GAGTAGAGTC CAGTCCCTGC 720
 CAGGAGAAAG GTCAGGGCCC TGAGTGAGCG CAGAGGGGAC CATCCACCCC AAAAGTGTGT 780
 AGAACTCAAG AGTGTCCAGC CGGCCCTCTT GACAGCACTG AGGGACCCGG GCTCTGCCCTG 840
 CAGTCTGCAG CCTAAGGGCC CCTCGATTCC TCTTCCAGGA GCTCCAGGAA GCAGGCAGGC 900
 50 CTTGGTCTGA GACAGTGTCC TCAGGTCCGA GAGCAGAGGA GACCCAGGCA GTGTCAAGCA 960
 TGAAGGTGAA GTGTTACACC TGAATGTGCA CCAAGGGCCC CACCTGCCCC AGCACACATG 1020
 GGACCCATA GCACCTGGCC CCATTCCCC TACTGTCACT CATAGAGCCT TGATCTCTGC 1080
 AGGCTAGCTG ACAGTGTGAT AGCCCTCTCA CTCTCTCCCT CAGGTCTCTG GGACAGGCTA 1140
 ACCAGGAGGA CAGGAGCCCC AAGAGGCCCC AGAGCAGCAC TGACGAAGAC CTGTAAGTCA 1200
 55 GCCTTTGTGA GAACCTCAA GGTTCGGTTC TCAGCTGAAG TCTCTCACAC ACTCCCTCTC 1260
 TCCCGAGGCC TGTGGGTCTC CATCGCCCAG CTCCCTGCCA CGCTCTGAC TGCTGCCCTG 1320
 ACCAGAGTCA TCATGTCTCT CGAGCAGAGG AGTCCGCACT GCAAGCCTGA TGAAGACCTT 1380
 GAAGCCCAAG GAGAGGACTT GGGCTGATG GGTGCACAGG AACCCACAGG CGAGGAGGAG 1440
 GAGACTACCT CCTCTCTGTA CAGCAAGGAG GAGGAGGTGT TGTCTGCTGG GTCATCAAGT 1500
 60 CCTCCCCATA GTCCCTCAGG AGGCGCTTCC TCCTCCATTT CCGTCTACTA CACTTTATGG 1560
 AGCCAAATCG ATGAGGGCTC CAGCAGTCAA GAAGAGGAAG AGCCAAAGCTC CTCGGTCCGAC 1620
 CCAGCTCAGC TGGAGTTCAT GTTCCAAGAA GCACTGAAAT TGAAGTGGC TGAGTTGGTT 1680
 CATTTCTCTG TCCACAAATA TCGAGTCAAG GAGCCGGTCA CAAAGGCAGA AATGTCTGGAG 1740
 AGCGTCACTA AAAATTACAA GCGCTACTTT CCTGTGATCT TCGGCAAGC CTCGAGTTTC 1800
 65 ATGCAAGTGA TCTTTGGCAC TGATGTGAAG GAGGTGGACC CCGCCGGCCA CTCCTACATC 1860
 CTTGTCACTG CTCTTGGCCT CTCGTGCGAT AGCATGCTGG GTGATGGTCA TAGCATGCCC 1920
 AAGGCCGCCCT TCCTGATCAT TGTCTTGGGT GTGATCCTAA CCAAAGACAA CTGCGCCCCCT 1980
 GAAGAGGTTA TCTGGGAAGC GTTGAGTGTG ATGGGGGTGT ATGTTGGGAA GGAGCACATG 2040
 70 TTCTACGGGG AGCCAGGAA GCTGCTCACC CAAGATTGGG TGCAGGAAAA CTACCTGGAG 2100
 TACCGGCAGG TGCCCGGCAG TGATCCTGCG CACTACGAGT TCCTGTGGGG TTCCAAGGCC 2160
 CACGCTGAAA CCAGCTATGA GAAGGTCAATA AATTATTTGG TCATGCTCAA TGCAAGAGAG 2220
 CCCATCTGCT ACCCATCCCT TTATGAAGAG GTTTTGGGAG AGGAGCAAGA GGGAGTCTGA 2280
 GCACCAAGCCG CAGCCGGGGC CAAAGTTTGT GGGGTGAGGG CCCCATCCAG CAGCTGCCCT 2340
 75 GCCCCATGTG ACATGAGGCC CATTCCTGCG TCTGTGTTTG AAGAGAGCAA TCAGTGTCTT 2400
 CAGTGGCAGT GGGTGGAAAT GAGCACACTG TATGTCATCT CTGGGTTCCT TGTCTATTGG 2460
 GTGATTGGA GATTATCCCT TGCTCCCTTT TGAATTTGTT CAAATGTTCT TTTAATGGTC 2520
 AGTTTAATGA ACTTACCAT CGAAGTTAAT GAATGACAGT AGTCACACAT ATTGCTGTTT 2580
 ATGTTATTTA GGAGTAAGAT TCTTGCTTTT GAGTCACATG GGGAAATCCC TGTATTTTTG 2640
 TGAATTGGGA CAAGATAACA TAGCAGAGGA ATTAATAAAT TTTTGAAGAC TTGAACCTTAG 2700
 80 CAGCAAAATA GAGCTATAA AGAAATAGTG AAATGAAAT GTAGTTAAT CTGCTTAT 2760
 ACCTCTTTCT CTCTCTGTGA AAATTAAGAC ATATACATGT ATACCTGGAT TTGCTTGGCT 2820
 TCTTTGAGCA TGAAGAGAA ATAAAAATTG AAAGAATAAT TTTTCTGTTT CACTGGCTCA 2880
 TTTTCTTCTT AGACACGCAC TGAACATCTG TTATTCGGAA CACCTTGGGT T

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Seq ID NO: 162 Protein sequence:
 Protein Accession #: AAA68877.1

1	11	21	31	41	51	
MSLEQRSPHC	KPDEDLEAQQ	EDLGLMGAQE	PTGEEEEETS	SSDSKEEEVS	AAGSSSPQPS	60
PQGASSSIS	VYYTLWSQFD	EGSSSQEERE	PSSSVDPACL	EFMFQELKL	KVAELVHLL	120
HKYRVKEPVT	KAEMLESVIK	NYKRYFPVIF	GKASEFMQVI	FGTDVKEVDP	AGHSYILVTA	180
LGLSCDSMLG	DGHSMPKAAAL	LIIVLGVILT	KDNCAPEEVI	WEALSVMGVY	VGKEHMFYGE	240
PRKLLTQDWV	QENYLEYRQV	PGSDPAHYEF	LWGSKAHAET	SYEKVINYL	MLNAREPICY	300
PSLYEEVLGE	EQEGV					

Seq ID NO: 163 DNA sequence
Nucleic Acid Accession #: AF292100
Coding sequence: 30-809

1	11	21	31	41	51	
GGGGGGGGAG	AGGCCTGGAG	GACACCAACA	TGAACAAGTT	GAAATCATCG	CAGAAGGATA	60
AAGTTCGTCA	GTTTATGATC	TTCACACAAT	CTAGTGAAAA	AACAGCAGTA	AGTTGTCTTT	120
CTCAAAATGA	CTGGAAGTTA	GATGTTGCAA	CAGATAATTT	TTTCCAAAAT	CCTGAACCTT	180
ATATACGAGA	GAGTGTAATA	GGATCATTTG	ACAGGAAGAA	GTTAGAAGAC	CTGTACAATA	240
GATACAAAGA	CCCTCAAGAT	GAGAATAAAA	TTGGAATAGA	TGGCATACAG	CAGTTCCTGT	300
ATGACCTGGC	ACTCGATCCA	GCCAGCATT	GTGTGTTGAT	TATTGCGTGG	AAGTTCAGAG	360
CAGCAACACA	GTGCGAGTTC	TCCAAACAGG	AGTTCATGGA	TGGCATGACA	GAATTAGGAT	420
GTGACAGCAT	AGAACAACTA	AAGGCCCAGA	TACCCAAGAT	GGAACAAGAA	TTGAAAGAAC	480
CAGGACGATT	TAAGGATTTT	TACCAGTTTA	CTTTTAATTT	TGCAAGAAT	CCAGGACAAA	540
AAGGATTAGA	TCTAGAAATG	GCCATTGCCCT	ACTGGAACCT	AGTGCTTAAT	GGAAGATTTA	600
AATTCTTAGA	CTTATGGAAT	AAATTTTGT	TGGAACATCA	TAAACGATCA	ATACCAAAAG	660
ACACTTGGAA	TCTTCTTTTA	GACTTCAGTA	CGATGATTGC	AGATGACATG	TCTAATTATG	720
ATGAAGAAGG	AGCATGGCCT	GTTCTTATTG	ATGACTTTGT	GGAATTTGCA	CGCCCTCAAA	780
TTGCTGGGAC	AAAAAGTACA	ACAGTGTAGC	ACTAAAGGAA	CCTTTTAGAA	TGTACATAGT	840
CTGTACAATA	ATACCAACAG	AAAATTGCAC	AGTCAATTC	TGCTGGCTGG	ACTGAACTGA	900
AGATCAATCC	TACCAATTC	GACTGAGGGT	TGAGACAAAA	CTTTAAGGAT	ACATCTTGGA	960
CCATATCGTA	TTTCATTCTT	CTAATGGTGG	TTTGGGCTTG	TCTTCTAGTC	TGGGCGGCTC	1020
TAAACATTTA	TAATTCACAC	ATTGTGGATT	TCATCTTATA	TCTGTGGACC	ATCTAGTTT	1080
ATTCTCCCAT	AAGTCTTAGA	AGCTTTATGG	TGATTATTTT	GAGGTTTTCA	TTCTCGCATA	1140
AAGCACAAAT	GCTGCTTCAT	CAGAAAACAG	TTGGCATAAG	AATTAACAT	ATGAACATCA	1200
CAAAACAATT	TATAAAACT	TCTTAAATAT	ACGCTTTGGG	CTAGTTGCAA	AGACTATGCT	1260
AATAGCACTT	CCAGTGAGAG	TGATATATTT	AAGTGTACTG	GATCTGGAAT	GGTGTTTTGG	1320
TTTGGGGGGA	ATTTTTTTTT	TTTCTGGGCA	AATCACATAT	GTGTGTGATG	TGAGTATCTG	1380
ATGAAAAAAC	AATGTCAGAA	TAACCGACAT	GAAAATTTT	TAGGATAACT	TGGTGCCTAC	1440
CTGAAAAATG	TATTGTGTTT	TAGACTCTTG	ATTTCAAAAG	GTTCACAGAG	ACTAGTCTGC	1500
GCTTACCTTA	CCCATGTTTA	TATATAGCTG	TCCTACAGGG	AGCTTTTATT	TAGAAAATGT	1560
CTGCATAAAT	TTAGATTCTT	CTCCTGTCTA	CATTATGCAC	TACATAATTG	GACTTCATTA	1620
TGCTTTTGAA	ATGCTTATCT	GCCTGTGACA	TAAATTAAC	TATTTAATTT	GTTTGTGAATG	1680
TTTTGGGATT	CTACACAATA	CAATATTCTA	AATTTAGGCA	TGAGGGTTTT	TTTGTTTTAT	1740
TTTTACTTTT	TTTTTGTCTA	TGCACTATGG	AACACAAATG	AAATCTCTCT	AATTTATAAG	1800
AAGATAGTAG	GAGTTAAATT	TTGAAAATGG	TTGTGATGAG	CCACGAAATT	CAATCTTTAT	1860
AATATAGGTA	CTGCTCTTTC	AGACAAACAG	TCCATTTTTA	ATGACTTCTT	ATTTTGTGTA	1920
AATTACTTTA	ACTGCTAATC	ACTGTGGTTG	CCAAATATTT	ACTTCAGAAG	CAAAGATTTT	1980
CAACAAGCA	TACACGATGC	AAAATACCAG	TCTGGCTTCT	AGTCTATTTA	CTGTTTGTGT	2040
TCATCTAGAT	TAGCTCAGTT	TTCTCATCAA	AGCAGAAATG	TATCTTGCGT	GTGTGTGTGT	2100
GTGTGTGTGT	GTGTGTGTGT	GTATGTGTGT	ATATATATAT	ATATATATAT	ATATATATTT	2160
TTTTTTTTTT	TTTTTTTTTA	ATTACAAAAG	CCATGAGCTG	CTTTTATGCT	GAAAATGGTC	2220
ATTTCCCTGT	TCACCTACTG	ACATGTGAAG	AAGGGTTTCT	TGCTTTCTTA	AACATTTCCG	2280
TAAGGCAGGC	TAGAAATGTA	ATACTTCAAA	TGTTTGATGA	TTATGGTCTT	TTGATAGGAA	2340
TAGATTCTGC	TTGGGATATA	TATCCAGGCA	CTCTCTAAGG	TCTAGGGTTG	ATATTACAA	2400
AGGAATGTAC	TTAGAATAGC	AGTACATTTT	ATGCAAAATAT	GGAATATTAT	TTAAGAAACA	2460
ATGACATATC	AAAATGCTCT	TTTACATGAT	TTTGAAATAG	ACTAGAAAGC	TTTCCCTATA	2520
GACATATTAA	TATTCCAAATC	ATAACTTTAA	TTCAAGAAATG	CAGTTTTTACC	AAAAGAAAAA	2580
TTTGAAATTT	TCTATTCAAG	CTACTGGAAT	TGGTTATTAA	AAGAAAAAGG	AAAAGAAAGA	2640
ATCTTGCTGC	TTCAGTATT	TCCTGATTTT	TTTGTAAATA	TAAAGAGGAA	CTTCAATTAT	2700
GAAAAATTTT	TAAAGATAT	ATATATCTAT	ATATCTATAT	ATATGTACTG	TTTTGTTTCC	2760
TGCTTGGAAG	ATTTTGAGTT	ATGGTTATTG	GTTCAGATT	GATTAATTCA	CATATGCTGT	2820
GTTTTCTTTA	AAAGTCATAT	GGGTTCTGTT	CCTAATGCCCT	TGGATTTTAC	ATATTTTCT	2880
TTTTAAATGC	AAAACCTTTT	CAACAAAATA	GTGTTTGTC	TCAGGTTGGT	ACTAAACATT	2940
TATAATTACT	GTGTAATTAT	AAACAAAAT	ACATAAGCT	TTGAATATAA	TTATGTAGCA	3000
TAAAAGTTAA	GGTTGTTTAC	TATGATGGCA	TCTTAGAATT	AAACAAAAT	TTTACTAGGG	3060
CTGAAAAGAG	AAGACTGATT	TAATGTGGTG	TGATTATTCT	GAAGATAAAT	GTCTGGCTAC	3120
AGGGAATATT	TTGTACTAAA	AAATGATTAC	ACATATGGCT	GTGTGTGTTT	GAGTCTGTGT	3180
CTGTGAGAGA	GCCAGAGAGA	GTGAGAGAGA	TTGACAGAGA	AAGGGAGAGA	CACACACACG	3240
CCCCTTGAAT	TGCTTTAACT	CCTAAGTGT	TCAGTCCCTA	TTCCGGTAAA	CTCCCCATGC	3300
TGATTCTTTG	TTTTAACTG	AACCATAGGT	ACAGTTTCCT	TTTTGCCAAA	TGTCAAAACA	3360
GGTACAAATT	TTAAATGTA	ATGCTTTTAA	AATAGAAAAA	TGTATAAAAT	TAGAAGTGCC	3420
CACATATAAA	AAATACTTGA	GATGAAGATT	ATCTTTAGTG	AATATCATCT	GCATATCTCT	3480
GTAAGTTCAA	TTGTGTTTCT	TACAGTCCCT	GTCATATTAC	CAACAGAGGC	AATAAAGCT	3540
GCAGTGAAT	TG					

Seq ID NO: 164 Protein sequence:
Protein Accession #: AAG00606

1	11	21	31	41	51	
MNKLKSSQKD	KVRQFMIFTQ	SSEKTAVSCL	SQNDWKLDVA	TDNFFQNPEL	YIRESVKGSL	60
DRKKLEQLYN	RYKDPQDENK	IGIDGIQQFC	DDLALDPASI	SVLIIANKFR	AAQCEFSKQ	120
EFMDGMTBLG	CDSIEQLKQAQ	IPKMEQELKE	PGRFKDFYQF	TFNFAKNPQ	KGLDLEMAIA	180
YWNVLVNGRF	KFLDLWNKFL	LEHHRKSIPK	DTWNLLLDPS	TMIADDSMNY	DEEGAWPVLI	240
DDFVEFARFQ	IAGTKSTTV					

Seq ID NO: 165 DNA sequence
Nucleic Acid Accession #: AF256215
Coding sequence: 220-2028

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	CTCCAGTCCG	CATGCTCAGT	AGCTGCTGCC	GGCCGGGCTG	CGGGGCGGGG	TCCGCTGCGC	60
	GCCTACGGCG	TGCGGTGGGG	GCCGCCGCGG	CACCCGGCAG	GGCCCGCCAG	TCCCCGCTTC	120
10	CCTGCTCCAG	AGCCGCCGCG	TGGGCGGGGG	CAGGCGGGGC	CGGGGGCTCC	TCCATGCTGC	180
	CAGCCGCGCG	GCTGCGGAGC	CGACCAAGTG	GCTCCTCGCA	TGGCGGCGGA	AGAGGAGGCT	240
	GCGGCGGGAG	GTAAAGTGTT	GAGAGAGGAG	AACCAGTGCA	TTGCTCCTGT	GGTTTCCAGC	300
	CGCGTGAGTC	CAGGGACAAG	ACCAACAGCT	ATGGGGTCTT	TCAGCTCACA	CATGACAGAG	360
15	TTTCCACGAA	AACGCAAAAG	AAGTGATTCA	GACCCATCCC	AAGTGAAGA	TGGTGAACAC	420
	CAAGTTAAAA	TGAAGGCCTT	CAGAGAAGCT	CATAGCCAAA	CTGAAAAGCG	GAGGAGAGAT	480
	AAAAATGAATA	ACCTGATTAT	AGAACTGTCT	GCAATGATCC	CTCAGTGCAA	CCCCATGGCG	540
	CGTAAACTGG	ACAAACTTAC	AGTTTAAAGA	ATGGCTGTTC	AACACTTGAG	ATCTTTAAAA	600
	GGCTTGACAA	ATTCCTATAT	GGGAAGTAAT	TATAGACCAT	CATTTCCTCA	GGATAATGAG	660
20	CTCAGACATT	TAATCCTTAA	GACTGCGAAA	GGCTTCTTAT	TTGTGGTTGG	ATGTGAAAGA	720
	GGAAAAATTC	TCTTCGTTTC	TAAGTCAGTC	TCCAAAATAC	TTAATTATGA	TCAGGCTAGT	780
	TTGACTGGAC	AAAGCTTATG	TGACTTCTTA	CATCCAAAG	ATGTTGCCAA	AGTAAAGGAA	840
	CAACTTCTCT	CTTTTGATAT	TTCAACCAAG	GAAAAGCTAA	TAGATGCCAA	AACGTGTTTG	900
	CAAGTTCACA	GTAATCTCCA	CGCTGGAAG	ACACGTGTGT	ATTCCTGGCTC	AAGACGATCT	960
25	TTTTTCTGTC	GGATAAAGAG	TTGTAAAATC	TCTGTCAAAG	AAGAGCATGG	ATGCTTACCC	1020
	AACTCAAAAG	AGAAAGAGCA	CAGAAAATTC	TATACTATCC	ATTGCACTGG	TTACTTGAGA	1080
	AGCTGSCCTC	CAAAATATTG	TGGAATGGAA	GAAGAAAGGA	ACAGTAAGAA	AGACAACAGT	1140
	AATTTTACCT	GCCTTGTGGC	CATTGGAAGA	TTACAGCCAT	ATATTGTTCC	ACAGAACAGT	1200
	GGAGAGATTA	ATGTGAAACC	AACCTGAATT	ATAACCCGGT	TTGCACTGAA	TGGAAAATTT	1260
30	GTCTATGTAG	ATCAAAGGCG	AACAGCGATT	TAGGATATC	TGCCCTCAGGA	ACTTTTGGGA	1320
	ACTTCTTGTT	ATGAATATTT	TCATCAAGAT	GACCAACAATA	ATTTGACTGA	CAAGCACAAA	1380
	GCAGTCTTAC	AGAGTAAGGA	GAAAATACCT	ACAGATTCCCT	ACAAATTCAG	AGCAAAAAGT	1440
	GGCTCTTTTG	TAACCTTAAA	AAGCCAATGG	TTTAGTTTCA	CAAACTCCTTG	GACAAAAGAA	1500
	CTGGAATATA	TTGTATCTGT	CAACACTTTA	GTTTTGGGAC	ATAGTGAGCC	TGGAGAAGCA	1560
35	TCATTTTAC	TTCTAGCTTC	TCAATCATCA	GAAGAATCCT	CTAGACAGTC	CTGTATGAGT	1620
	GTACCTGGAA	TGTCTACTGG	AACAGTACTT	GGTGTGGTGA	GTATTGGAAC	AGATATTGCA	1680
	AATGAAATTC	TGGATTTACA	GAGGTTACAG	TCTTCTTCAT	ACCTTGATGA	TTCGAGTCCA	1740
	ACAGGTTTAA	TGAAAGATAC	TCATACTGTA	AACCTGCAGGA	GTATGTCAA	TAAGGAGTTG	1800
	TTTCACCAA	GTCCCTCTGA	AATGGGGGAG	CTAGAGGCTA	CCAGGCAAAA	CCAGAGTACT	1860
40	GTTGCTGTCC	ACAGCCATGA	GCCACTCCTC	AGTGATGGTG	CACAGTTGGA	TTTCGATGCC	1920
	CTATGTGACA	ATGATGACAC	AGCCATGGCT	GCAATTATGA	ATTACTTAGA	AGCAGAGGGG	1980
	GGCCTGGGAG	ACCCTGGGGA	CTTCAGTGAC	ATCCAGTGGA	CCCTCTAGCC	TTTGATTTT	2040
	AACTCCAAAA	ATGAGAAACA	TTTTAAAGCA	TTATTTACGA	AAAAACTGTC	TCAACTATTC	2100
	TTAAGTACTG	TATTGATATT	GTTTGTATCT	TTTATTAATG	TTCTACCACT	TTTTATAGAT	2160
45	TTGCATCTTC	CTGTACACAG	GATGTGGGGA	AATACGTTTT	CCTCCCAAGA	GAACCAAGTT	2220
	TATTATAGAC	TCCCTTATCT	AGTGAAATGG	CTTATAATCC	ACTAGTTGCC	ATATTTTGGC	2280
	TAAAAATATT	CTAACCAAGA	ATACTACTTA	CATATTGTTT	TGGCTTTGTT	TTATTTTGA	2340
	TGCAGTTTTT	TTTAGTTGAG	GTAATGTAAT	ATATTGATGT	TTCTCTTTGT	GTCCTAAGATT	2400
	GATTTATAAT	AGTAGGTTTG	TATAATTTGG	AACATTTTCC	ATGCCTTGCG	AATTTCTTTA	2460
50	ATTGAGGATA	GGGCTTACAC	ACTTTAAGAA	AACAGTGAGT	ACTTGAAAT	TTAAGGGGAC	2520
	AGTGCAATTT	ATAGTCATAA	TCACATTGAA	TACTGTATTT	GATCTTTGGA	GACTTAGGCA	2580
	AGCACAGAGC	TGGGATATTT	ATGCTCAGTT	GAGCACTTTA	AGATGAATTT	TAAGTGAGAT	2640
	GATTTCTTGC	TTAAACTCTA	GAAAGTCAAA	AGAGTTTCAG	CTTTCCTTAC	AGAAAAGGAA	2700
55	GGATCTTGGG	CCCTAGATCT	TGGGGATTAA	CCTCTGCATA	TAAGATTAC	TCTTAATAGG	2760
	CCAGAGCTGG	TGCTCAGGCC	TGTAATCCCA	GTACTTTGGG	AGGCTGAGAC	GGGCAGATCA	2820
	CTTGAGGTCA	GGAGTTCAAG	ACCAGCCTGG	CCAATATGGT	GAAACCCCGT	TTCTACTAAA	2880
	AATACAAAAA	AAATTACCCA	GGCACTCACT	CTTGAGGTAA	CTAACCAACT	CCCACGATAA	2940
	TGACAGTCCA	TTCAATGAGG	CAAAAGCCCTC	ATGACCTAAT	GGCACACACC	TGTAATCCCA	3000
60	ACTGCTTGGG	AGGCTTGGG	GAGAGGATTG	CTTGAACCTG	GGAGGCAGAG	GTTGCACTGA	3060
	GCCGAGATCG	CACCACTGCA	CTCCAGTCTG	GGCAACAGAG	TGAGACTTCA	TCTCAAAAAA	3120
	AGTAAAAAAA	AAGATTTAAT	ATAATCACTG	AAGATCTCTA	TTATAGATAG	ATTAGGTTTT	3180
	TGACATTGGA	AACATCTTAA	GGGATAGATT	TGTCTCTAAAG	GAAAAAAGTA	GGCCCGGGCA	3240
	GATTAAATGT	CTTGTGTAAA	GTACACACAT	AAATTCAGTC	ACACATTAAA	TTCTAGAGAT	3300
	TTTAAATGTT	TAATGTATAT	AAACCAAGTT	CTTTATACAC	ATTTGGGAAA	ACATTGGTCT	3360
65	CACAGATTAA	ATGATTAACT	AACTGACCCA	GGAAGTATGT	GTAGCTTTCT	AAGTAATTAG	3420
	GCAATTACAG	TTATTGCCCTG	TAACCAAGAG	TAATAAAACA	AAATGACAG	TACATGTTTA	3480
	AAATTTAGAG	GCAATGAGAA	ATAATTTAAA	AACCAATTTT	CTAGTTATAA	TTTAAAAATT	3540
	GGAGAGCATT	TTTAACAGTA	ATTAATCCAG	AGGTGGCTCA	AATTGAGTAT	AAGAATTAA	3600
	ATTATTTAAA	ATACTGCATG	TCTACCTTCT	CGGGGATCAT	ACTTTATAAC	ACTTCTGCT	3660
70	TCAGTAGCTC	TTCTAGCTTT	GCCAAGTATG	CTCCCATATT	TTCTCTCTCG	TGCCCTCGCA	3720
	ATGAAAGTCA	GATAGGCTGG	GAACTCATGG	GGCAGCCCTC	AGACTTCAAT	GTGGGCTTCA	3780
	AATCCAGTTT	CCTGTTCTAT	ATGGTGCTAC	ATCTTTCCAG	AAAATTTCCC	TCAGAGCCCC	3840
	TCGCCAAAAA	AAAGCATTAT	TTTGACCCCTG	CATGCTATTT	CTTTAGCTGT	AGGTGATAGA	3900
	TTAGAACTTC	TGTGACAGAT	GTAAATGACA	AACATACCAA	CAGACAATAA	CCAAGCAAAA	3960
75	TGTTTCTCTC	AAGTGTGAAA	TGTGAGGGG	CTCGTGGGCA	AGGATGTATT	GGCACACTGT	4020
	CCTCTTGAAC	TGATAGTGTC	CCAGCAATGT	TGGAGGTTGG	CACCATTCCT	GGTCCGACAC	4080
	TTGAGGACCT	GAGAGACATC	AGGTTTAGAA	TGAGCCAAAG	AAATCCTACA	AGATGGGGAG	4140
	AAATGGTGTG	CAGCAGCCCTA	AGTGTATATG	TTAAGTCTAA	AGAAAGTATGA	AAGATCCCTC	4200
	GTGTTCTCTA	AATTGAGCAG	AGGGGCTTGC	CTACCAATAT	CACTTTCTAG	GGGACTGAAC	4260
	CATTGCGAGT	TAGACTTGGC	TTCCAAAGAG	TCTGCCTAAG	CCAGGGGTGG	CAGGGTAGGC	4320
80	CATCATAGCT	GGATGGCCCT	AAAAAGCAGAT	GGGGGCGAGC	TTGCCCTCGT	GATGCCAGGA	4380
	TTTGAGAGGC	AGAGTTTCTA	GAGGGAGACC	AGTGCTGCCCT	CTCACAGTGG	CAGTTTCTTC	4440
	TCTTTGCAAG	AGGAGGGGCT	GTTCATTTCC	ATAGACCACT	GGGCAGATAG	CCAGTTGAAT	4500
	ACTCTGTGCA	TGGTTTGATC	CTTTATTAAT	TCGCTCTAAT	ATTTTCTCTG	AGATCCTTTT	4560
85	GTCTCTGACT	CAAAATCTAA	TCCATGCATT	GTATGATACC	GTAGCTCTCC	TAAGGTTTGT	4620
	GTTCCTCTCA	AAATGTTTTA	GTTTTCTTCA	ACTAAATTTG	ATTTTGTCTG	TTAGAAGTGA	4680
	CATATTTTAA	TGGTATACAC	TATGTTCCCT	TTTCTACTG	CGAGTCAATT	TTTTGAATTT	4740
	TCGTGAGAAA	GAATATATCT	ACAAATTGCA	CGAAAGTATC	ATAAAACAG	TACTCTAGAG	4800

	CAGCGCTGTC	CAATAGAAAT	ATAATCTGAG	CCACATGTAT	AATTTTATTT	TCTTCTAGCC	4860
	ACATTAAAGA	AGTAAAAAGA	TACAAGTAGA	ACTAATTTTA	ATGTTTAAAT	TCAGTATATC	4920
	CAAAATATCA	TTTGACATG	TAATTAATAT	AAAAATTATTA	ATGTGATATT	TTACATTCTT	4980
5	TTGGTAATAC	TAGTCTTCAA	AATCTGGTAT	GTATCTTACA	TTGATAGCAC	ATCTCACTTT	5040
	GTACTAGCCA	CATTGCAAGT	GCTCAGTAGC	CACATGTGGC	TAGTGGCTAC	TGCACTGGAC	5100
	AGCACAGTTC	TAGGTTCCAC	CCTAACACCC	AAGTCTCTGT	GATTAGAATC	CCAGAATCAG	5160
	AGCTGGAGT	AAACATAGAG	ATCAAACCTC	CTTTTAAAAA	TGAGGACGCT	GAGGCACAGA	5220
	GTTTAAATGG	CTTGATGAG	GTCATACAGC	TAAATTCAGC	CTCAACAGGG	TCTTCTGATT	5280
10	CCAGGCACCT	TTCCCACTCC	ACTACATTAC	TGTAGTGGTA	ATTCTTAGGG	TTAAAAAAG	5340
	TGTAGAGTAG	GCCGGGCGCA	GTGGCTCATG	CCTGTAATCC	CAGCACTTGG	GGAGGCCGAA	5400
	GTGGGCGGAT	CACGAGGTCA	GGAGATCGAG	ACCATCCTGG	CCAACATGGT	GAAACCCCGT	5460
	CTCTACTGAA	AATACAAAGC	AAAATTAGCC	AGGTGTGGTG	GCGGGCGCCT	GTGGTCCCAG	5520
	CTGCTCTGGA	GGCTGAGGCA	GAATGGCGTG	AACCCAGGAG	GCAGAGATGG	CAGTGAGCCA	5580
15	AGATCGCGCC	ACTGCACCCC	AGCCTGGGCG	ACAGAGCGAG	ACTCCATCTC	AAAAAAGAAA	5640
	AAAAAAGAAA	AAGAAAAGAA	AAGAAAAGTC	TAGAGAACAT	TATATTAAGT	GGTTATTATT	5700
	GAAGTAGACC	AAAGTTTATA	CCATAAGGAT	ATTTTTCCTT	AAATACCATG	TTTGAAGAAC	5760
	AATTTATTTAT	TGATCCTTGA	ATCTGTAAGA	TCAAATAACA	AGTCTCTATC	CATGTTACCA	5820
	AATTTAACCT	TTTGAATAATA	ATAAACTTTA	AAATATCAGA	TGTGTTATTA	CAGGATGATA	5880
20	CTTGAATCA	AGTGAATGA	GTTATATGGT	CATCACTAAA	TTTAGAAATC	TATTGTGAAA	5940
	CAAGACAAA	CAGGAAAGTA	CAGAAATAGAG	ACTTTTAGTA	AATAAATGGA	ATTTAAAAAGA	6000
	AAGTGTTTAT	TTACAGTGTG	ACGACAGAAA	AGGATGTCTT	TGTTGTCATA	GTCTTTGAGG	6060
	GATCTCCGTA	AAATCTGGGG	CACAGGTACA	AGAAATAGCC	AATATTTAGT	TCCCAGACCA	6120
	TGTTTAGTAG	TGTCAGTTT	CAGATCATGC	TGCCAAGAGG	TATCTCCCCC	TCAGGTGGGT	6180
25	CATCACTGAG	CCCTGGAAAT	GGAGACTCAT	ACTTGCCCG	CACAATGTTA	CGGGCAGACA	6240
	GGCCGACATC	TATGATTAGC	TAGAAGCCAT	AAAGAAAAGC	TGCTAAGTGG	CCACTAGGTG	6300
	CCACTTTTCT	GTTTTTGTAA	TGCTTTCATT	AGCAGATCTT	TTTTTTCCAA	GCTCCATGGG	6360
	GCCTATGAGA	GGCATTATAG	ATTTTGTGTC	CTACAATAAG	TCAGCCTGTC	TGGTGTGAGT	6420
	TGTTTTATGA	GAAATGCTTT	CCAAGGGAGG	TCTAGGAAGA	TCCTGACACA	TAAGAACTTT	6480
30	GGCTTAGAGA	GCTTTCCAGG	TGTAGTGCCA	ATAAAACTG	ACCTGGAAAG	AAAACCTGCC	6540
	CAGCACGGAA	CATGCTTTCT	GAACTCACTT	GAGAGTGTAT	GGTGTATGTC	ACTTCTCATA	6600
	TATTTCTGAG	TTTAGATTGG	TCTTTTATAC	AATTTTATAG	TCTTTTCCAG	TTCACTTGTG	6660
	CTCGTCTGTA	TATTGGTATT	TTTAAATTTT	TGTGGTAAAT	AATGAAAAGA	GTGAAATTAT	6720
35	ATTTTATAAT	TACTCATTG	TAGTTTTTTT	TTTTAATTTA	ATAAACTTCC	TCCAAAAAGT	6780
	GCTCCCTTAA	AA					

Seq ID NO: 166 Protein sequence:
Protein Accession #: AAG34652

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	MAAEEEAAG	GKVLREENQC	IAPVVSSRV	PGTRPTAMGS	FSSHMTFEP	KRKGSDDSP	60
	QVEDGEHQV	MKAFREAHQ	TEKRRRDKM	NLIEELSAMI	PQCNPMARK	DKLTVLRMA	120
45	QHLRLSLK	NSYVGSNYR	SFLQDNELR	LILKTAEGFL	FVVGCGERK	LFVSKSVSKI	180
	LNVDQASLT	QSLFDFLHP	DVAKVKEQL	SFDISPREKL	IDAKTGLQV	SNLHAGRTV	240
	YSGSRRSFF	RIKSKISIVK	EEHGCPLNS	KKEHRKFYTI	HCTGYLRSW	PNIVGMEER	300
	NSKKDMSNF	CLVATGRLQ	YIVPQMSGE	NVKPTEFITR	FAVNGKFVY	DQRATAILGY	360
	LPQELLGTS	YEFYFHQDD	NLTDKHKAV	QSKEKILTDS	YKFRKADG	VTLKSQWFS	420
50	TNPWTKELE	IVSVNTLVLG	HSEPGEASF	PCSSQSSESR	SRQSCMSVP	MSTGTVLGAG	480
	SIGTDIANEI	LDLQRLQSS	YLDSSPTGL	MKDTHTVNC	SMSNKELFP	SPSEMGELE	540
	TRQNQSTVA	HSHEPLLSG	AQLDFDALC	NDDTMAAFM	NYLEAEGGL	DPGDFSDIQ	600
	TL						

Seq ID NO: 167 DNA sequence
Nucleic Acid Accession #: NM_014400
Coding sequence: 86-1126

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	GATCTGGACT	GCAGGCTGGC	TGCTGCTGCT	GCTGCTTCGC	GGAGGAGCGC	AGGCCCTGGA	180
	GTGCTACAGC	TGCGTGCAGA	AAGCAGATGA	CGGATGCTCC	CCGAACAAGA	TGAAGACAGT	240
65	GAAAGTCGCG	CGGGCGGTGG	ACGCTGTCAC	CGAGGCCGTG	GGGGCGGTGG	AGACCATCCA	300
	CGGACAAATC	TGCTGGCGAG	TGCGGGGTTG	CGGTTGCGGA	CTCCCCGGCA	AGAATGACCG	360
	CGGCCCTGG	CTTACCGGCG	TTCTGGCGTT	CATCCAGCTG	CAGCAATGCG	CTCAGGATCG	420
	CTGCAACGCC	AAGCTCAACC	TCACCTCGCG	GGCGCTCGAC	CCGGCAGGTA	ATGAGAGTGC	480
	ATACCCGCCC	AACGGCGTGG	AGTGTACAG	CTGTGTGGGC	CTGAGCCGGG	AGGCGTGCCA	540
70	GGGTACATCG	CGCCGGTTCG	TGAGCTGCTA	CAACGCCAGC	GATCATGTCT	ACAAGGGCTG	600
	CTTCGACGCG	AACGTCACTT	TGACGGCAGC	TAATGTGACT	GTGTCTCTGC	CTGTCCGGGG	660
	CTGTGTCCAG	GATGAATCTT	GCACTCGGGA	TGGAGTAACA	GGCCCAGGGT	TCACGCTCAG	720
	TGGCTCCTGT	TGCCAGGGGT	CCCGCTGTAA	CTCTGACCTC	CGCAACAAGA	CCTACTTCTC	780
	CCCTCGAATC	CCACCCCTTG	TCCGGCTGCC	CCCTCCAGAG	CCCACGACTG	TGGCCTCAAC	840
75	CACATCTGTC	ACCACTTCTA	CCTCGGCCCC	AGTGAGACCC	ACATCCACCA	CCAAACCCAT	900
	GCCAGCGCCA	ACCACTCAGA	CTCCGAGACA	GGGAGTAGAA	CACGAGGCCT	CCCGGGATGA	960
	GGAGCCCCAG	TTGACTGGAG	GCGCGCTGG	CCACCAAGG	CGCAGCAATT	CAGGGCAGTA	1020
	TCTGTCAAAA	GGGGGGCCCC	AGCAGCCCCA	TAATAAAGGC	TGTGTGGCTC	CCACAGCTGG	1080
	ATTGGCAGCC	CTTCTGTTGG	CGGTGGCTGC	TGGTGTCTTA	CTGTGAGCTT	CTCCACCTGG	1140
80	AAATTTCCCT	CTCACTTACT	TCTCTGGCCC	TGGGTACCCC	TCTTCTCATC	ACTTCTCTGT	1200
	CCCACCACTG	GACTGGGCTG	GCCCAGCCCC	TGTTTTTCCA	ACATTTCCCA	GTATCCCCAG	1260
	CTTCTGCTGC	GCTGTTTTCG	GGCTTTGGGA	AATAAAATAC	CGTTGTATAT	ATTCTGGCAG	1320
	GGGTGTTCTA	GCTTTTTGAG	GACAGTCCCT	GTATCCTTCT	CATCCTTGTC	TCTCCGCTTG	1380
	TCCTCTTGTG	ATGTTAGGAC	AGAGTGAGAG	AAGTCAGCTG	TCACGGGGAA	GGTGAGAGAG	1440
85	AGGATGCTAA	GCTTCTTACT	CACTTTCTCC	TAGCCAGCCT	GGACTTTGGA	GCGTGGGGTG	1500
	GGTGGGACAA	TGGTCCCCCA	CTCTAAGCAC	TGCTTCCCTT	ACTCCCCGCA	TCTTTGGGGA	1560
	ATCGGTTCCC	CATATGTCTT	CCTTACTAGA	CTGTGAGCTC	CTCGAGGGCA	GGGACCGTGC	1620
	CTTATGCTCG	TGTGTGATCA	GTTTCTGGCA	CATAAATGCC	TCAATAAAGA	TTTAATTACT	1680

TTGTATAGTG AAAAAAAA

Seq ID NO: 168 Protein sequence:
Protein Accession #: NP_055215

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CTEAVGAVET IHGQFSLAVX GCGSGLPGKN DRGLDLHGLL AFIQLQQCAQ DRCNAKLNLT 120
SRALDPAGNE SAYPPNGVEC YSCVGLSREA CQGTSPFVVS CYNASDHVYK GCFDGNVTLT 180
AANVTVSLPV RGCVDDEFCT RDGVTGPGFT LSGSCCQGSR CNSDLRNKTY FSPRIPLVR 240
LPPPEPTTVA STTSVTSTTS APVRPTSTTK PMPAPTSQTP RQGVHEASR DEEPRLTGGA 300
AGHQDRSNG QYPAKGPPQ PHNKGCVAPT AGLAALLLAV AAGVLL

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Seq ID NO: 169 DNA sequence
Nucleic Acid Accession #: NM_006875
Coding sequence: 186-1190

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1      11      21      31      41      51
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GAATTGCGCA CGAGCGCGCG GCGAATCTCA ACGCTGCGCC GTCTGCGGGC GCTTCCGGGC 60
CACCAGTTTC TCTGCTTTCC ACCCTGGCGC CCCCCAGCCC TGGCTCCCCA GCTGCGCTGC 120
CCCGGGCGTC CACGCCCTGC GGGCTTAGCG GGTTCAGTGG GCTCAATCTG CGCAGCGCCA 180
CTTCCATGTT GACCAAGCCT CTACAGGGGC CTCCCGCGCC CCCCAGGACC CCCACGCGC 240
CGCCAGGAGG CAAGGATCGG GAAGCGTTCG AGGCCGAGTA TCGACTCGGC CCCCTCCTGG 300
GTAAGGGGGG CTTTGGCACC GTCTTCGCAG GACACCGCCT CACAGATCGA CTCCAGGTGG 360
CCATCAAAAGT GATTCCCCGG AATCGTGTGC TGGGCTGGTC CCCCTTGTCA GACTCAGTCA 420
CATGCCCACT CGAAGTCGGA CTGCTATGGA AAGTGGGTGC AGGTGGTGGG CACCCTGGCG 480
TGATCCGCCT GCTTGACTCG TTTGAGACAC AGGAAGGCTT CATGCTGGTC CTCGAGCGGC 540
CTTTGCCCGC CCAGGATCTC TTTGACTATA TCACAGAGAA GGGCCCACTG GGTGAAGGCC 600
CAAGCCGCTG CTCTTTTGCC CAAGTAGTGG CAGCCATCCA GCACTGCCAT TCCCCTGGAG 660
TTGTCCATCG TGACATCAAG GATGAGAACA TCCTGATAGA CCTACGCCGT GGCTGTGCCA 720
AACTCATTGA TTTTGGTTCT GGTGCCCTGC TTCATGATGA ACCCTACACT GACTTTGATG 780
GGACAAGGGT GTACAGCCCC CCAGAGTGGG TCTCTCGACA CCAGTACCAT GCACTCCCGG 840
CCACTGTCTG GTCACTGGGC ATCCTCCTCT ATGACATGGT GTGTGGGGAC ATTCCCTTTG 900
AGAGGGACCA GGAGATCTCG GAAGCTGAGC TCCACTTCCC AGCCCATGTC TCCCAGACT 960
GCTGTGCCCT AATCGGCCG TGCTGGCCCG CCAAACCTTC TTCCCGACCC TCACTGGAAG 1020
AGATCCTGCT GGACCCCTGG ATGCAAAACAC CAGCCGAGGA TGTATCCCTT CAACCCCTCC 1080
AAAGGAGGCC CTGCCCCCTT GGCCTGGTCC TTGCTACCCT AAGCCTGGCC TGGCCTGGCC 1140
TGGCCCCCAA TGGTCAGAAG AGCCATCCCA TGGCCATGTC ACAGGGATAG ATGGACATT 1200
GTTGACTTGG TTTTACAGGT CATTACCAGT CATTAAAGTC CAGTATTACT AAGGTAAGGG 1260
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TCATATGCTT TTACTTGGGC AAGGGTGCTT TCCTTCCAAT ACCCCAGTAG CTTTATTTT 1560
AGTAAAGGGA CCCTTTCCCC TAGCTTAGGG TCCCATATTG GGTCAGCTG CTTACCTGCC 1620
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CTGGTGAGAA GAACCTTAAT TCCATAATT GGAAGGAAT GGAAGATGGA CACCACCGGA 1800
CACCACCAGA CAATAGGATG GGATGGATGG TTTTGGGGG GATGGGCTAG GGGAAATAAG 1860
GCTTGCTGTT TGTTTTCCCT GGGCGCTCCC TCCAATTTTG CAGATTTTGG CAACCTCCTC 1920
CTGAGCCGGG ATGTGCCAAT TACTAAATG TAAATAATCA CGTATTGTGG GGAGGGGAGT 1980
TCCAAGTGTG CCTCCTTTT TTTTCTGCTC TGGATTATTT AAAAAAGCAT GTGTGGAAC 2040
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Seq ID NO: 170 Protein sequence:
Protein Accession #: NP_006866

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KVIPRNRVLG WSPLSDSVTC PLEVALLWKV GAGGGHPGVI RLLDWFETQE GFMLVLERPL 120
PAQDLFDYIT EKQPLGEGPS RCFFGQVVAA IQHCHSRGVV HRDIKDENIL IDLRRGCAKL 180
IDFGSGALLH DEPYTDFDGT RVYSPEWIS RHQYHALPAT VWSLGILLYD MCVGDIPFER 240
DQEILEAELH FPAHVSPDCC ALIRRLAPK PSSRPSLEEI LLDPMWQTPA EDVTPQPLQR 300
RPCPFLGLVA TSLAWPGLA PNGQKSHPM MSQG

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Seq ID NO: 171 DNA sequence
Nucleic Acid Accession #: NM_003646
Coding sequence: 89..2875

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GAGCAGCGAC TCCGAGTCGG CTTCGCCCTC GTCCAGCGGC TCCGAGCGCG ACGCCGGTCC 180
CGAGCCGGAC AAGGCCCGCG GCGGACTCAA CAAGCGGCGC TTCCCGGGGC TGCGGCTCTT 240
CGGGCACAGG AAAGCCATCA CCAAGTCGGG CCTCCAGCAC CTGGCCCCCC CCGCGCCAC 300
CCCTGGGGCC CGTGACGCG AGTCAGAGCG GCAGATCCGG AGTACAGTGG ACTGGAGCGA 360
GTCAGCGACA TATGGGGAGC ACATCTGGTT CGAGACCAAC GTGTCCGGGG ACTTCTGCTA 420
CGTTGGGGAG CAGTACTGTG TAGCCAGGAT GCTGAAGTCA GTGTCTCGAA GAAAGTGCGC 480
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GCACCACTGG GTACACAGAC GACGCCAGGA CGGCAAGTGT CGGCACTGTG GGAAGGGATT 660
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Seq ID NO: 172 Protein sequence:
Protein Accession #: NP_003637

Seq ID NO: 173 DNA sequence
Nucleic Acid Accession #: AF232772
Coding sequence: 1-1662

252

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	CTCATTCCTG	TGTCCATCTG	GGTGGCAGTT	CTCCTGGAGG	GGCTGGCCTA	CACAGCTTAT	1500
5	TGCCAGGACC	TGTTCACTGA	GACAGAGCTA	GCCTTCCTTG	TCCTCGGGGC	TATACTGTAT	1560
	GGCTGCTACT	GGGTGGCCCT	CCTCATGCTA	TATCTGGCCA	TCATCGCCCG	GCGATGTGGG	1620
	AAGAAGCCGG	AGCAGTACAG	CTTGGCTTTT	GCTGAGGTGT	GACATGGCCC	CCAAGCAGAG	1680
	CGGGTAAAGT	GCAATGGGTA	AGGGAGGGAA	GGGGAATGGA	AGAGAAAAGA	CAGGGTGGGA	1740
	GGGAGGAGGG	AGTGCCTGTG	TTTAGTCTCT	TAATGGTCCA	AAGGACAAAT	CTAAATGCA	1800
	AAGAACGGTG	ATGTAGTATG	GCCTGACAGC	TCTGTTTAGA	GGAGGCAACA	CTGATCCCCC	1860
10	AGATGCAGGG	CTGCAGGGGA	TTCTGTGTTT	TCAGACTGCC	TGCTGTCTTG	CATCTGCACA	1920
	TAGGCAGTAG	CCTCCTCCTG	GGCTCCAGAG	GGCACTCAGA	AGTTGTGCTA	AACCAAGTTA	1980
	AGTCCCATTG	AGTGGCAACT	TGTGATAGGT	ACCTGAGTGA	CGGCAACCTG	CGGAAGGAGG	2040
	TTCTCCACGC	CCATCTGAAC	ACAACCAGAG	GTGGCAGGAG	AATTTCTACT	GAGCGAGGTG	2100
15	GGCCGGTTAG	TGTATGTCAC	CCCCACCCCA	CCCATAGTA	GTCATCAATG	CAATAAGATT	2160
	GGCGCTGAGA	TACAAGGCC	AGAAGCCTGA	TCTTTGGGCA	TCAGAAAACA	GGGTCCAGGA	2220
	ATGGTGTCTT	ATGTGAGATA	CCCCACTCCA	CATCAACATT	CCAGGGATGA	GCCAAACCAG	2280
	CAGGGAGTTA	GCACTGAAC	GCTTTTAAAA	GTGCACATTA	AAAAGGAAG	TTTGGCAGGA	2340
	GGAACAAAGA	GATTGTGGTG	GTGCTAAAGG	AGGCCATAAG	CTACACAGAG	GCCTTGGGTG	2400
20	TTCCACCTGG	AAACTGAGCA	GACGCTCTAG	TGGGTTCTTA	GCTTGTCTGT	GATCTCTGCT	2460
	GGGGAGATAA	AAAGATTAAG	CCCCAACATG	TTCAGAAAAG	AAGTGAAGTC	TTGGGTATT	2520
	TAACCTGTAT	ACTCTTGAAT	TCCTCTCAAA	TTAGCTCTG	ATCTGAGGCT	AAGACACACT	2580
	CCCCACTTCA	CTTTCTTCAA	AGCCACATTT	TTTGAGGTAT	CACTGCAGTC	ACCTCTTCTA	2640
	CCCTCATCAT	CATAGGTAAG	GTTTTCAAGG	TGGCAATTGG	GGCGGAGCCC	CGGCTTCTTA	2700
25	TAGAAGCTTC	AGCAGGAGGC	AAGCGTGTTC	TCAGCACATA	TGGGAACAT	GAGGAGCCTC	2760
	TGATCAAATT	GGCTACAATC	TTGGAGCTGC	TTGGACGGAT	TCCTTGGCAG	CCGGGTAGC	2820
	ATGTGTGACT	TTCAGGCTAC	TGTTCTTGAC	AATCATCTCC	AATGGAAAGC	TTTTCACTGT	2880
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	GGCTTCTCCA	GGGAATTCTT	ACAGCCAAGT	TGTGACAGTC	ACTGCATTG	CCTGCTTCTT	3000
30	TCCAGAAACC	AAACTAGGAG	ATGAAACTGG	TTCTTACATG	CTAAGGTTCT	TGCTTCTCT	3060
	CTCATGCCTC	CTGAGGCTGT	TTTTGGCTGT	TTTCCCTCTG	CTGCTTTTGG	GGAATGAGGG	3120
	GAAGCCATTG	TCCAAGTGAC	TGCAATCCCA	GGCTGTTCTC	AGCGTTTGA	GTTTAAACC	3180
	TGGGATCCTG	TGACTAGCCTT	TGACTTAAGG	GTGCTTGCT	TGCCCTCCAA	ATGCTCTTTC	3240
	TCAAAGGGGC	CAACTAACCC	GTGCAGAAC	AGCACTAAGG	TGGACAGCAG	ACAAGAGGGC	3300
35	AAGCCTCTAA	TGTACCAAGT	GCTTCTCTACA	AAGACGCAAG	GTGTGCTCCG	AACCACAGAT	3360
	GGGCAAAACC	TGGTGCTTTC	CTTCATCTCC	CACGAACCTA	AGGGTTTTC	AAGTGTAGCT	3420
	ACAGTGTGCC	ACATCACACA	GACCTCCAGT	TTCTGGTAAG	ACTGCTGGTT	GACATCAGAC	3480
	CCAACCATTT	GAAGGCTGGA	AGGCAGCAGG	CATTTGCTAA	GGCAGCTGAT	CCAGGCAATC	3540
	GTTCTGCTGG	CCAAGAAGTT	AAACTATTTT	GAGCATTAGA	ATGGAGGAAA	TCCGGTCAGC	3600
40	CAAGTGCAGA	GTTCAGACTT	CGCTAAGGGC	TTGTTTTTCT	TCAGCATTTA	CTTGAAGATT	3660
	AATGTAGGAT	GACAGGCTCT	CCTGGCTGTC	CTACCATCAG	CTCTGCCTTG	CACTGTGGTC	3720
	GTCAACTTTC	CTCAAATCAA	AAACAGGCAG	GTACAGGTAG	TGGGCTCACA	ACGTTTGACC	3780
	TCGACTGGTT	TTTCTAAGTT	ATTTTGTACA	TTTTTCAGCA	GCAAAACCAA	ACTGGGTCTT	3840
45	GACGCTTATC	CCCGTTTCTT	GCAAGGGAAG	AGCCTTTATA	CAATTGGACG	CATTTTGGTT	3900
	TTTCTCTATT	GAGAATTCAA	ATCCTCTTTT	GTATTGTTTC	TACAATAATT	TGTAAACATA	3960
	TTTATTTTTA	CTGCTTTTTT	TTTTTTTTTT	TAATTTTCAG	GTCAAGTTTT	TTATACTGCA	4020
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Seq ID NO: 174 Protein sequence:
Protein Accession #: AAF36984

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55	LFAFLEHRRM	RRAGQALKLP	SPRRGSVALC	IAAYQEDPDY	LRKCLRSAQR	ISFPDLKVVM	120
	VVDGNRQEDA	YMLDIFHEVL	GGTEQAGFFV	WRSNFHEAGE	GETEASLQEG	MDRVRDVVRA	180
	STFSIMQKW	GGKREVMYTA	FKALGDSVDY	IQVCDSDTVL	DPACTIEMLR	VLEEDPQVGG	240
	VGGDVQILNK	YDSWISFLSS	VRWMAENVE	RACQSYFGCV	QCISGPLGMY	RNSLLQQFLE	300
	DWYHQKFLGS	KCSFGDDRHL	TNRVLSLGYR	TKYTARSKCL	TETPTKYLRW	LNQQTWRWSK	360
60	YFREWLNSL	WFHKHHLWMT	YESVVTGFFP	FFLIATVIQL	FYRGRWNL	LFLLTVQLVG	420
	LIKATYACFL	RGNAEMIFMS	LYSLLYMSSL	LPAKIFAIAI	INKSGWGTSG	RKTIVVNFIG	480
	LIPVSIWVAV	LEGLAYTAY	CQDLFSETEL	APLVSGAILY	GCYWVALLML	YLAIIRRCG	540
	KKPEQYSLAF	AEV					

Seq ID NO: 175 DNA sequence
Nucleic Acid Accession #: NM_000691
Coding sequence: 43..1404

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75	TTCCAGCAGC	TGAGAGCGCT	GCAGCGCCTG	ATCCAGGAGC	AGGAGCAGGA	GCTGGTGGGC	180
	GCGCTGGCCG	CAGACCTGCA	CAAGAATGAA	TGGAACGCCT	ACTATGAGGA	GGTGGTGATC	240
	GCTCTAGAGG	AGATCGAGTA	CATGATCCAG	AAGCTCCCTG	AGTGGGCCCG	GGATGAGCCC	300
	GTGGAGAAGA	CGCCCCAGAC	TACGACAGAC	GAGCTCTACA	TCCACTCGGA	GCCACTGGGC	360
	GTGGTCCCTG	TCACTGGCAC	CTGGAACACT	CCCTTCAACC	TCACCATCCA	GCCCATGGTG	420
	GGCGCCATCG	CTGCAGGGAA	CGCAGTGGTC	CTCAAGCCCT	CGGAGCTGAG	TGAGAACATG	480
80	GCGAGCCTGC	TGGCTACCAT	CATCCCCCAG	TACCTGGACA	AGGATCTGTA	CCCAGTAATC	540
	AATGGGGGTG	TCCCTTGAGAC	CACGGAGCTG	CTCAAGGAGA	GGTTCGACCA	TATCCTGTAC	600
	ACGGGCAGCA	CGGGGGTGGG	GAAGATCATC	ATGACGGCTG	CTGCCAAGCA	CCTGACCCCT	660
	GTACAGCTGG	AGCTGGGAGG	GAAGAGTCCC	TGCTACGTGG	ACAAGAAGCT	TGACCTGGAC	720
	GTGGCCTGCG	GACGCAATCG	CTGGGGGAAA	TTTATGAACA	GTGGCCAGAC	CTGCGTGGCC	780
85	CCAGACTACA	TCCTCTGTGA	CCCTCTGATC	CAGAAACCAA	TTGTGGAGAA	GCTCAAGAG	840
	TCACGTAAAG	AGTCTTACGG	GGAAGATGCT	AAGAAATCCC	GGGACTATGG	AAGAATCATT	900
	AGTGCCCGGC	ACTTCCAGAG	GGTGATGGGC	CTGATTGAGG	GCCAGAAAGT	GGCTTATGGG	960
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 CCCCAGCCCA GCCCACTCC TCTGCTGACC TGCTGACCTG TGCACACCCC ACTCCCAT 1560
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 CAATTTTCTA ACTCGG

Seq ID NO: 176 Protein sequence:
 Protein Accession #: NP_000682

1 11 21 31 41 51
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 YEEVVVLEE IEYMIQKLPE WADEPVEKT PQTQQDELYI HSEPLGVVLV IGTWNYPPNL 120
 TIQPMVGAIA AGNAVVLKPS EISENMAALL ATTIPOYLDK DLYPVGNGV PETTELLKER 180
 FDHILYTGST GVGKIIMTAA AKHLTPVTLE LGGKSPCYVD KNCDLDVACR RIAWGKFMNS 240
 GQTCVAPDYI LCDPSIQNQI VEKLKSLKE FYGEDAKKSR DYGRISARH FQRVMGLIEG 300
 QKVAYGGTGD AATRYIAPT I LTVDPQSPV MQEEIFGPVL PIVCVRSLEE AIQFINQREK 360
 PLALYMFSSN DKVIKKMIAE TSSGGVAAND VIVHITLHSL PFGGVNGNSGM GSYHGKKSFE 420
 TFSHRRSCLV RPLMNDGLK VRYPPSPAKM TQH

Seq ID NO: 177 DNA sequence
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 Coding sequence: 108-4703

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 AGAAAAGACT GTCTGTGAA AGAATCTATC AAAAGAAAAC ACAATTGGA CATATTTTGC 240
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	ATTTGTGGAA	AGAAGACTTG	GCTACATTTA	TTGAAGAATT	GGAGGCTGTT	GAAGCCAAGG	3660
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	TCAAAAAAGG	AAAGAAGAGA	AATCCCTGGC	CTGATTGAGA	ATCAGATAGG	AGCAGTGACG	4020
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15	AATTACAAT	GGATTGGAT	TCAGATGAAG	ATTTCTCAGA	TTTTGATGAA	AAAACGTATG	4140
	ATGAAGATTT	TGTCCCATCA	GATGCTAGTC	CACCTAAGAC	CAAACTTCC	CCAAAACTTA	4200
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	CAGTCACAAG	CAAGAAATCC	AAGGGGGAGA	GTGATGACTT	CCATATGGAC	TTTGACTCAG	4620
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25	CAGATGAAGA	TGATCTGTTT	TAAAATGTGA	GGCGATTATT	TAAAGTAAAT	ATCTTACCAA	4740
	GCCCAAGACT	GGTTTTAAAG	TTACCTGAAG	CTCTTAACTT	CCTCCCTCT	GAATTTAGTT	4800
	TGGGAAGGT	GTTTTTAGTA	CAAGACATCA	AAGTGAAGTA	AAGCCCAAGT	GTTCTTTAGC	4860
	TTTTTATAAT	ACTGTCTAAA	TAGTGACCAT	CTCATGGGCA	TTGTTTTCTT	CTCTGCTTTG	4920
	TCTGTGTTTT	GAGTCTGCTT	TCTTTTGTCT	TAAACCTG	ATTTTTAAGT	TCTTCTGAAC	4980
30	TGTAGAAATA	GCATCTGAT	CACCTCAGCG	TAAAGCAGTG	TGTTTTATTAA	CCATCCACTA	5040
	AGCTAAACT	AGAGCAGTTT	GATTTAAAG	TGTCACCTCT	CCTCCTTTTC	TACTTTCAGT	5100
	AGATATGAGA	TAGAGCATAA	TTATCTGTTT	TATCTTAGTT	TTATACATAA	TTTACCATCA	5160
	GATAGAAGCT	TATGGTTCTA	GTACAGATAC	TCTACTACAC	TCAGCCTCTT	ATGTGCCAAG	5220
	TTTTTCTTTA	AGCAATGAGA	AATTGCTCAT	GTCTTCAATC	TTCTCAAAAT	ATCAGAGGCC	5280
35	AAAGAAAAAC	ACTTTGGCTG	TGCTATAAC	TTGACACAGT	CAATAGAATG	AAGAAAAATTA	5340
	GAGTAGTTAT	GTGATTATTT	CAGCTCTTGA	CCTGTCCCTT	CTGGCTGCCT	CTGAGTCTGA	5400
	ATCTCCCAAA	GAGAGAAACC	AATTTCTAAG	AGGACTGGAT	TGCAGAAGAC	TCGGGGACAA	5460
	CATTGTATCC	AAGATCTTAA	ATGTTATATT	GATAACCATG	CTCAGCAATG	AGCTATTAGA	5520
	TTCATTTTGG	GAAATCTCCA	TAATTTCAAT	TTGTAAACTT	TGTTAAGACC	TGCTCTACAT	5580
40	GTTATATGTT	TGTGACTTGA	GTAATGTTAT	CAACGTTTTT	GTAATAATTT	ACTATGTCTT	5640
	TCTATTAGCT	AAATTTCAAC	AATTTGTATC	TTTAATAAAA	TGTTCTAAAC	ATTGTC	

Seq ID NO: 178 Protein sequence:
Protein Accession #: NP_001058.1

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	MEVSPLQPVN	ENMQVNKIKK	NEDAKKRLSV	ERIYQKKTQL	EHILLRPDXY	IGSVELVTQQ	60
	MWVYDEDVGI	NYREVTVPVG	LYKIFDEILV	NAADNKQRDP	KMSCIRVTID	PENNLISIWN	120
50	NGKGIPIVVEH	KVEKMYVPAL	IFGQLLTSSN	YDDDEKKTG	GRNGYGAALC	NIFSTKFTVE	180
	TASREYKKMF	KQTMWDMNGR	AGEMELKPFN	GEDYTCITFQ	PDLSEKFMQS	LDKDIVALMV	240
	RRAYDIAGST	KDVKVFNLGN	KLPVKGFRRS	VDMYLKDKLD	ETGNSLKVH	EQVNRHWEVC	300
	LTMSEKGFQ	ISFVNSIATS	KGRHVDYVA	DQIVTKLVDV	VKKKNKGGA	VKAHQVKNHM	360
	WTFVNALLEN	PTFDSQTKEN	MTLPKPSFGS	TCQLSEKFIK	AAIGCGIVES	ILNWVKFKAQ	420
55	VQLNKKCSAV	KHNRIKGIPI	LDNDANDAGR	NSTECTLIIT	EGDSAKTLAV	SGLGVVGRDK	480
	YGVFPLRGKI	LNVRASHKQ	IMENAEINNI	IKIVGLQYKK	NYEDEDLSKT	LRYGKIMIMT	540
	DQDQDQSHIK	GLLINFIIHN	WPSLLRHRFL	EEFITPIVKV	SKNKQEMAFY	SLPEFEWKS	600
	STPNHKKWV	KYKGLGTST	SKEAKEYFAD	MKRHRIOFKY	SGPEDDAATS	LAFSKKQIDD	660
	RKEWLTFNME	DRRQRKLLGL	PBDYLVGQTT	TYLTYNDFIN	KELILFNSND	NERSIPSMVD	720
60	GLKPGQRKVL	FTCFKRNDKR	EVKVAQLAGS	VAEMSSYHHG	EMSLMNTIIN	LAQNFVGSNN	780
	LNLLQPIQGF	GTRLIHGKDS	ASPRYIFTML	SSLARLLFPF	KDDHTLKFLY	DDNQRVPEW	840
	YIPILPMVLI	NAGAEIGTGW	SKKIPNFDVR	EIVNNIRRLM	DGEEPLPLML	SYKNFKGTIE	900
	ELAPNQYVIS	GEVAILNSTT	IEISELPVRT	WTQTYKEQVL	EPMLNGTEKT	PPLITDYREY	960
	HTDITVVKFV	KMTEBKLAEA	ERVGLHKVFK	LQTSITCNSM	VLFHDHVGCLK	KYDITVLDILR	1020
65	DFEELRLKYY	GLRKEWLLGM	LGAESAKLNN	QARFILEKID	GKIIENKFK	KELIKVLIQR	1080
	GYSDDPKVKA	KEAQKQVPDE	EENESDNEK	ETEKSDSVTD	SGPTFNYLLD	MPLWYLTKEK	1140
	KDELCLRLNE	KEQELDTLKR	KSPSDLWKED	LATFIEELEA	VEAKEKQDEQ	VGLPGKGGKA	1200
	KGKKTKMAEV	LPSPRGRQVI	PRITIEKMAE	AEKKNKKKIK	NENTEGSPQE	DGVELEGLKQ	1260
	RLEKKQKREP	GTKTKKQTTL	AFKPIKKGKK	RNPWPDSSED	RSSDESNDIV	PPRETEPRRA	1320
70	ATKTKFTMDL	DSDEDFDFD	EKTDDDFVP	SDASPPKTKT	SPKLSNKKEL	PQKSVVSDLE	1380
	ADDVKGSVPL	SSSPPATHFF	DETEITNPVP	KKNVTVKKTA	AKSQSSTSTT	GAKKRAAPKG	1440
	TKRDPALNSG	VSQKPDPAKT	KNRRKRKPST	SDDSDSNFEK	IVSKAVTSKK	SKGESDDFHM	1500
	DFDSAVAPRA	KSVRAKKPKK	YLEESDEDDL	F			

Seq ID NO: 179 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 148-7095

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	CAAAAAAACC	ATTTCCCTTG	CTCCCCCTCC	CTCTCCACTC	TGAGAAGCAG	AGGAGCCGCA	120
	CGGCGAGGGG	CCGCAGACCG	TCTGGAAATG	CGAATCCTAA	AGCGTTTCCT	CGCTTGCATT	180
	CAGCTCCTCT	GTGTTTGGCC	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240
85	CTGTGTGAAG	AGATTGGCTG	GTCCATATACA	GGAGCACTGA	ATCAAAAAAA	TTGGGGAAAG	300
	AAATATCCAA	CATGTAATAG	CCCAAAACAA	TCTCCTATCA	ATATTGATGA	AGATCTTACA	360
	CAAGTAAATG	TGAATCTTAA	GAAACTTAAA	TTTCAGGGTT	GGGATAAAAC	ATCATTGGAA	420

	AACACATTCA	TTCATAACAC	TGGGAAAACA	GTGGAAATTA	ATCTCACTAA	TGACTACCGT	480
	GTCAGCGGAG	GAGTTTCAGA	AATGGTGT	AAAGCAAGCA	AGATAACTTT	TCAGTGGGGA	540
	AAATGCAATA	TGTCATCTGA	TGGATCAGAG	CATAGTTTAG	AAGGACAAAA	ATTTCACCTT	600
	GAGATGCAAA	TCTACTGCTT	TGATGCGGAC	CGATTTTCAA	GTTTTGAGGA	AGCAGTCAAA	660
5	GGAAAAGGGA	AGTTAAGAGC	TTTATCCATT	TGTTTGAGG	TGGGACAGA	AGAAAATTG	720
	GATTTCAAAG	CGATTATTGA	TGGAGTCGAA	AGTGTTAGTC	GTTTTGGGAA	GCAGGCTGCT	780
	TTAGATCCAT	TCATACTGTT	GAACCTTCTG	CCAAACTCAA	CTGACAAAGTA	TTACATTTAC	840
	AATGGCTCAT	TGACATCTCC	TCCCTGCACA	GACACAGTTG	ACTGGATTGT	TTTTAAAGAT	900
10	ACAGTTAGCA	TCTCTGAAAG	CCAGTTGGCT	GTTTTTGTG	AAGTCTTAC	AATGCAACAA	960
	TCTGGTTATG	TCATGCTGAT	GGACTACTTA	CAAAACAATT	TTCGAGAGCA	ACAGTACAAG	1020
	TTCTCTAGAC	AGGTGTTTTT	CTCATACACT	GGAAAAGGAA	AGATTCAATG	AGCAGTTTGT	1080
	AGTTCAGAAC	CAGAAAATGT	TCAGGCTGAC	CCAGAGAAAT	ATACCAGCCT	TCTTGTATCA	1140
	TGGGAAAGAC	CTCGAGTCGT	TTATGATACC	ATGATTGAGA	AGTTTGCAGT	TTTGTACCAG	1200
15	CAGTTGGATG	GAGAGGACCA	AACCAAGCAT	GAATTTTTGA	CAGATGGCTA	TCAAGACTTG	1260
	GGTGCTATTG	TCAATAAATT	GCTACCCAAT	ATGAGTTATG	TTCTTCAGAT	AGTAGCCATA	1320
	TGCATTAATG	GCTTATATGG	AAAAATACAG	GACCAACTGA	TTGTGACAT	GCCTACTGAT	1380
	AATCCTGAAC	TTGATCTTTT	CCCTGAATTA	ATTGGAACGT	AAGAAATAAT	CAAGGAGGAG	1440
	GAAGAGGGAA	AAGACATTGA	AGAAGGCGCT	ATTGTGAATC	CTGGTAGAGA	CAGTGCTACA	1500
20	AACCAAATCA	GGAAAAGGGA	ACCCAGATTT	TCTACCACAA	CACACTACAA	TCGCATAGGG	1560
	ACGAAATACA	ATGAAAGCAA	GACTAACCGA	TCCCCAACAA	GAGGAAGTGA	ATTCTCTGGA	1620
	AAGGTGATG	TCCCAATAC	ATCTTTAAAT	TCCACTTCCC	AACCACTCAC	TAAATTAGCC	1680
	ACAGAAAAAG	ATATTTCCCT	GACTTCTCAG	ACTGTGACTG	AACCTGCCAC	TCACACTGTG	1740
	GAAGGTACTT	CAGCCTCTTT	AAATGATGGC	TCTAAAACGT	TTCTTAGATC	TCCACATATG	1800
25	AACCTGTGCG	GGACTGCAGA	ATCCTTAAAT	ACAGTTTCTA	TAAACAGATA	TGAGGAGGAG	1860
	AGTTTATTGA	CCAGTTTCAA	GCTTGATACT	GGAGCTGAAG	ATTCTTCAGG	CTCCAGTCCC	1920
	GCAACTTCTG	CTATCCCAAT	CATCTCTGAG	AACATATCCC	AAGGGTATAT	ATTTTCTCTC	1980
	GAAAACCCAG	AGACAATAAC	ATATGATGTC	CTTATACCAG	AATCTGTATG	AAATGCTTCC	2040
	GAAGATTCAA	CTTCACTCAG	TTTCAAGAA	TCACTAAAGG	ATCCTTCTAT	GGAGGGAAAT	2100
30	GTGTGGTTTC	TGAGTCTGAC	AGACATAACA	GCACAGCCCG	ATGTTGGATC	AGGCAGAGAG	2160
	AGCTTTCTCC	AGACTAATTA	CAGTGAGATA	CGTGTGATG	AATCTGAGAA	GACAACCAAG	2220
	TCCTTTTCTG	CAGGCCCACT	GATGTACAG	GGTCCCTCAG	TTACAGATCT	GGAAATGCCA	2280
	CATTATTCTA	CCTTTGCGCTA	CTTCCCAACT	GAGGTAACAC	CTCATGCTTT	TACCCCATCC	2340
	TCCAGACAAC	AGGATTTGCT	CTCCACGGTC	AACGTGGTAT	ACTCGCAGAC	AACCCAAACG	2400
35	GTATACAATG	GTGAGACACC	TCTTCAACCT	TCCTACAGTA	GTGAAGTCTT	TCTCTAGTC	2460
	ACCCCTTTGT	TGCTTGACAA	TCAGATCCTC	AACACTACCC	CTGCTGCTTC	AAGTAGTGAT	2520
	TCGGCCTTGC	ATGCTACGCC	TGATTTTCCC	AGTGTGATG	TGTCATTGTA	ATCCATCTGT	2580
	TCTTCTCATG	ATGGTGACCC	TTTGCTTCCA	TTTCTCTG	CTTCTCTCAG	TAGTGAATTG	2640
	TTTCGCCATC	TGCATACAGT	TTCTCAAATC	CTTCCACAAG	TTACTTCAGC	TACCGAGAGT	2700
40	GATAAGGTGC	CCTTGATCAT	TTCTCTGCCA	GTGGCTGGGG	GTGATTGCTT	ATTAGAGCCC	2760
	AGCCTTGCTC	AGTATTCTGA	TGTGCTGTCC	ACTACTCATG	CTGCTTCAGA	GACGCTGGAA	2820
	TTTGTGATG	AATCTGGTGT	TCTTTATAAA	ACGCTTATGT	TTTCTCAAGT	TGAACCAACC	2880
	AGCAGTGATG	CCATGATGCA	TGCACGTTCT	TCAGGGCCTG	AACCTTCTTA	TGCCTGTGCT	2940
	GATAATGAGG	GCTCCCAACA	CATCTTCACT	GTTTCTTACA	GTTCTGCAAT	ACCTGTGCAT	3000
45	GATTTCTGTG	GTGTAACCTA	TCAGGGTTCC	TTATTTAGCG	GCCCTAGCCA	TATACCAATA	3060
	CCTAAGTCTT	CGTTAATAAC	CCCAACTGCA	TCATTACTGC	AGCCTACTCA	TGCCCTCTCT	3120
	GGTGATGGGG	AATGGTCTGG	AGCCTCTTCT	GATAGTGAAT	TTCTTTTACC	TGACACAGAT	3180
	GGGCTGACAG	CCCTTAACAT	TTCTTCACTT	GTTTCTGTAG	CTGAATTTAC	ATATACAACA	3240
50	TCTGTGTTTG	TGAAGTGAATA	TAAGGGCGCT	TCTAAAAGTG	AAATAATATA	TGGAATGAG	3300
	ACTGAACTGC	AAATTCCTTC	TTTCAATGAG	ATGGTTTACC	CTTCTGAAAG	CACAGTCAATG	3360
	CCCAACATGT	ATGATAATGT	AAATAAGTTG	AATGCGTCTT	TACAAGAAAC	CTCTGTTTCC	3420
	ATTTCTAGCA	CCAAGGGCAT	GTTTCCAGGG	TCCCTTGCTC	ATACCACCAC	TAAGGTTTTT	3480
	GATCATGAGA	TTAGTCAAGT	TCCAGAAAAT	AACCTTTTCA	TTCAACCTAC	ACATACTGTC	3540
55	TCTCAAGCAT	CTGGTGACAC	TTGCTTAA	CCTGTGCTTA	GTGCAAACTC	AGAGCCAGCA	3600
	TCCTCTGACC	CTGCTTCTAG	TGAAATGTTA	TCTCCTTCAA	CTCAGCTCTT	ATTTTATGAG	3660
	ACCTCAGCTT	CTTTTAGTAT	TGAAGTATTG	CTACAACCTT	CCTTTTAGGC	TTCTGATGTT	3720
	GACACCTTGC	TTAAAACCTG	TCTTCCAGCT	GTGCCCAAGT	ATCCAATATT	GGTTGAAACC	3780
	CCCAAGTTTG	ATAAAATTAG	TTCTACAATG	TTGCATCTCA	TTGTATCAAA	TTCTGCTTCA	3840
60	AGTGAACA	TGCTGCATCT	TACATCTGTA	CCAGTTTTTG	ATGTTGTCGC	TACTTCTCAT	3900
	ATGCACTCTG	CTTCACTTCA	AGGTTTGACC	ATTTCTATG	CAAGTGAGAA	ATATGAACCA	3960
	GTTTTGTAA	AAAGTGAAAG	TTCCCAACAA	GTGGTACCTT	CTTTGTACAG	TAATGATGAG	4020
	TTGTTCCAAA	CGGCCAATT	GGAGATTAA	CAGGCCCATC	CCCCAAAAGG	AAGGCATGTA	4080
	TTTGCTACAC	CTGTTTTATC	AATTGATGAA	CCATTAAATA	CACTAATAAA	TAAGCTTATA	4140
	CATTCCGATG	AAATTTTAAC	CTCCACCAAA	AGTTCTGTTA	CTGGTAAGGT	ATTTGCTGGT	4200
65	ATTCCAACAG	TGCTTCTGTA	TACATTGTTA	TCTACTGATC	ATTCGTGTTCC	TATAGGAAAT	4260
	GGGCAATGTT	CCATTACAGC	TGTTTCTCCC	CACAGAGATG	GTTCTGTAA	CTCAACAAAG	4320
	TTGCTGTTTC	CTTCTAAGGC	AACCTTCTGAG	CTGAGTCATA	GTGCCAAATC	TGATGCCGGT	4380
	TTAGTGGGTG	GTGGTGAAGA	TGGTGACACT	GATGATGATG	GTGATGATGA	TGATGATGAC	4440
	AGAGGTAGTG	ATGGCTTATC	CATTCAATA	TGTATGTCAT	GCTCATCTTA	TAGAGAATCA	4500
70	CAGGAAAAGG	TAATGAATGA	TTCAAGACAC	CACGAAAACA	GTCTTATGGA	TCAGAATAAT	4560
	CCAATCTCAT	ACTCACTATC	TGAGAATTCT	GAAGAAGATA	ATAGAGTCAC	AAGTGATATC	4620
	TCAGACAGTC	AAACTGGTAT	GGACAGAAGT	CCTGGTAAAT	CACCATCAGC	AAATGGGCTA	4680
	TCCCAAAAGC	ACAATGATGG	AAAAGAGGAA	AATGACATTC	AGACTGGTAG	TGCTCTGCTT	4740
	CCTCTCAGCC	CTGAATCTAA	AGCATGGGCA	GTCTTGACAA	GTGATGAAGA	AAGTGGATCA	4800
75	GGGCAAGGTA	CCTCAGATAG	CCTTAATGAG	AATGAGACTT	CCACAGATT	CAGTTTGTCA	4860
	GACACTAATG	AAAAGATGTC	TGATGGGATC	CTGGCAGCAG	GTGACTCAGA	AATAACTCCT	4920
	GGATTCCCAC	AGTCCCCAAC	ATCATCTGTT	ACTAGCGAGA	ACTCAGAAGT	GTTCCACGTT	4980
	TCAGAGGCG	AGGCCAGTAA	TAGTAGCCAT	GAGTCTCGTA	TTGGTCTAGC	TGAGGGGTG	5040
	GAATCCGAGA	AGAAGGCAGT	TATACCCCTT	GTGATCGTGT	CAGCCCTGAC	TTTTATCTGT	5100
	CTAGTGGTTC	TTGTGGGTAT	TCTCATCTAC	TGGAGGAAAT	GCTTCCAGAC	TGCACACTTT	5160
80	TACTTAGAGG	ACAGTACATC	CCCTAGAGTT	ATATCCACAC	CTCCAACACC	TATCTTTCCA	5220
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	CATGCAAGTA	GTGGGTTTAC	TGAAGAATT	GAGACACTGA	AAGAGTTT	CCAGGAAGTG	5340
	CAGAGCTGTA	CTGTTGACTT	AGGTATTACA	GCAGACAGCT	CCAACCACCC	AGACAACAAG	5400
	CACAAGAAATC	GATACATAAA	TATCGTTGCC	TATGATCATA	GCAGGGTTAA	GCTAGCACAG	5460
85	CTTGCTGAAA	AGGATGGACA	ACTGACTGAT	TATATCAATG	CCAATTATGT	TGATGGCTAC	5520
	AACAGACCAA	AAGCTTATAT	TGCTGCCCAA	GGCCCACTGA	AATCCACAGC	TGAAGATTTC	5580
	TGGAGAATGA	TATGGGAACA	TAATGTGGAA	GTTATTGTCA	TGATAACAAA	CCTCGTGGAG	5640

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	CTAAGAAACA	CAAAAATAAA	AAAGGCTCC	CAGAAAGGAA	GACCCAGTGG	ACGTGTGGTC	5820
5	ACACAGTATC	ACTACACGCA	GTGGCTGAC	ATGGGAGTAC	CAGAGTACTC	CCTGCCAGTG	5880
	CTGACCTTTG	TGAGAAAAGGC	AGCCTATGCC	AAGCGCCATG	CAGTGGGGCC	TGTTGTCTGC	5940
	CACTGCAGTG	CTGGAGTTGG	AAGAACAGGC	ACATATATTTG	TGCTAGACAG	TATGTTGCAG	6000
	CAGATTCAAC	ACGAAGGAAC	TGTCAACATA	TTTGGCTTCT	TAAAACACAT	CCGTTCACAA	6060
	AGAAATTATT	TGGTACAAC	TGAGGAGCAA	TATGTCTTCA	TTCATGATAC	ACTGGTTGAG	6120
10	GCCATACCTA	GTAAGAAGAC	TGAGGTGCTG	GACAGTCATA	TTCATGCCTA	TGTTAATGCA	6180
	CTCCTCATTC	CTGGACCCAGC	AGGCAAAACA	AAGCTAGAGA	AACAATTCCA	GCTCCTGAGC	6240
	CAGTCAAATA	TACAGCAGAG	TGACTATTCT	GCAGCCCTAA	AGCAATGCNA	CAGGGAAG	6300
	AATCGAATCT	CTTCTATCAT	CCCTGTGGAA	AGATCAAGGG	TTGGCATTTC	ATCCCTGAGT	6360
	GGAGAAGGCA	CAGACTACAT	CAATGCCTCC	TATATCATGG	GCTATTACCA	GAGCAATGAA	6420
15	TTCATCATT	CCCAGCACCC	TCTCCTTCAT	ACCATCAAGG	ATTTCTGGAG	GATGATATGG	6480
	GACCATATG	CCCACTGGT	GGTTATGATT	CCTGATGGCC	AAAACATGGC	AGAAGATGAA	6540
	TTTGTTTACT	GGCCAAATAA	AGATGAGCCT	ATAAATTGTG	AGAGCTTTAA	GGTCACTCTT	6600
	ATGGCTGAAG	AACACAAATG	TCTATCTAAT	GAGGAAAAC	TTATAATTCA	GGACTTTATC	6660
	TTAGAAGCTA	CACAGGATGA	TTATGTACTT	GAAGTGAGGC	ACTTTCAGTG	TCCTAAATGG	6720
20	CCAAATCCAG	ATAGCCCAT	TAGTAAACT	TTTGAACCTA	TAAGTGTTAT	AAAAGAAGAA	6780
	GCTGCCAATA	GGGATGGGCC	TATGATTGTT	CATGATGAGC	ATGGAGGAGT	GACGGCAGGA	6840
	ACTTCTCTGT	CTCTGACAA	CCTTATGCAC	CAACTAGAAA	AAGAAAATTC	CGTGGATGTT	6900
	TACCAGGTAG	CCAAGATGAT	CAATCTGATG	AGGCCAGGAG	TCTTTGCTGA	CATTGAGCAG	6960
	TATCAGTTTC	TCTACAAAGT	GATCCTCAGC	CTTGTGAGCA	CAAGGCAGGA	AGAGAATCCA	7020
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	GACAGTAAT	TTCATGACAT	AGGATTCTGC	CGCCAAATTT	ATATCATTA	CAATGTGTGC	7260
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30	TATTTCTAAG	AATGGAATTG	TGGTATTTT	TCTGTATTG	ATTTTAAACAG	AAAATTTCAA	7380
	TTTATAGAGG	TAGGAATTC	CAAACTACAG	AAAATGTTTG	TTTTTAGTGT	CAAAATTTTA	7440
	GCTGTATTG	TAGCAATTAT	CAGGTTTGCT	AGAAATATA	CTTTTAATAC	AGTAGCCTGT	7500
	AAATAAAACA	CTCTTCCATA	TGATATTCAA	CATTTTACAA	CTGCAGTATT	CACCTAAAGT	7560
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	GTTTAGTTTA	ATGACGTAGT	TCATTAGCTG	GTCTTACTCT	ACCAGTTTTC	TGACATTGTA	7740
	TTGTGTTACC	TAAGTCATTA	ACTTTGTTTC	AGCATGTAAT	TTTAACTTTT	GTGGAAAAATA	7800
	GAAATACCTT	CATTTTGAAA	GAAAGTTTTA	TGAGAATAAC	ACCTTACCAA	ACATTGTTCA	7860
40	AATGGTTTTT	ATCCAAGGAA	TTGCAAAAT	AAATATAAAT	ATTGCCATTA	AAAAAAAAAA	7920
	AAAAAAAAAA	AAAAAAAAAA	AAAA				

Seq ID NO: 180 Protein sequence:
Protein Accession #: Eos sequence

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	QSPINIDEDL	TQVNVNLKKL	KFQGWDKTSL	ENTFIHNTGK	TVEINLTNDY	RVSGGVSEMV	120
	FKASKITPFH	GKCNMSSDGS	EHSLEGQKFP	LEMQUIYCFDA	DRFSSFEEAV	KGKGLRLALS	180
50	ILFEVGTEN	LDFKAIIDGV	ESVSRFGKQA	ALDPFILLNL	LPNSTDKYYI	YNGSLTSPPC	240
	TDTVDWIVFK	DTVSISESGL	AVFCBVLTMQ	QSGYVMLMDY	LQNNFREQQY	KFSRQVFSSY	300
	TGKEEIEHAV	CSSEPENVQA	DPENYTSLLV	TWERPRVVVD	TMIEKFAVLY	QQLDGEDQTK	360
	HEFLTDGYQD	LGAILNNLFP	NMSYVLQIVA	ICTNGLYGYK	SDQLIVDMPT	DNPELDLFFE	420
	LIGTEEIIKE	EEEGKDIEEG	AIVNPGRDSA	TNQIRKKEPQ	ISTTTHYNRI	GTKYNEAKTN	480
55	RSPTRGSEFS	GKGDVNTSL	NSTSPQVTKL	ATEKDISLTS	QTVTELPFHT	VEGTSASLND	540
	GSKTVLRSFH	MNLSGTABSL	NTVSI TEYEE	ESLLTSFKLD	TGAEDSSGSS	PATSAIPFIS	600
	ENISQGYIFS	SENPEITITYD	VLIPESARNA	SEDSTSSGSE	ESLKDPSMEG	NVWFPSSTDI	660
	TAQPDVGSGR	ESFLQNTYTE	IRVDESEKTT	KSFSAQPVMS	QQPSVTDLEM	PHYSTFAYFP	720
60	TEVTPHAFTP	SSRQODLVST	VNVVYSQTTQ	PVYNGETPLQ	PSYSSEVFPL	VTPLLLDNQI	780
	LMTTPAASSS	DSALHATPVF	PSVDVSFESI	LSSYDGAPLL	PFSSASFSE	LFRHLHTVSQ	840
	ILPQVTSATE	SDKVPLHASL	PVAGGDLLE	PSLAQYSDVL	STTHAASETL	EFGSESGVLY	900
	KTLMFSQVEP	PSSDAMMHAR	SSGPEPSYAL	SDNEGSQHIF	TVSYSSAIPV	HDSVGVITYQG	960
	SLFSGPSHIP	IPKSLITPT	ASLLQPTHAL	SGDGEWSGAS	SDSEFLLEPT	DGLTALNISS	1020
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	KPVLSPANSE	ASSDPASSE	LSPSTQLLFY	ETSASFSTEV	LLQPSFQASD	VDTLTKTVLP	1200
	AVPSDPILVE	TPKVDKISST	MLHLIVSNSA	SSENMLHSTS	VPVFDVSPTS	HMHASLQGL	1260
70	TISYASEKEYE	PVLLKSESSH	QVPSLSYND	ELFQTANLEI	NQAHPPKGRH	VFATPVLSID	1320
	EPLNTLINKL	IHSDEILTST	KSSVTGKVFA	GIPTVASDTF	VSTDHSPVIG	NGHVAITAVS	1380
	PHRDGSVTST	KLLFPKATS	ELSHSAKSDA	GLVGGGEDGD	TDDDGDDDD	DRGSDGLSIH	1440
	KCMSCSSYRE	SQEKVMNDSD	THENSLMDQN	NPISYSLSEN	SEEDNRVTSV	SSDSQTGMDR	1500
	SPGKSPSANG	LSQKHNDGKE	ENDIQTSAL	LPLSPESKAW	AVLTSDDESG	SGQGTSDSLN	1560
75	ENETSTDFSF	ADTNEKDADG	ILAAAGDSEIT	PGFPQSPTSS	VTSENSEVFH	VSEAEASNS	1620
	HESRIGLAEG	LESEKKAIVP	LVIVSALTPI	CLVVLVGILI	YWRKCFQTAH	FYLEDSTSPR	1680
	VISTPPTPIF	PISDDVGAIP	IKHFPKHVAD	LHASSGFTEE	FETLKEFYQE	VQSCTVDLGI	1740
	TADSSNHPDN	KHKNYRINIV	AYDHSRVKLA	QLAEKDGKLT	DYINANYVDG	YNRPKAYIAA	1800
	QGFLKSTAE	FWRMIWEHNV	EVIVMITNLV	EKGRKCDQY	WPADGSEBYG	NFLVTQKSVQ	1860
80	VLAYITVRNF	TLRNTKIKKG	SQKGRPSGRV	VTQYHYTQWP	DMGVPEYSLP	VLTFVRKAA	1920
	AKRHAVGPVV	VHCSAGVGRT	GTIYVLDMSL	QQIQHEGTVN	IFGFLKHIRS	QRNYLVQTEE	1980
	QYVFIHDTLV	EAILSKETEV	LDSHIHAYVN	ALLIPGPAK	TKLEKQFQLL	SQSNIQQSDY	2040
	SAALKQCNR	KNRTSSIIIP	ERSRVGISSL	SGEGTDYINA	SYIMGYYSQN	EFITQHPPLL	2100
	HTIKDFWRMI	WDHNAQLVVM	IPDGMMAED	EFVYWPKNDE	PINCESFKVT	LMAEHHKCL	2160
	NBEKLIQDF	ILEATQDDVY	LEVRHFQCPK	WPNPDSPIK	NFELISVIKE	BAANRDGPM	2220
85	VHDEHGGVTA	GTFCALTITM	HQLEKENSVD	VYQVAKMINL	MRPGVFADIE	QYQFLYKVL	2280
	SLVSTRQEEN	PSTSLDSNGA	ALPDGNIAES	LESIV			

Seq ID NO: 181 DNA sequence
Nucleic Acid Accession #: Eos sequence

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	CGGCGAGGGG	CGCGAGACCG	TCTGGAAATG	CGAATCCTAA	AGCGTTTCCT	CGCTTGCAAT	180
	CAGCTCCTCT	GTGTTTGCCG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240
10	CTTGTTGAAG	AGATTGGCTG	GTCCCTATACA	GGAGCACTGA	ATCAAAAAAA	TTGGGGAAAG	300
	AAATATCCAA	CATGTAATAG	CCCAAAACAA	TCTCCTATCA	ATATTGATGA	AGATCTTACA	360
	CAAGTAAATG	TGAATCTTAA	GAAACTTAAA	TTTCAGGGTT	GGGATAAAAC	ATCATTTGAA	420
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	GATTTCAAAG	CGATTATTGA	TGGAGTCGAA	AGTGTTAGTC	GTTTTGGGAA	GCAGGCTGCT	780
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20	AATGGCTCAT	TGACATCTCC	TCCCTGCACA	GACACAGTTG	ACTGGATTGT	TTTTAAAGAT	900
	ACAGTTAGCA	TCTCTGAAAG	CCAGTTGGCT	GTTTTTTGTG	AAGTTCCTAC	AATGCAACAA	960
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	AGTTTCAGAA	CAGTAAATGT	TCAGGCTGAC	CCAGAGAAAT	ATACCAGCCT	TCTTGTTACA	1140
25	TGGGAAAGAC	CTCGAGTCGT	TTATGATACC	ATGATTGAGA	AGTTTGCAGT	TTTGTACCAG	1200
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	GGTGTCTATC	TCAATTAATT	GCTACCCAAT	ATGAGTTATG	TTCTTCAGAT	AGTAGCCATA	1320
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	TTGGAAATCC	AGAAGAAGCG	AGTTATACCC	CTTGTGATCG	TGTGAGCCCT	GACTTTTATC	2520
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	TTTTTACTTAG	AGGACAGTAC	ATCCCTTAGA	GTTATATCCA	CACCTCCAAC	ACCTATCTTT	2640
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	TGCCTTTTTG	CAAGACTTGT	AATTTACTTA	TTATGTTTGA	ACTAAAATGA	TTGAATTTTA	4740
85	CAGTATTTCT	AAGAAATGGA	TTGTGGTATT	TTTTTCTGTA	TTGATTTTAA	CAGAAAATTT	4800
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	TTAGCTGTAT	TTGTAGCAAT	TATCAGGTTT	GCTAGAAATA	TAACTTTTAA	TACAGTAGCC	4920
	TGTAAATAAA	ACACTCTTCC	ATATGATATT	CAACATTTTA	CAACTGCAGT	ATTCACCTAA	4980

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Seq ID NO: 182 Protein sequence:
 Protein Accession #: Eos sequence

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Seq ID NO: 183 DNA sequence
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	AAACTACAGA	AAATGTTTTG	TTTTAGTGTC	AAATTTTTAG	CTGTATTTGT	AGCAATTATC	4860
	AGGTTTGCTA	GAAATATAAC	TTTTAATACA	GTAGCCTGTA	AATAAAACAC	TCTTCCATAT	4920
	GATATTCAAC	ATTTTACAAC	TGCAGTATTC	ACCTAAAGTA	GAAATAATCT	GTTACTTTAT	4980
	GTAATACTG	CCCTAGTGTC	TCCATGGACC	AAATTTATAT	TTATAATTGT	AGATTTTTAT	5040
45	ATTTTACTAC	TGAGTCAAGT	TTTCTAGTTC	TGTGTAATTG	TTAGTTTAA	TGACGTAGTT	5100
	CATTAGCTGG	TCTTACTCTA	CCAGTTTTCT	GACATTGTAT	TGTGTTACCT	AAGTCATTAA	5160
	CTTTGTTTCA	GCAATGTAAT	TTAATTTTTG	TGGAAAAATG	AAATACCTTC	ATTTTGAAAG	5220
	AAGTTTTTAT	GAGATAACAA	CCTTACCAAA	CATTGTTTCA	ATGGTTTTTA	TCCAAGGAAT	5280
	TGCAAAAATA	AATATAAATA	TTGCCATTAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	5340
50	AAA						

Seq ID NO: 184 Protein sequence:
Protein Accession #: EOS sequence

	1	11	21	31	41	51	
55	MRILKRLFLAC	IQLLCVCRLD	WANGYYRQQR	KLVEEIGWSY	TGALNQKNWG	KKYPTCNSEPK	60
	QSPINIDEDL	TQVNVNLKKL	KFQGWKTSLS	ENTFIHNTGK	TVEINLTNDY	RVSGGVSEMV	120
	FKASKITPHW	GKCNMSSDGS	EHSLEGQKFP	LEMQUIYCFDA	DRFSSFEEAV	KGKGLRLALS	180
60	ILFEVGTEN	LDFKALIDGV	ESVSRFGKQA	ALDPPILLNL	LPNSTDKYYI	YNGSLTSPPC	240
	TDVTDWIVFK	DVTSISESQL	AVFCEVLTMQ	QSGYVMLMDY	LQNNFREQQY	KFSRQVFSY	300
	TGKEEIHFAV	CSSEPENVQA	DPENYTSLLV	TWERPRVVVD	TMIEKFAVLY	QQLDGEDQTK	360
	HEFLTDGYQD	LGAILNNLLP	NMSYVLQIVA	ICTNGLYKGY	SDQLIVDMPT	DNPELDLFE	420
	LIGTEEIIKE	EEEGKDIEEG	AIVNPNRDSA	TNQIRKKEPQ	ISTTTHYNRI	GTKYNEAKTN	480
65	RSPTRGSEFS	GKGDVNTSL	NSTSQPVTKL	ATEKDISLTS	QTVTELPPHT	VEGTSASLND	540
	GSKTVLRSFH	MNLSGTAEBS	NTVSI TEYEE	ESLLTSFKLD	TGAEDSSGSS	PATSAIPFIS	600
	ENISQGYIFS	SENPEITITYD	VLIPESARNA	SEDSTSSGSE	ESLKDPSMEG	NWFPSSSTDI	660
	TAQPPDVGSR	ESFLQNTYTE	IRVDESEKTT	KFSFAGPVMS	QGPSVTDLEM	PHYSTFAYFP	720
	TEVTTHAFTP	SSRQQLVST	VNVVYSQTQ	PVYNEASNS	HESRIGLAEG	LESEKKAVIP	780
70	LVIVSALTFI	CLVVLVGILI	YWRKCFQTAH	FYLEDSTSPR	VISTPPTPIF	PISDDVGAIP	840
	IKHFPKHVAD	LHASSGFTEE	FEEVQSCSTD	LGITADSSNH	PDNKHKNRYI	NIVAYDHSRV	900
	KLAQLAEKDG	KLTDYINANY	VDGYNRPKAY	IAAQGPLKST	AEDFWRMIWE	HNVEIVMIT	960
	NLVEKGRRKC	DQYWPADGSE	EYGNFLVTQK	SVQVLAYYTV	RNFTLRNTKI	KKGSQKGRPS	1020
	GRVVVTQYHYT	QWPDMDGVEY	SLPVLTFVRK	AAAYAKRHAVG	PVVVHCSAGV	GRTGTIYIVLD	1080
75	SMLQQIQHEG	TVNIFGFLKH	IRSQRNYLVQ	TEEQYVFIHD	TLVEAILSKE	TEVLDSHIHA	1140
	YVNALLIPGP	AGKTKLEKQF	QLLSQSNIIQ	SDYSALKQKC	NREKNRTSSI	IPVERSRVGI	1200
	SSLSGEGBTG	INASYIMGYI	QSNFIITQH	PLLHTIKDFW	RMIWDHNAQL	VVMIPDGQNM	1260
	ABDEFVYWN	DEBPINCESF	KVTLMABEHL	CLSNEEKLII	QDFILEATQD	DYVLEVRHFQ	1320
	CPKWPNDPSP	ISKTFELISV	IKEEAANRDG	PMIVHDEHGG	VTAGTFCAIT	TLMHQLEKEN	1380
80	SVDVYQVAKM	INLMRPGVFA	DIEQYQFLYK	VILSLVSTRQ	EENPSTSLDS	NGAALPDGNI	1440
	AESLESLSV						

Seq ID NO: 185 DNA sequence
Nucleic Acid Accession #: EOS sequence
Coding sequence: 501-4514

85	1	11	21	31	41	51
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	CAAAAAAAAC	ATTTCTCTCG	CTCCCCCTCC	CTCTCCACTC	TGAGAAGCAG	AGGAGCCGCA	120
5	CGGCGAGGGG	CCGCAGACCG	TCTGGAAATG	CGAATCCTAA	AGCGTTTCCT	CGCTTGCATT	180
	CAGCTCCTCT	GTGTTTGCGT	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240
	CTTGTTGAAG	AGATTGGCTG	GTCTTATACA	GGAGCACTGA	ATCAAAAAAT	TGGGGAAAGA	300
	AATATCCAAC	ATGTAATAGC	CCAAAACAAT	CTCCTATCAA	TATTGATGAA	GATCTTACAC	360
	AAGTAAATGT	GAATCTTAAG	AAACTTAAAT	TTCAAGGTTG	GGATAAAACA	TCATTGGAAA	420
10	ACACATTTCAT	TCATAACACT	GGGAAAACAG	TGGAAATTAA	TCTCACTAAT	GACTACCGTG	480
	TCAGCGGAGG	AGTTTCAGAA	ATGGTGTTTA	AAGCAAGCAA	GATAACTTTT	CACTGGGGAA	540
	AATGCAATAT	GTCACTCGAT	GGATCAGAGC	ATAGTTTAGA	AGGACAAAAA	TTTCCACTTG	600
	AGATGCAAAAT	CTACTGCTTT	GATGCGGACC	GATTTTCAAG	TTTTGAGGAA	GCAGTCAAAG	660
	GAAAAGGGAA	GTTAAGAGCT	TTATCCATTT	TGTTTGAGGT	TGGGACAGAA	GAAAAATTGG	720
15	ATTTCAAAGC	GATTATTGAT	GGAGTCGAAA	GTGTTAGTCG	TTTTGGGAAG	CAGGCTGCTT	780
	TAGATCCATT	CATACTGTTG	AACCTTCTGC	CAAACCTCAAC	TGACAAGTAT	TACATTTACA	840
	ATGGCTCATT	GACATCTCCT	CCCTGCACAG	ACACAGTTGA	CTGGATTGTT	TTTAAAGATA	900
	CAGTTAGCAT	CTCTGAAAGC	CAGTTGGCTG	TTTTTTGTGA	AGTTCTTACA	ATGCAACAAT	960
	CTGGTTATGT	CATGCTGATG	GACTACTTAC	AAAACAATTT	TCGAGAGCAA	CAGTACAAGT	1020
20	TCTCTAGACA	GGTGTCTTCC	TCATACACTG	GAAAGGAAGA	GATTTCATGAA	GCAGTTTGTA	1080
	GTTTCAGAAC	AGAAAAATGT	CAGGCTGACC	CAGAGAATTA	TACCAGCCTT	CTTGTTTACAT	1140
	GGGAAAGACC	TCGAGTCGTT	TATGATACCA	TGATTGAGAA	GTTTGCAAGT	TTGTACCAGC	1200
	AGTTGGATGG	AGAGGACCAA	ATCAAGCATG	AATTTTTGAC	AGATGGCTAT	CAAGACTTGG	1260
	GTGCTATTCT	CAATAATTGT	CTACCCAATA	TGAGTTATGT	TCTTCAGATA	GTAGCCATAT	1320
25	GCACCTAATGG	CTTATATGGA	AAATACAGCG	ACCAACTGAT	TGTCGACATG	CCTACTGATA	1380
	ATCCTGAAC	TGATCTTTTC	CCTGAATTAA	TTGGAACCTG	AGAAATAATC	AAGGAGGAGG	1440
	AAGAGGGAAA	AGACATTGAA	GAAGGCGCTA	TTGTGAATCC	TGGTAGAGAC	AGTGCTACAA	1500
	ACCAATCAG	GAAAAAGGAA	CCCCAGATTT	CTACCAACAAC	ACACTACAAT	CGCATAGGGA	1560
	CGAAATACAA	TGAAGCCAAG	ACTAACCGAT	CCCCAACAAAG	AGGAAGTGAA	TTCTCTGGAA	1620
30	AGGGTGATGT	TCCCAATACA	TCTTTAAATT	CCACTTCCCA	ACCAGTCACT	AAATTAGCCA	1680
	CAGAAAAAGA	TATTTCTCTG	ACTTCTCAGA	CTGTGACTGA	ACTGCCACCT	CACACTGTGG	1740
	AAGGTACTTC	AGCCTCTTTA	AATGATGGCT	CTAAAACCTGT	TCTTAGATCT	CCACATATGA	1800
	ACTTGTCCGG	GACTGCAGAA	TCCTTAAATA	CAGTTTCTAT	AACAGAAATAT	GAGGAGGAGA	1860
	GTTTATTGAC	CAGTTTCAAG	CTTGATACTG	GAGCTGAAGA	TTCTTCAGGC	TCCAGTCCCG	1920
35	CAACTTCTGC	TATCCCATTC	ATCTCTGAGA	ACATATCCCA	AGGGTATATA	TTTTCTCCG	1980
	AAAACCCAGA	GACATAAACA	TATGATGTCC	TTATACCAGA	ATCTGCTAGA	AATGCTTCCG	2040
	AAGATTCAAC	TTCATCAGGT	TCAGAAGAAT	CACTAAAGGA	TCCTTCTATG	GAGGGAAATG	2100
	TGTGGTTTCC	TAGCTCTACA	GACATACACG	CACAGCCCGA	TGTTGGATCA	GGCAGAGAGA	2160
	GCTTTCTCCA	GACTAATTAC	ACTGAGATAC	GTGTTGATGA	ATCTGAGAAG	ACAACCAAGT	2220
40	CCTTTTCTGC	AGGCCCAAGT	ATGTCACAGG	GTCCCTCAGT	TACAGATCTG	GAAATGCCAC	2280
	ATTATCTTAC	CTTTGCCCTAC	TTCCCAACCT	AGGTAACACC	TCATGCTTTT	ACCCCATCCT	2340
	CCAGACAACA	GGATTGGTTC	TCCACGGTCA	ACGTGGGTATA	CTCGCAGACA	ACCCAACCCG	2400
	TATACAATGA	GGCCAGTAAT	AGTAGCCATG	AGTCTCGTAT	TGGTCTAGCT	GAGGGGTTGG	2460
45	AATCCGAGAA	GAAGGCAGTT	ATACCCCTTG	TGATCGTGTC	AGCCCTGACT	TTTATCTGTC	2520
	TAGTGGTTCT	TGTGGGTATT	CTCATCTACT	GGAGGAAATG	CTTCCAGACT	GCACACTTTT	2580
	ACTTAGAGGA	CAGTACATCC	CCTAGAGTTA	TATCCACACC	TCCAACACCT	ATCTTTCCAA	2640
	TTTCAGATGA	TGTCGGAGCA	ATTCCAATAA	AGCACITTTCC	AAAGCATGTT	GCAGATTTAC	2700
	ATGCAAGTAG	TGGGTTTACT	GAAGAATTTG	AGACACTGAA	AGAGTTTTAC	CAGGAAGTGC	2760
	AGAGCTGTAC	TGTTGACTTA	GGTATTACAG	CAGACAGCTC	CAACCACCCA	GACAACAAGC	2820
50	ACAAGAATCG	ATACATAAAT	ATCGTTGCCT	ATGATCATAG	CAGGGTTAAG	CTAGCACAGC	2880
	TTGCTGAAAA	GGATGGCAAA	CTGACTGATT	ATATCAATGC	CAATTATGTT	GATGGCTACA	2940
	ACAGACCAAA	AGCTTATATT	GCTGCCCAAG	GCCCCACTGAA	ATCCACAGCT	GAAGATTTCT	3000
	GGAGAATGAT	ATGGGAACAT	AATGTGGAAG	TTATTGTCTAT	GATAACAAAC	CTCGTGGAGA	3060
	AAGGAAGGAG	AAAATGTGAT	CAGTACTGGC	CTGCCGATGG	GAGTGAGGAG	TACGGGAACT	3120
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	AGAAACACAC	AAAAATAAAA	AAGGGCTCCC	AGAAAGGAAG	ACCCAGTGGA	CGTGTGGTCA	3240
	CACAGTATCA	CTACACGAGT	TGGCCTGACA	TGGGAGTACC	AGAGTACTCC	CTGCGAGTGC	3300
	TGACCTTTGT	GAGAAAGGCA	GCCTATGCCA	AGCGCCATGC	AGTGGGGCCT	GTTGTGCTCC	3360
	ACTGCAGTGC	TGGAGTTGGA	AGAACAGGCA	CATATATTGT	GCTAGACAGT	ATGTTGCAGC	3420
60	AGATTCAACA	CGAAGGAAC	GTCAACATAT	TTGGCTTCTT	AAAACACATC	CGTTCACAAA	3480
	GAAATATTAT	GGTACAAACT	GAGGAGCAAT	ATGCTTCTAT	TCATGATACA	CTGGTTGAGG	3540
	CCATACCTTAG	TAAAGAAACT	GAGGTGCTGG	ACAGTCATAT	TCATGCCTAT	GTTAATGCAC	3600
	TCCTCATTTCC	TGGACACAGC	GGCAAAACAA	AGCTAGAGAA	ACAATTCCAG	CTCCTGAGCC	3660
65	AGTCAAAATAT	ACAGCAGAGT	GACTATTCTG	CAGCCCTAAA	GCAATGCAAC	AGGGAAAAGA	3720
	ATCGAACTTC	TTCTATCATC	CCTGTGGAAA	GATCAAGGGT	TGGCATTTCA	TCCCTGAGTG	3780
	GAGAAGGCAC	AGACTACATC	AATGCCTCCT	ATATCATGGG	CTATTACCAG	AGCAATGAAT	3840
	TCATCATTTAC	CCAGCACCCT	CTCCTTCATA	CCATCAAGGA	TTTCTGGAGG	ATGATATGGG	3900
	ACCATAATGC	CCAACCTGGT	GTTATGATTC	CTGATGGCCA	AAACATGGCA	GAAGATGAAT	3960
70	TTGTTTACTG	GCCAAATAAA	GATGAGCCTA	TAAATTGTGA	GAGCTTTAAG	GTCACTCTTA	4020
	TGGCTGAAGA	ACACAAATGT	CTATCTAATG	AGGAAAAACT	TATAATTTCAG	GACTTTTATCT	4080
	TAGAAGCTAC	ACAGGATGAT	TATGTACTTG	AAGTGAGGCA	CTTTCAGTGT	CCTAAATGGC	4140
	CAATCCAGTA	TAGCCCCATT	AGTAAAAACT	TTGAACCTTAT	AAGTGTATTA	AAAGAAGAAG	4200
	CTGCCAATAG	GGATGGGCCT	ATGATTGTTT	ATGATGAGCA	TGGAGGAGTG	ACGGCAGGAA	4260
75	CTTTCTGTGC	TCTGACAACC	CTTATGCACC	AACTAGAAAA	AGAAAATTCC	GTGGATGTTT	4320
	ACCAGGTAGC	CAAGATGATC	AACTCTGATG	GGCCAGGAGT	CTTTGCTGAC	ATTGAGCAGT	4380
	ATCAGTTTCT	CTACAAAGTG	ATCCTCAGCC	TTGTGAGCAC	AAGGCAGGAA	GAGAATCCAT	4440
	CCACCTCTCT	GGACAGTAAT	GGTGCAAGAT	TGCCTGATGG	AAATATAGCT	GAGAGCTTAG	4500
	AGTCTTTAGT	TTAACACAGA	AAGGGGTGGG	GGGACTCACA	TCTGAGCATT	GTTTCTCTCT	4560
80	TCCTAAAAAT	AGGCAGGAAA	ATCAGTCTAG	TTCTGTTATC	TGTTGATTTT	CCATCACCTG	4620
	ACAGTAACTT	TCTAGACATA	GGATTCTGCC	GCCAAATTTA	TATCATTAAC	AATGTGTGCC	4680
	TTTTTGCAAG	ACTTGTAATT	TACTTATTAT	GTTTGAACCTA	AAATGATTGA	ATTTTACAGT	4740
	ATTTCTAAGA	ATGGAATGTG	GGTATTTTTT	TCTGTATTGA	TTTTTAACAGA	AAATTTCAAT	4800
	TTATAGAGGT	TAGGAATTCC	AAACTACAGA	AAATGTTTGT	TTTTAGTGTC	AAATTTTAG	4860
	CTGTATTGTG	AGCAATTATC	AGGTTTGCTA	GAAATATAAC	TTTTAATACA	GTAGCCTGTA	4920
85	AATAAACAC	TCTTCCATAT	GATATTCAAC	ATTTTACAAC	TGCAGTATTC	ACCTAAAGTA	4980
	GAAATAATCT	GTTACTTTAT	GTAAATACTG	CCCTAGTGTC	TCCATGGACC	AAATTTATAT	5040
	TTATAATTGT	AGATTTTAT	ATTTTACTAC	TGAGTCAAGT	TTTCTAGTTC	TGTGTAATTG	5100
	TTTAGTTTAA	TGACGTAGTT	CATTAGCTGG	TCTTACTCTA	CCAGTTTTCT	GACATTGTAT	5160

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Seq ID NO: 186 Protein sequence:
 Protein Accession #: EOS sequence

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PCTDTVDWIV	FKDTVSISES	QLAVFCEVLT	MQQSGYVMLM	DYLNQNNFREQ	QYKFSRQVFS	180
SYTGKEEIHG	AVCSSEPENV	QADPENYTSI	LVTWERPRVV	YDTMIEKFAV	LYQQLDGEDQ	240
TKHEFLTDTG	QDLGAILNNL	LPNMSYVLQI	VAICTNGLYG	KYSDQLIVDM	PTDNPDLDF	300
PELIGTEBII	KEBEEGKDIE	EGAIVNPGRD	SATNQIRKKE	POISTTTTHYN	RIGTKYNEAK	360
TNRSPTRGSE	PSGKGDPVNT	SLNSTSQPVT	KLATEKDIDL	TSQVTTELPP	HTVEGTSASL	420
NDGSKTVLRS	PHMNLSGTAE	SLNTVSIIEY	EEESLLTSFK	LDTGAEDSSG	SSPATSAIPP	480
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DITAPDVGVS	GRESFLQTNV	TEIRVDESEK	TTKSFSAGPV	MSQGSFVTDL	EMPHYSTFAY	600
FPTTEVTPHAF	TPSSRQQDLV	STVNIVYSQT	TQPVYNEASN	SSHESRIGLA	EGLESEKKAV	660
IPLVIVSALT	FICLVVLVGI	LIYWRKCFQT	AHFYLEDSTS	PRVISTPPTP	IFPISDDVGA	720
IPIKHPKPHV	ADLHASSGFT	EEFTLKEFY	QEVQSCVVDL	GITADSSNHP	DNKHKNRVIN	780
IVAYDHSRVK	LAQLAEKDKG	LTDYINANYV	DGYNRPKAYI	AAQGPLKSTA	EDFWRMIWEH	840
NVEVIVMITN	LVEKGRRCDD	QYWPADGSEE	YGNFLVTQKS	VQVLAAYTVR	NFTLRNTKIK	900
KGSQKGRPSG	RVVYQYHTQ	WPDMDGVPEYS	LPVLTFFVRKA	AYAKRHAVGP	VVVHCSAGVG	960
RTGTIYVLDS	MLQIQHBEGT	VNIFGFLKHI	RSQRNYLVQT	EEQYVFIHDT	LVEAILSKET	1020
EVLDSDIHAY	VNALLIPGPA	GKTKLEKQFQ	LLSQSNIIQS	DYSAALKQCN	REKNRTSSII	1080
PVERSIVGIS	SLSEGTYDI	NASYIMGYIQ	SNEFIITQHP	LLHTIKDFWR	MIWDHNAQLV	1140
VMIPDQNMMA	BDEFVYWNPK	DEPNICESFK	VTLMAEEHKC	LSNEEKLIQ	DFILEATQDD	1200
YVLEVRHFQC	PKWPNPDSPI	SKTFELISVI	KEEAANRDGP	MIVHDEHGGV	TAGTFCALTT	1260
LMHQLKENS	VDVYQVAKMI	NLMRPGVFAD	IEQYQFLYKV	ILSLVSTRQE	ENPSTSLDSN	1320
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Seq ID NO: 187 DNA sequence
 Nucleic Acid Accession #: EOS sequence
 Coding sequence: 148-4632

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CAGCTCCTCT	GTGTTTGGCG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240
CTTGTGGAAG	AGATTGGCTG	GTCCTATACA	GGAGCACTGA	ATCAAAAAAA	TGGGGGAAAG	300
AAATATCCAA	CATGTAATAG	CCCCAAACAA	TCTCCTATCA	ATATTGATGA	AGATCTTACA	360
CAAGTAAATG	TGAATCTTAA	GAAACTTAAA	TTTCAGGGTT	GGGATAAAAC	ATCATTGGAA	420
AACACATTCA	TTCATAACAC	TGGGAAAACA	GTGGAAATTA	ATCTCACTAA	TGACTACCGT	480
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AAATGCAATA	TGTCATCTGA	TGGATCAGAG	CATAGTTTAG	AAGGACAAAA	ATTTCCACTT	600
GAGATGCAAA	TCTACTGCTT	TGATGCGGAC	CGATTTTCAA	GTTTGTAGGA	AGCAGTCAAA	660
GGAAAAGGGA	AGTTAAGAGC	TTTATCCATT	TTGTTTGAGG	TTGGGACAGA	AGAAAAATTG	720
GATTTCAAAG	CGATTATTGA	TGGAGTCGAA	AGTGTTAGTC	GTTTGGGAAA	GCAGGCTGCT	780
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AATGGCTCAT	TGCATCTTCC	TCCCTGCACA	GACACAGTTG	ACTGGATTGT	TTTTAAAGAT	900
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TCTGGTTATG	TGATGCTGAT	GGACTACTTA	CAAAACAATT	TTCGAGAGCA	ACAGTACAA	1020
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AACCTGTGGG	GGACTGCAGA	ATCCTTAAAT	ACAGTTTCTA	TAACAGAATA	TGAGGAGGAG	1860
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GAAAACCCAG	AGACAATAAC	ATATGATGTC	CTTATACCAG	AATCTGCTAG	AAATGCTTCC	2040
GAAGATTCAA	CTTCATCAGG	TTCAGAAAG	TCACTAAAGG	ATCCTTCTAT	GGAGGGAAAT	2100
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CATTATTCTA	CCTTTGCCCTA	CTTCCCACT	GAGGTAACAC	CTCATGCTTT	TACCCCATCC	2340
TCCAGACAAC	AGGATTTGGT	CTCCACGGTC	AACGTGGTAT	ACTCGCAGAC	AACCCAACCG	2400
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GAATCCGAGA	AGAAGGCAGT	TATACCCCTT	GTGATCGTGT	CAGCCCTGAC	TTTTATCTGT	2520
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CATGCAAGTA	GTGGGTTTAC	TGAAGAATTT	GAGACACTGA	AAGAGTTTTA	CCAGGAAGTG	2760
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	CTTGCTGAAA	AGGATGGCAA	ACTGACTGAT	TATATCAATG	CCAATTATGT	TGATGGCTAC	2940
	AACAGACCAA	AAGCTTATAT	TGCTGCCCAA	GGCCCACTGA	AATCCACAGC	TGAAGATTTC	3000
5	TGGAGAATGA	TATGGGAACA	TAATGTGGAA	GTATTGTGCA	TGATAACAAA	CCTCGTGGAG	3060
	AAAGGAAGGA	GAAAATGTGA	TCAGTACTGG	CCTGCCGATG	GGAGTGAGGA	GTACGGGAAC	3120
	TTTCTGGTCA	CTCAGAAGAG	TGTGCAAGTG	CTTGCCTATT	ATACTGTGAG	GAATTTTACT	3180
	CTAAGAAACA	CAAAAATAAA	AAAGGGCTCC	CAGAAAAGGA	GACCCAGTGG	ACGTGTGGTC	3240
	ACACAGTATC	ACTACACGCA	GTGGCCTGAC	ATGGGAGTAC	CAGAGTACTC	CCTGCCAGTG	3300
10	CTGACCTTTG	TGAGAAAGGC	AGCCTATGCC	AAGCGCCATG	CAGTGGGGCC	TGTTGTCTGC	3360
	CACCTGCAGT	CTGGAGTTGG	AAGAACAGGC	ACATATATTG	TGCTAGACAG	TATGTTGCAG	3420
	CAGATTCAAC	ACGAAGGAAC	TGTCAACATA	TTTGGCTTCT	TAAAAACACAT	CCGTTTCAAA	3480
	AGAAATTAAT	TGGTACAAAC	TGAGGAGCAA	TATGTCTTCA	TTTATGATAC	ACTGGTTGAG	3540
	GCCATACTTA	GTAAAGAAAC	TGAGGTGCTG	GACAGTCATA	TTTATGCCCTA	TGTTAATGCA	3600
15	CTCCTCATTC	CTGGACCAGC	AGGCAAAACA	AAGCTAGAGA	AACAATTCCA	GGGTCTCACT	3660
	CTGTCAACCA	GGCTGGAGTG	CAGAGGCACA	ATCTCGGCTC	ACTGCAACCT	TCCTCTCCCT	3720
	GGCTTAACCT	ATCCTCTTAC	CTCAGCCTCC	CGAGTGGCTG	GGACTATACT	CTGAGCCAG	3780
	TCAAATATAC	AGCAGAGTGA	CTATTCTGCA	GCCCTAAAGC	AATGCAACAG	GGAAAAGAA	3840
	CGAATCTTCT	CTATCATCCC	TGTGGAAGA	TCAAGGGTTG	GCATTTTCATC	CCTGAGTGGA	3900
20	GAAGGCACAG	ACTACATCAA	TGCTCTCTAT	ATCATGGGCT	ATTACAGAG	CAATGAATTC	3960
	ATCATTACCC	AGCACCTCT	CCTTCATACC	ATCAAGGATT	TCTGGAGGAT	GATATGGGAC	4020
	CATAATGCC	AACCTGGTGG	TATGATTCCT	GATGGCCAAA	ACATGGCAGA	AGATGAATTT	4080
	GTTTACTGGC	CAAAATAAGA	TGAGCCTATA	AATTGTGAGA	GCTTTAAGGT	CACCTCTTATG	4140
	GCTGAAGAAC	AGAAATGTCT	ATCTAATGAG	GAAAACTTA	TAATTGAGGA	CTTTATCTTA	4200
25	GAAGCTACAC	AGGATGATTA	TGTAATGAA	GTGAGGCACT	TTTCAAGTCC	TAAATGGCCA	4260
	AATCCAGATA	GCCCCATTAG	TAAACTTTT	GAACTTATA	GTGTTATAAA	AGAAGAAGCT	4320
	GCCAATAGGG	ATGGGCCCTAT	GATTGTTTAT	GATGAGCATG	GAGGAGTGAC	GGCAGGAAC	4380
	TTCTGTGCTC	TGACAACCTT	TATGCACCAA	CTAGAAAAAG	AAAATTCCGT	GGATGTTTAC	4440
	CAGGTAGCCA	AGATGATCAA	TCGTGATGAG	CCAGGAGTCT	TTGCTGACAT	TGAGCAGTAT	4500
30	CAGTTTCTCT	ACAAAGTGA	CCTCAGCCTT	GTGGGCACAA	GGCAGGAAGA	GAATCCATCC	4560
	ACCTCTCTGG	ACAGTAATGG	TGCAGCATTG	CCTGATGGAA	ATATAGCTGA	GAGCTTAGAG	4620
	TCCTTAGTTT	AACACAGAAA	GGGGTGGGGG	GACTCACATC	TGAGCATTGT	TTTCTCTTTC	4680
	CTAAAATTAG	GCAAGAAAAT	CAGTCTAGTT	CTGTTATCTG	TTGATTTCCT	ATCACCTGAC	4740
	AGTAACCTTC	ATGACATAGG	ATTCTGCCCG	CAAATTATA	TCATTACAA	TGTGTGCCTT	4800
35	TTTGCAAGAC	TTGTAATTTA	CTTATTATGT	TTGAACTAAA	ATGATTGAAT	TTTACAGTAT	4860
	TTCTAAGAAT	GGAAATGTGG	TATTTTTTTC	TGTATTGATT	TTAACAGAAA	ATTTCAATTT	4920
	ATAGAGGTGA	GGAAATCCAA	ACTACAGAAA	ATGTTTGTGT	TTAGTGTCAA	ATTTTGTAGT	4980
	GTATTTGTAG	CAATTATCAG	GTTTGTCTAG	AATATAACTT	TTAATACAGT	AGCCTGTAAA	5040
	TAAAACACTC	TTCCATATGA	TATTCACAT	TTTACAACCT	CAGTATTCAC	CTAAAGTAGA	5100
40	AATAATCTGT	TACTTATTTT	AAATACTGCC	CTAGTGTCTC	CATGGACCAA	ATTTATATTT	5160
	ATAATTGTAG	ATTTTATAT	TTTACTACTG	AGTCAAGTTT	TCTAGTCTG	TGTAATGTGT	5220
	TAGTTTAAAT	ACGTAGTTCA	TTAGCTGGTC	TTACTCTACC	AGTTTCTCGA	CATTGTATTG	5280
	TGTTACCTAA	GTCATTAAC	TTGTTTCAGC	ATGTAATTTT	AACTTTTGTG	GAAAAATAGAA	5340
45	ATACCTTCAT	TTTGAAAGAA	GTTTTTATGA	GAATAACACC	TTACCAACAA	TTGTTCAAA	5400
	GGTTTTTATC	CAAGGAATTG	CAAAAATAAA	TATAAATATT	GCCATTAAAA	AAAAAATAAA	5460
	AAAAAAAAAA	AAAAAAAAAA	A				

Seq ID NO: 188 Protein sequence:
Protein Accession #: EOS sequence

50	1	11	21	31	41	51	
	MRILKRFLAC	IQLLCVCRLD	WANGYYRQQR	KLVEEIGWSY	TGALNQKNWG	KKYPTCNSPK	60
	QSPINIDEDL	TQVNVNLKKL	KPQGWDKTSL	ENTFIHNTGK	TVEINLTNDY	RVSGGVSEMV	120
55	FKASKITFWH	GKCNMSSDGS	EHSLEGQKFP	LEMQIYCFDA	DRFSSFEEAV	KGKGLRALS	180
	ILFEVGTENN	LDFKAIIDGV	ESVSRFGKQA	ALDPFILLNL	LPNSTDKYII	YNGSLTSPPC	240
	TDTVDWIVFK	DTVSISISFL	AVFCEVLTMQ	QSGYVLMMDY	LQNNFREQQY	KFSRQVFSSY	300
	TGKEIHEAV	CSSEPENVQA	DPENYTSLLV	TWERPRVVDY	TMIEKFVAVLY	QQLDGEDQTK	360
	HEFLTDGYQD	LGAILNNLLP	NMSYVLQIVA	ICTNGLYQKY	SDQLIVDMPT	DNPELDLFE	420
60	LIGTEEIIKE	EEBEGKIEEG	AIVNPGRDSA	TNQIRKKEPQ	ISTTTHYNRI	GTKYNEAKTN	480
	RSPTRGSEFS	GKGDVPTNSL	NSTSQPVTKL	ATEKDILSLT	QTVTELPPIH	VEGTSASLND	540
	GSKTVLRSPH	MNLSGTAEAL	NTVSITEYEE	ESLLTSFKLD	TGAEDSSGSS	PATSAIPFIS	600
	ENISQGYIFS	SENPETITYD	VLPESARNA	SEDSTSSGSE	ESLKDPMEG	NVWFPSSTDI	660
	TAQPDVGSGR	ESFLQNTYTE	IRVDESEKTT	KSFSGAPVMS	QGPSVIDLEM	PHYSTFAYFP	720
65	TEVTPHAFPT	SSRQDLVST	VNVVYSQTTQ	PVYNEASNSS	HESRIGLAEG	LESEKKAVIP	780
	LVIVSALTFI	CLVVLVGLIL	YWRKCFQTAH	FYLEDDSTSPR	VISTPPTPIF	PISEDDVGAIP	840
	IKHFPKHVAD	LHASSGFTEE	FETLKEFYQE	VQSCITVDLGI	TADSSNHDPN	KHKNRYINIV	900
	AYDHSRVKLA	QLAEKDGKLT	DYINANYVDG	YNRPKAYIAA	QGPKLSTAE	FWRMIWEHNV	960
	EVIVMITNLV	EKGRKCKDQY	WPADGSEYEG	NFLVTQKSVQ	VLAYYTVRNF	TLRNTKIKKG	1020
70	SQKGRPSGRV	VTQVHYTQWP	DMGVPEYSLP	VLTFFVRKAAY	AKRHAVGPVV	VHCSAGVGRT	1080
	GTYYVLDSML	QQIQHEGTVN	IFGFLKHRS	QRNVLVQTEE	QYVFIDHTLV	EALSKETEV	1140
	LDSHIHAYVN	ALLIPGPAGK	TKLEKQFQGL	TLSPRLCECRG	TISAHCNLPL	PGLTDPPTSA	1200
	SRVAGTILLS	QSNIQQSDYS	AALKQCNREK	NRTSSIIIPVE	RSRVGISSLS	EGGTDYINAS	1260
	YIMGYQYSNE	FIITQHPLLL	TIKDFWRMIW	DHNAQLVMI	PDGQNMAEDE	FVYWPKNKDEP	1320
75	INCESFKVTL	MAEBHKCLSN	EELKLIQDFI	LEATQDDYVL	EVHRFQCPKW	PNPDSPISKT	1380
	FELISVIKEE	AANRDGPMIV	HDEHGGVTAG	TFCALTLMH	QLEKENSVDV	YQVAKMINLM	1440
	RPGVFADIEQ	YQFLYKVLIS	LVGTRQEENP	STSLDSNGAA	LPGDNIAESL	ESLV	

Seq ID NO: 189 DNA sequence
Nucleic Acid Accession #: NM_002820
Coding sequence: 304..831

80	1	11	21	31	41	51	
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	CCCTGTTCCA	CGAACCCAGG	AGAACTGCTG	GCCAGATTAA	TTAGACATTG	CTATGGGAGA	120
85	CGTGTAACA	CACACTTAT	CATTGATGCA	TATATAAAC	CATTTTATT	TCGTATTAT	180

5 TTCAGAGGAA GCGCCTCTGA TTGTTTCTT TTTTCCCTTT TTGCTCTTTC TGGCTGTGTG 240
 GTTTGGAGAA AGCACAGTTG GAGTAGCCGG TTGCTAAATA AGTCCCAGAG GCGAGCGGAG 300
 ACGATGCAGC GGAGACTGGT TCAGCAGTGG AGCGTCGCGG TGTTCCTGCT GAGCTACGCG 360
 GTGCCCTCCT GCGGGCGCTC GGTGGAGGGT CTCAGCCGCC GCCTCAAAAG AGCTGTGTCT 420
 10 GAACATCAGC TCCTCCATGA CAAGGGGAAG TCCATCCAAG ATTTACGGCG ACGATTCTTC 480
 CTTCAACATC TGATCGCAGA AATCCACACA GCTGAAATCA GAGCTACCTC GGAGGTGTCC 540
 CCTAACTCCA AGCCCTCTCC CAACACAAAG AACCACCCCG TCCGATTTTG GTCTGATGAT 600
 GAGGGCAGAT ACCTAACTCA GGAAACTAAC AAGGTGGAGA CGTACAAAGA GCAGCCGCTC 660
 AAGACACCTG GGAAGAAAAA GAAAGCAAG CCCGGGAAAC GCAAGGAGCA GGAAAAGAAA 720
 15 AAACGGCGAA CTCGCTCTGC CTGGTTAGAC TCTGGAGTGA CTGGGAGTGG GCTAGAAGGG 780
 GACCACCTGT CTGACACCTC CACAACGTCG CTGGAGCTCG ATTCACGGTA ACAGGCTTCT 840
 CTGGCCCGTA GCCTCAGCGG GGTGCTCTCA GCTGGGTTTT GGAGCCTCCC TTCTGCCTTG 900
 GCTTGACAAA ACCTAGAATT TTCTCCCTTT ATGTATCTCT ATCGATTGTG TAGCAATTGA 960
 CAGAGAATAA CTCAGAATAT TGTCTGCCTT AAAGCAGTAC CCCCCTACCA CACACACCCC 1020
 20 TGTCCTCCAG CACCATAGAG AGGCGCTAGA GCCCATTCCT CTTTCTCCAC CGTCACCCAA 1080
 CATCAATCCT TTACACTCT ACCAAATAAT TTCATATTCA AGCTTCAGAA GCTAGTGACC 1140
 ATCTTCATAA TTGCTGGAG AAGTGTATT CTTCCTCTTA CTCTCACACC TGGGCAAACT 1200
 TTCTTCAGTG TTTTTCATTT CTACGTTCT TCACTTCAA GGGAGAATAT AGAAGCATTT 1260
 GATATTATCT ACAAACACTC CAGAACAGCA TCATGTCATA AACGATTCTG AGCCATTAC 1320
 25 ACTTTTATAT TAATTAATTA TATTTAATTA AATCTCAAAT TTATTTAAT GTAAAGAACT 1380
 TAAATTATGT TTTAAACACA TGCTTAAAT TTGTTTAAAT AAATTTAACT CTGGTTTCTA 1440
 CCAGCTCATA CAAAATAAAT GGTTCCTGAA AATGTTTAA TATTAACCTA CAAGGATATA 1500
 GGTTCCTCTC ATGTATCTTT TTGTTTATTG GCAAGATGAA ATAATTTTTC TAGGGTAATG 1560
 CCGTAGGAAA AATAAAACTT CACATTTAAA AAAAA

Seq ID NO: 190 Protein sequence:
Protein Accession #: NP_002811

30 1 11 21 31 41 51
 | | | | | |
 MQRRLVQQWS VAVFLLSYAV PSCGRSVEGL SRRLKRAVSE HQLLHDKGKS IQDLRRRFFL 60
 35 HHLIAEIHIA EIRATSEVSP NSKPSPTNKN HPVRFSGSDE GRYLTQETNK VETYKEQPLK 120
 TPGKKKKGKP GRRKKEQKKK RRTRSAWLDS GVTGSGLEGD HLSDTSTTSL ELDSR

Seq ID NO: 191 DNA sequence
Nucleic Acid Accession #: XM_059328
Coding sequence: 52..1023

40 1 11 21 31 41 51
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 GGGCTGTCCG GCCACTCCCC CTGGGAGCGC GAGCGGTGGA CCCAGGCGGC CATGTCCCGC 60
 45 CCTCGCATGC GCCTGGTGGT CACCGCGGAC GACTTTGGTT ACTGCCCGCG ACGCGATGAG 120
 GGATATCGTG AGGCCTTTCT GGCCGGGGCT GTGACCAGCG TGTCCCTGCT GGTCAACGGT 180
 GCGGCCACCG AGAGCGCGGC GGAGCTGGCC CGCAGGCACA GCATCCCCAC GGGCCTCCAC 240
 GCCAACCTGT CCGAGGGCGC CCCCCTGGGT CCGGCCCGCC GTGGCGCCTC ATCGCTGCTC 300
 50 GGCCCGGAAG GTTCTTCTCT TGGCAAGATG GGATTCCGGG AGGCGGTGGC GGCCGGAGAC 360
 GTGGATTGTC CTCAGGTGGC GGAGGAGCTC GAGGCCAAC TAAGCTGCTT CCGGGAGCTG 420
 CTGGGCAGGG CCCCCACGCA CGCGGACGGG CACCAGCAGC TGCACGTGCT CCCAGGCGTG 480
 TGCCAGGTGT TGCCTGAGGC GCTGCAAGGC TATGGGGTGC GCTTTACGCG ACTGCCGCTG 540
 GAGCGCGGTG TGGGTGGCTG CACTTGGCTG GAGGCCCGCG CGCGTGCTT CGCCTGCGCC 600
 55 GTGGAGCGCG AGCCCGGGC CGCCGTGGGC CCCTTCTCCC GCCACGGCCT GCGGTGGACA 660
 GACGCCTTCG TGGCCTGAG CACTTGGCGC CGGCACATGT CCGCTCACCG CGTGTCCGGG 720
 GCCCTGGCGC GGGTCTTGGA AGGTACCCTA GCGGGCCACA CCCTGACAGC CGAGCTGATG 780
 GCGCACCCCG GCTACCCAG TGTGCCTCCC ACCGGCGGCT GCGGTGAAGG CCCCAGCGCT 840
 60 TTCTCTTGCT CTGGGAGCG GCTGCATGAG CTGCGCGTCC TCACCGCGCC CACGCTGCGG 900
 GCCCAGCTTG CCCAGGATGG CGTGCACTT TGCGCCCTCG ACGACCTGGA CTCCAAGAGG 960
 CCAGGGGAGG AGGTCCCCTG TGAGCCCACT CTGGAACCC CTCCCTACTC 1020
 TGACCCCTTA CAGACAACCA AGCACTAATC CCCTTAGTAC CAAGAAAGGG GAGCCAGGAT 1080
 65 TTAGTCTTGG CCCAGCCGAC AGCTGGGACC TGGAGCACGA TCTGTTGACT TCCCTGGGTA 1140
 GGACACTGCC ACCTCTGGGC TCAGGTCTCT ATGCCTCAA ATGGCATCTA GAGTTTGAGC 1200
 AGCCTTCTTG GCTGAGGCA GGCCTAGCCT GTGGCAGCG GCTAGGGCCC GCAGAGCATT 1260
 TGGTGCCCTT CATGTTGCA ATGCAACAC CTTCACTACT GGGGCGAGTG GGAGAGATG 1320
 CTATATTAAT AAAATAACGT GTGCTTTTC

Seq ID NO: 192 Protein sequence:
Protein Accession #: XP_059328

70 1 11 21 31 41 51
 | | | | | |
 MSRPRMRLVV TADDFGYCPR RDEGIVEAFL AGAVTSVSLI VNGAATESAA ELARRHSIPT 60
 75 GLHANLSEGR PVGPARRGAS SLLGPEGFFL GKMFGREAVA AGDVLDPQVR EELEAQLSCF 120
 RELLEGAPTH ADGHQHVHVL PGVCQVFAEA LQAYGVRFTF LPLERGVGGC TWLEAPARAF 180
 ACAVERDARA AVGPFSRHGL RWTDAFVGLS TCGRHMSAHR VSGALARVLE GTLAGHTLTA 240
 ELMAHFPGYS VPPTGGCGEG PDAFSCSWER LHELRLVTAP TLRQLAQDQ VQLCALDLDL 300
 SKRPGEEVPC EPTLEPFLEP SLL

Seq ID NO: 193 DNA sequence
Nucleic Acid Accession #: NM_005688.1
Coding sequence: 126..4439

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 85 AGGGCGCAG GAATTCGTAT GTGAAACTAA CAGTCTGTGA GCCCTGGAAC CTCCGCTCAG 120

	AGAAGATGAA	GGATATCGAC	ATAGGAAAAG	AGTATATCAT	CCCCAGTCCT	GGGTATAGAA	180
	GTGTGAGGGA	GAGAACCCAGC	ACTTCTGGGA	CGCACAGAGA	CCGTGAAGAT	TCCAAGTTCA	240
	GGAGAACTCG	ACCGTTGGAA	TGCCAAGATG	CCTTGGAAAC	AGCAGCCCCA	GCCGAGGGCC	300
5	TCTCTCTTGA	TGCCTCCATG	CATTCTCAGC	TCAGAATCCT	GGATGAGGAG	CATCCCAAGG	360
	GAAAGTACCA	TCATGGCTTG	AGTGCTCTGA	AGCCCATCCG	GACTACTTCC	AAACACCCAGC	420
	ACCCAGTGGA	CAATGCTGGG	CTTTTTCTCT	GTATGACTTT	TTCGTGGCTT	TCTTCTCTGG	480
	CCCGTGTGGC	CCACAGAAG	GGGGAGCTCT	CAATGGAAGA	CGTGTGGTCT	CTGTCCAAGC	540
	ACGAGTCTTC	TGACGTGAAC	TGCAGAAGAC	TAGAGAGACT	GTGGCAAGAA	GAGCTGAATG	600
10	AAGTTGGGCC	AGACGCTGCT	TCCCTGCGAA	GGTTGTGTG	GATCTTCTGC	CGCACCAGGC	660
	TCATCCTGTC	CATCGTGTG	CTGATGATCA	CGCAGCTGGC	TGGCTTCAGT	GGACCAGCCT	720
	TCATGGTGAA	ACACCTCTTG	GAGTATACCC	AGGCAACAGA	GTCTAACCTG	CAGTACAGCT	780
	TGTTGTAGT	GCTGGGCCTC	CTCCTGACGG	AAATCGTGGC	GTCTTGGTGC	CTTGCACTGA	840
	CTTGGGCATT	GAATTACCGA	ACCGGTGTCC	GCTTGCGGGG	GGCCATCCTA	ACCATGGCAT	900
15	TTAAGAAGAT	CCTTAAGTTA	AAGAACATTA	AAGAGAAATC	CCTGGGTGAG	CTCATCAACA	960
	TTTGTCTCAA	CGATGGGCGAG	AGAATGTTTG	AGGCAGCAGC	CGTTGGCAGC	CTGCTGGGCTG	1020
	GAGGACCCGT	TGTTGCCATC	TTAGGCATGA	TTTATAATGT	AATTATTCTG	GGACCAACAG	1080
	GCCTCCTGGG	ATCAGCTGTT	TTTATCCTCT	TTTACCCAGC	AATGATGTTT	GCATCACGGC	1140
	TCACAGCATA	TTTCAGGAGA	AAATGCGTGG	CCGCCACGGA	TGAACGTGTC	CAGAAGATGA	1200
20	ATGAAGTTCT	TACTTACATT	AAATTTATCA	AAATGTATGC	CTGGGTCAA	GCATTTTCTC	1260
	AGAGTGTTC	AAAAATCCGC	GAGGAGGAGC	GTCCGATATT	GGAAAAAGCC	GGGTACTTCC	1320
	AGGGTATCAC	TGTGGGTGTG	GCTCCCATTG	TGGTGGTGAT	TGCCAGCGTG	GTGACCTTCT	1380
	CTGTTTCATAT	GACCTTGGGC	TTCGATCTGA	CAGCAGCACA	GGCTTTCACA	GTGGTGACAG	1440
	TCTTCAATTC	CATGACTTTT	GCTTTGAAAG	TAACACCGTT	TTCAGTAAAG	TCCCTCTCAG	1500
25	AAGCCTCAGT	GGCTGTGAC	AGATTTAAGA	GTTTGTCTT	AATGGAAGAG	GTTTACATGA	1560
	TAAAGAACAA	ACCAGCCAGT	CCTCACATCA	AGATAGAGAT	GAAAAATGCC	ACCTTGGCAT	1620
	GGGACTCCTC	CCACTCCAGT	ATCCAGAACT	CGCCCAAGCT	GACCCCAAAA	ATGAAAAAAG	1680
	ACAAGAGGGC	TTCAGGGGCG	AAGAAAGAGA	AGGTGAGGCA	CTGTCAGCGC	ACTGAGCATC	1740
	AGGCGGTGCT	GGCAGAGCAG	AAAGGCCACC	TCCTCCTGGA	CAGTGACGAG	CGGCCACATC	1800
30	CCGAAGAGGA	AGAAGGCAAG	CACATCCACC	TGGGCCACCT	CGCCTTACAG	AGGACACTGC	1860
	ACAGCATCGA	TCTGGAGATC	CAAGAGGGTA	AACTGGTTGG	AATCTGCGGC	AGTGTGGGAA	1920
	GTGGAAAAAC	CTCTCTCATT	TCAGCCATTT	TAGGCCAGAT	GACGCTTCTA	GAGGGCAGCA	1980
	TTGCAATCAG	TGGAAACCTTC	GCTTATGTGG	CCCAGCAGGC	CTGGATCCTC	AATGCTACTC	2040
	TGAGAGACAA	CATCCTGTTT	GGGAAGGAAT	ATGATGAAGA	AAGATAACAAC	TCTGTGCTGA	2100
	ACAGCTGCTG	CCTGAGGCCCT	GACCTGGCCA	TTCTTCCCAG	CAGCGACCTG	ACGGAGATTG	2160
35	GAGAGCGAGG	AGCCAAACCTG	AGCGGTGGGC	AGCGCCAGAG	GATCAGCCTT	GCCCCGGCCT	2220
	TGTATAGTGA	CAGGAGCATC	TACATCCTGG	ACGACCCCTC	CAGTGCCCTA	GATGCCCATG	2280
	TGGCAACCA	CATCTTCAAT	AGTGCTATCC	GGAAACATCT	CAAGTCCAAG	ACAGTTCTGT	2340
	TTGTTACCCA	CCAGTTACAG	TACCTGGTTG	ACTGTGATGA	AGTGATCTTC	ATGAAAGAGG	2400
40	GCTGTATTAC	GGAAAGAGGC	ACCCATGAGG	AACTGATGAA	TTTAAATGGT	GACTATGCTA	2460
	CCATTTTAA	TAACTTGTGG	CTGGGAGAGA	CACCGCCAGT	TGAGATCAAT	TCAAAAAAGG	2520
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45	TCTCTGTTAT	TATGGCCCTT	TTTATGCTGA	ATGTAGGCAG	CACCGCCTTC	AGCACCTGGT	2760
	GGTTGAGTTA	TGTGATCAAG	CAAGGAAGCG	GGAACACCCAC	TGTGACTCGA	GGGAACGAGA	2820
	CCTCGGTGAG	TGACAGCATG	AAGGACAATC	CTCATATGCA	GTAATATGCC	AGCATCTACG	2880
	CCCTCTCCAT	GGCAGTCTAG	CTGATCCTGA	AAGCCATTCC	AGGAGTTGTC	TTTGTCAAGG	2940
	GCACGCTGCG	AGCTTCTCTC	CGGCTGCATG	ACGAGCTTTT	CCGAAGGATC	CTTCGAAGCC	3000
50	CTATGAAGTT	TTTTGACACG	ACCCCCACAG	GGAGGATTCT	CAACAGGTTT	TCCAAAGACA	3060
	TGGATGAAGT	TGACGTGCGG	CTGCCGTTCC	AGGCCGAGAT	GTTTCATCCAG	AACGTTATCC	3120
	TGGTGTCTTT	CTGTGTGGGA	ATGATCGCAG	GAGTCTTCCC	GTGGTTCTCT	GTGGCAGTGG	3180
	GGCCCCCTGT	CATCCTCTTT	TCAGTCTGTC	ACATTTGCTC	CAGGGTCTCT	ATTCGGGAGC	3240
	TGAAGCGTCT	TGAGATCAAG	ACGCACTCAC	CTTTCCTCTC	CCACATCAGC	TCCAGCATAC	3300
55	AGGGCCTTGC	CACCATCCAC	GCCTACAATA	AAGGGCAGGA	GTTTCTGCAC	AGATACCAGG	3360
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	CTGTGCGGCT	GGACCTCATC	AGCATCGCCC	TCATCACCCAC	CACGGGGCTG	ATGATCGTTC	3480
	TTATGACCGG	GCAGATTCCC	CCAGCCTATG	CGGGTCTCGC	CATCTCTTAT	GCTGTCCAGT	3540
	TAAAGGGGCT	GTTCCAGTTT	ACGGTCAGAC	TGGCATCTGA	GACAGAAGCT	CGATTACCTT	3600
60	CGGTGGAGAG	GATCAATCAC	TACATTAAGA	CTCTGTCTCT	GGAAGCACCT	GCCAGAATTA	3660
	AGAACAAGGC	TCCCTCCCCC	GACTGGCCCC	AGGAGGGAGA	GGTGACCTTT	GAGAACGCGAG	3720
	AGATGAGGTA	CCGAGAAAAAC	CTCCCTCTTG	TCCTAAAGAA	AGTATCCTTC	ACGATCAAAAC	3780
	CTAAAGAGAA	GATTGTCATT	GTGGGGCGGA	CAGGATCAGG	GAAGTCTCTG	CTGGGGATGG	3840
	CCCTCTTCCG	TCTGGTGGAG	TTATCTGGAG	GCTGCATCAA	GATTGATGGA	GTGAGAATCA	3900
65	GTGATATTGG	CCTTGGCCGAC	CTCCGAAGCA	AACTCTCTAT	CATTCTCTCA	GAGCCGGTGC	3960
	TGTTCAAGTG	CACTGTGAGA	TCAAATTTGG	ACCCCTTCAA	CCAGTACACT	GAAGACCAGA	4020
	TTTGGGATGC	CCTGGAGAGG	ACACACATGA	AAGAATGTAT	TGCTCAGCTA	CCTCTGAAAC	4080
	TTGAATCTGA	AGTGATGGAG	AATGGGGATA	ACTTCTCAGT	GGGGGAACGG	CAGCTCTTGT	4140
	GCATAGCTAG	AGCCCTGCTC	CGCCACTGTA	AGATTCTGAT	TTTAGATGAA	GCCACAGCTG	4200
70	CCATGGACAC	AGAGACAGAC	TTATTGATTC	AAGAGACCAT	CCGAGAAGCA	TTTGCAAGCT	4260
	GTACCATGCT	GACCATTGCC	CATCGCTGTC	ACACGGTTCT	AGGCTCCGAT	AGGATTATGG	4320
	TGCTGGCCCA	GGGACAGGTG	GTGGAGTTTG	ACACCCCATC	GGTCTTCTCT	TCCAACGACA	4380
	GTTCGCCGAT	CTATGCCATG	TTTGCTGCTG	CAGAGAACAA	GGTCGCTGTC	AAGGGCTGAC	4440
	TCCTCCTCTG	TGACGAAGTC	TCTTTTCTTT	AGAGCAATTG	CATTCCCTGC	CTGGGGCGGG	4500
75	CCCCTCATCG	CGTCCCTCTA	CCGAAACCTT	GCCTTTCTCG	ATTTTATCTT	TGCGACAGCA	4560
	GTTCCGGATT	GGCTTGTGTG	TTTCACTTTT	AGGGAGAGTC	ATATTTTGTAT	TATTGTATTT	4620
	ATTCCATATT	CATGTAACCA	AAATTTAGTT	TTTGTCTCTA	ATTGCACTCT	AAAAGGTTCA	4680
	GGGAACCGTT	ATTATAATTG	TATCAGAGGC	CTATAATGAA	GCTTTATACG	TGTAGCTATA	4740
	TCTATATATA	ATTCTGTACA	TAGCCTATAT	TTACAGTGAA	AATGTAAGCT	GTTTATTTTA	4800
80	TATTAATAATA	AGCACTGTGC	TAATAACAGT	GCATATTCCT	TTCTATCATT	TTTGTACAGT	4860
	TTGCTGTACT	AGAGATCTGG	TTTGTCTATT	AGACTGTAGG	AAGAGTAGCA	TTTCACTCTT	4920
	CTCTAGCTGG	TGGTTTCAAG	GTGCCAGGTT	TTCTGGGTGT	CCAAAGGAAG	ACGTGTGGCA	4980
	ATAGTGGGCC	CTCCGACAGC	CCCCTCTGCC	GCCTCCCCAC	AGCCGCTCCA	GGGGTGGCTG	5040
	GAGACGGGTG	GGCGGCTGGA	GACCATGCGAG	AGCGCCGTGA	GTTCTCAGGG	CTCCTGCCTT	5100
	CTGTCTCTGGT	GTCACTTACT	GTTTCTGTCA	GGAGAGCAGC	GGGGCGAAGC	CCAGGCCCTT	5160
85	TTTCACTCCC	TCCATCAAGA	ATGGGGATCA	CAGAGACATT	CCTCCGAGCC	GGGGAGTTTC	5220
	TTTCTGTCCT	TCTTCTTTTT	GCTGTGTTT	CTAAACAAGA	ATCAGTCTAT	CCACAGAGAG	5280
	TCCCCTGCTC	TCAGGTTCTT	ATGGCTGGCC	ACTGCACAGA	GCTCTCCAGC	TCCAAGACCT	5340

GTTGGTTCCA AGCCCTGGAG CCAACTGCTG CTTTTGAGG TGGCACTTTT TCATTGCTCT 5400
 ATTCACACAC CTCCACAGTT CAGTGGCAGG GCTCAGGATT TCGTGGGTCT GTTTTCCTTT 5460
 CTCACCGCAG TCGTCGCACA GTCTCTCTCT CTCTCTCCCC TCAAAGTCTG CAACTTTAAG 5520
 CAGCTCTTGC TAATCAGTGT CTCACACTGG CGTAGAAGTT TTTGTACTGT AAAGAGACCT 5580
 5 ACCTCAGGTT GCTGGTTGCT GTGTGGTTTG GTGTGGTCCC GCAAAACCCC TTTGTGCTGT 5640
 GGGGCTGGTA GCTCAGGTGG GCGTGGTCAC TGCTGTCATC AGTTGAATGG TCAGCGTTGC 5700
 ATGTCGTGAC CAACTAGACA TTCTGTGCGC TTAGCATGTT TGCTGAACAC CTTGTGGAAG 5760
 CAAAAATCTG AAAATGTGAA TAAATATTATT TTGGATTTTG TAAAAAATAA AAAAAAATAA 5820
 AAAAAAATAA AAAAAAATAA

Seq ID NO: 194 Protein sequence:
 Protein Accession #: NP_005679.1

1 11 21 31 41 51
 MKDIDIGKEY IIPSPGYRSV RERTSTSGTH RDREDSKFRR TRPLECQDAL ETAARAEGLS 60
 LDASMHSQLR ILDEEHFKGK YHHGLSALKP IRTTSKHQHP VDNAGLFSCM TFSWLSLAR 120
 VAHKKGELSM EDVWSLSKHE SSDVNCRRLE RLWQEEELNEV GPDAASLRRV VWIFCRTLRI 180
 20 LSIIVCLMITQ LAGFSGPAFM VKHLLLEYTQA TESNLQYSL LVLGLLLTEI VRSWSLALTW 240
 ALNYRTGVRL RGAILTMAFK KILKLNKIKE KSLGELINIC SNDGORMFEA AAVGSLLAGG 300
 PVVAILGMIY NVIILGPTGF LGSASFILFY PAMMFASRLT AYFRKRCVAA TDERVQKMNE 360
 VLTYYIKFIKM YANVKAQSQS VQKIREBERR ILEKAGYFQG ITVGVAPIV VIASVVTFSV 420
 HMTLGFDELTA AQAFVTVTVF NSMTFALKVT PFSVKSLSEA SVAVDRFKSL FLMEEVHMIK 480
 25 NKPPASPHIKI EMKNATLAWD SSHSSIQNSP KLTPEKMKDK RASRGKKEKV RQLQRTHEQA 540
 VLABQKGLHL LDDSDERSPE EEEGKHIHLG HRLRLQRTLHS IDLEIQEGKL VGICGSVSGS 600
 KTSLSAILG QMTLLEGSIA ISGTFAYVAQ QAWILNATLR DNILFGKEYD EERYNSVLNS 660
 CCLRPDLAIL PSSDLTIGE RGNALSGGQR QRISLARALY SDRSIYILDD PLSALDAHVG 720
 NHIFNSAIRK HLKSKTVLFV THQLQYLVD C DEVIFMKEGC ITERGTHEEL MNLNGDYATI 780
 30 FNNLLLGETP PVEINSKKT SGSQKKSQDK GPKTGSVKKE KAVKPEEQQL VQLEEKQGS 840
 VPWSVYGVYI QAAGGPLAFL VIMALFMLNV GSTAFSTWWL SYWIKQSGSN TTVTRGNETS 900
 VSDSMKDNPH MQYYASIAL SMAVMLILKA IRGVVFKGT LRASSRLHDE LFRRLRSPM 960
 KFFDTPPTGR ILNRFSDMD EVDVRLPFOA EMFIQNVILV FFCVGMIAGV FPWFLVAVGP 1020
 LVILFSLVHI VSRVLIRELK RLDNITQSPF LSHITSSIQG LATIHAYNKG QEFHLRYQEL 1080
 35 LDDNQAPFFL FTCAMRWLAV RLDLISIALI TTTGLMIVLM HGQIPPAYAG LAISYAVQLT 1140
 GLFQFTVRLA SETEARFTSV ERINHYIKTL SLEAPARIKN KAPSPDPQGE GEVTFENAEM 1200
 RYRENLPVLV KKVSTFIKPK EGTIVGRGT SGKSSLGMAL FRLVELSGGC IKIDGVRISD 1260
 IGLADLRSKL SIIPQEPVLF SKTVRSNLD PNOYTEDQIW DALERTHMEK CIAQLPLKLE 1320
 SEVMENGDNF SVGERQLICI ARALLRHCKI LILDEATAAM DTETDLLIQE TIREAFADCT 1380
 40 MLTIAHRLHT VLGS DRIMVL AQGQVVEFDT PSVLLSNDSS RFYAMFAAAE NKVAVKG

Seq ID NO: 195 DNA sequence
 Nucleic Acid Accession #: NM_006470
 Coding sequence: 228..1922

1 11 21 31 41 51
 GCTGTCTCTGA GCCTGAGTAC TCTAGCTGCC TTGTCGCCAT CGCATCTGGC TGCCATCCAG 60
 CGCCAGCACAC CAGTAATGAG TGGCCGAGCT TCCTCTGGGA GGGAGGAAAC AGTTAAAAATC 120
 TTGCAGCAGC TGCAATCATC TAGGCGTGGT TCTCTGTCT GACTTGGGCT GCACAGATCC 180
 TGGGCCAAGG GACAGAAGAA AGACAGCCTA GGAGCAGAGC CTCCAGATG GCTGAGTTGG 240
 ATCTAATGGC TCCAGGGCCA CTGCCAGGG CCACTGCTCA GCCCCAGGCC CCTCTCAGCC 300
 55 CAGACTCTGG GTACCCAGC CCAGATTCTG GGTGAGCCAG CCCAGTGGAA GAAGAGGACG 360
 TGGGCTCCTC GGAGAAGCTT GGCAGGGAGA CGGAGGAACA GGACAGCGAC TCTGCAGAGC 420
 AGGGGGATCC TGCTGGTGAG GGGAAAGAGG TCCTGTGTGA CTTCTGCCCTT GATGACACCA 480
 GAAGAGTGAA GGCAGTGAAG TCCTGTCTAA CCTGTCATGT GAATTAAGT GAAGAGCACT 540
 TGCAGCCGCA TCAGTGTAAC ATCAAAGTGC AAAGCCACCT GCTGACCGAG CCAGTGAAGG 600
 ACCACAACCT GCGATACTGC CCGTCCCACT ACAGCCCACT GTCTGCTTTC TGCTGCCCTG 660
 60 ATCAGCAGTG CATCTGCCAG GACTGTTGCC AGGAGCACAG TGGCCACACC ATAGTCTCCC 720
 TGGATGCAGC CCGCAGGGAC AAGGAGGCTG AACTCCAGTG CACCCAGTTA GACTTGGAGC 780
 GGAAACTCAA GTTGAATGAA AATGCCATCT CCAGGCTCCA GGCTAACCA AAGTCTGTTC 840
 TGGTGTCCGT GTCCAGAGTC AAAGCGGTGG CTGAAATGCA GTTTGGGGAA CTCCTTGCTG 900
 CTGTGAGGAA GGCCAGGCC AATGTGATGC TCTTCTTAGA GGAGAAGGAG CAAGCTGCCG 960
 65 TGAGCCAGGC CAACGGTATC AAGGCCCACT TGGAGTACAG GAGTGCCGAG ATGGAGAAGA 1020
 GCAAGCAGGA GCTGGAGAGG ATGGCGGCCA TCAGCAACAC TGTCCAGTTC TTGGAGGAGT 1080
 ACTGCAAGTT TAAGAACACT GAAGACATCA CCTTCCCTAG TGTTTACGTA GGGCTGAAGG 1140
 ATAAACTCTC GGGCATCCGC AAAGTTATCA CGGAATCCAC GTTACACTTA ATCCAGTTGC 1200
 TGGAGAACTA TAAGAAAAAG CTCCAGGAGT TTTCGAAGGA AGAGGAGTAT GACATCAGAA 1260
 70 CTCAAGTGTG TGCCGTGTGT CAGCGCAAAAT ATTGGACTTC CAAACCTGAG CCCAGCACCA 1320
 GGGAAACAGT CTCTCAATAT GCGTATGACA TCACGTTTGA CCCGACACA GCACACAAGT 1380
 ATCTCCGGCT GCAGGAGGAG AACCGCAAGG TCACCAACAC CACGCCCTGG GAGCATCCCT 1440
 ACCCGGACCT CCCAGCAGG TTCTGCACT GCGCGCAGGT GCTGTCCAG CAGAGTCTGT 1500
 75 ACCTGCACAG GTACTATTTT GAGGTGGAGA TCTTCGGGGC AGGCACCTAT GTTGGCTGTA 1560
 CTGCAAAAGG CATCGACCGG AAAGGGGAGG AGCGCAACAG TTGCATTTC GGAACAACCT 1620
 TCTCTGGAG CCTTCAATGG AACGGGAAGG AGTTACAGGC CTGGTACAGT GACATGGAGA 1680
 CCCCACTCAA AGCTGGCCCT TTCCGAGGC TCGGGTCTA TATCGACTTC CCGGGAGGGA 1740
 TCCTTTCCTT CTATGGCGTA GAGTATGATA CCATGACTCT GGTTCACAA TTTGCTGCA 1800
 80 AATTTTCAGA ACCAGTCTAT GCTGCTTCT GGCTTTCCTA GAAGGAAAAC GCCATCCGGA 1860
 TTGTAGATCT GGGAGAGGAA CCGAGAAGC CAGCACCGTC CTTGGGGGTG ACTGCTCCCT 1920
 AGACTCCAGG AGCCATATCC CAGACCTTTG CCAGCTACAG TGATGGGATT TGCAATTTAG 1980
 GGTGATTGT GGGCAGAAAT AACTGCTGAT GGTAGCTGGC TTTTGAATC CTATGGGGTC 2040
 TCTGAATGAA AACATTCTCC AGCTGCTCTC TTTTGCTCCA TATGGTGCTG TTCTCTATGT 2100
 GTTTGCACTA ATTCTTTTGT TTTTCTTTGA GACGGAGTCT CGCACTGTTG CCCAGGCTGG 2160
 85 AGAGCAGTGG CGCATCTTGT GCTCACTGCA AGCTCCGCTT CCCGAGTTCA AGCAATCTCT 2220
 CTGCCCTCAG CTCCCGAGTA GCTGGGATTA CAGGTGCCTG CCACCAACAC CAGCTAATGT 2280
 TTTGTATTTT TAGTAGAGAT GGGGTTTCAC CATGTTGGCC AGGCAGATCT CAAACTCCTG 2340

ACCTCGTGAT GCACCCACCT CGGCCTCCCA AAGTGCTGGG ATTACATGCG TGAGCCACTG 2400
 CGCCCTGCCT GTTTGTAGTA ATTTTTAGGC ACCAAATCTC CCTCATCTTC TAGTGCCATT 2460
 CTCCTCTCTG TTCAGGTAA TGTCACTG TGCCAGAAAT GGATGACCAG GAACCTTAAA 2520
 GAGTGGCTGA AAAGATTGCA GAGTTATCAT AATAAATTGC TAACTTGCCT

Seq ID NO: 196 Protein sequence:
 Protein Accession #: NP_006461

1 11 21 31 41 51
 MAELDLMAFG PLPRATAQFP AFLSPDSGSP SPDSGSASPV EEEDVGSSEK LGRETEEQDS 60
 DSAEQGDPAG EGKEVLCDFC LDDTRRVKAV KSCLTCMVNY CEEHLQPHQV NIKLQSHLLT 120
 EPVKDHNWRY CPAHHSPLSA FCCPDQQCIC QDCCQEHSGH TIVSLDAARR DKEAELQCTQ 180
 LDLEKRLKLN ENAISRLLQAN QKSVLVSVSE VKAVAEMQFG ELAALAVRKAQ ANVMFLFLEEK 240
 EQAALSQANG IKAHLEYRSA EMEKSKQELE RMAAISNTVQ FLEEYCKFKN TEDITFPSPVY 300
 VGLKDKLSGI RKVITESTVH LIQLLENYKK KLQEFSSKEEE YDIRTQVSAV VQRKYWTSKP 360
 EPSTREQFLQ YAYDITDFDP TAHKYLRLOE ENRKVINTTP WEHPYPDLPS RFLHWRQVLS 420
 QQSLVLRHY FEVEIFGACT YVGLTCKGID RKGEERNSCI SGNFNSWSLQ WNGKEFTAWY 480
 SDMETPLKAG PFRRLGVIYD FPGGILSFYG VEYDNTMLVH KFAKCFSEPV YAAFWLSKKE 540
 NAIRIVDLGE EPEKPAPSLG VTAP

Seq ID NO: 197 DNA sequence
 Nucleic Acid Accession #: NM_004316
 Coding sequence: 433-1149

1 11 21 31 41 51
 CCGGAGACCC GGCGCAAGAG AGCGCAGCCT TAGTAGGAGA GGAACGCGAG ACGCGGCAGA 60
 GCGCGTTCAG CACTGACTTT TGCTGCTGCT TCTGCTTTT TTTTCTTAG AAACAAGAAG 120
 GCGCCAGCCG CAGCCTCACA CGCGAGCGCC ACGCGAGGCT CCCGAAGCCA ACCCGCGAAG 180
 GGAGGAGGGG AGGGAGGAGG AGGCGGCGTG CAGGGAGGAG AAAAAGCATT TTCACCTTTT 240
 TTGCTCCAC TCTAAGAAGT CTCGCGGGGA TTTGTATAT ATTTTAAAC TTCGCTCAGG 300
 GCTCCCGCTT CATATTTCTT TTTCTTTCCC TCTCTGTTCC TGCACCCAAG TTCTCTCTGT 360
 GTCCCCCTCG CGGGCCCCCG ACCTCGCGTC CCGGATCGCT CTGATTCGCG GACTCCTTGG 420
 CCGCCGCTGC GCATGGAAGC CTCTGCCAAG ATGGAGAGCG GCGGCGCCGG CCAGCAGCCC 480
 CAGCCGACGC CCCAGCAGCC CTCTCTGCC CCGCAGCCT GTTCTTTGC CACGGCCGCA 540
 GCCGCGCGCG CCGCAGCCGC CGCAGCGGCA GCGCAGAGCG CGCAGCAGCA GCAGCAGCAG 600
 CAGCAGCAGC AGCAGCAGCA GCAGGCGCGC CAGCTGAGAC CGGCGGCCGA CGGCCAGCCC 660
 TCAGGGGCGG GTCACAAAGT AGCGCCCAAG CAAGTCAAGC GACAGCGCTC GTCTTCGCCC 720
 GAACCTGATG GCTGCAAAAG CCGGCTCAAC TTCAGCGGCT TTGGCTACAG CCTGCCGCGAG 780
 CAGCAGCCGG CGCCCGTGGC GCGCCGCAAC GAGCGCGAGC GCAACCGCGT CAAGTTGGTC 840
 AACCTGGGCT TTGCCACCTT TCGGGAGCAC GTCCCCAACG CGCGGCCCAA CAAGAAGATG 900
 AGTAAGGTGG AGACACTGCG CTCGCGGCTC GAGTACATCC GCGCGCTGCA GCAGCTGCTG 960
 GACGAGCATG ACGCGGTGAG CGCCGCTTC CAGGCAGGCG TCCTGTGCGC CACCATCTCC 1020
 CCAACTACT CCAACGACTT GAACTCCATG GCCGGCTCGC CGGTCTCATC CTACTCGTCG 1080
 GACGAGGGCT CTTACGACCC GCTCAGCCCC GAGGAGCAGG AGCTTCTCGA CTTACCAAC 1140
 TGGTTCTGAG GGGCTCGGCC TGGTCAGGCC CTGGTGCAGG TGGACTTTGG AAGCAGGGTG 1200
 ATCGCACAA CTTGATCTTT AGTGCTTTCT TGTCAGTGGC GTTGGGAGGG GGAGAAAAGG 1260
 AAAAGAAAA AAAAGAAGAA GAAGAAGAAA AGAGAAGAAG AAAAAAACGA AAACAGTCAA 1320
 CCAACCCCAT CGCCAACTAA GCGAGGCATG CCTGAGAGAC ATGGCTTTCA GAAACCGGGA 1380
 AGCGCTCAGA ACAGTATCTT TGCATCCAA TCATTACAGG AGATATGAAG AGCAACTGGG 1440
 ACCTGAGTCA ATGCGCAAAA TGCAGTTGT GTGCAAAAGC AGTGGGCTCC TGGCAGAAGG 1500
 GAGCAGCACA CGCGTTATAG TAACTCCCAT CACCTCTAAC ACGCACAGCT GAAAGTTCTT 1560
 GCTCGGGTCC CTTACCTCC CGGCCCTTC TTAGAGTGCA GTTCTTAGCC CTCTAGAAAC 1620
 GAGTTGGTGT CTTTC

Seq ID NO: 198 Protein sequence:
 Protein Accession #: NP_004307

1 11 21 31 41 51
 MESSAKMESG GAGQQPQPQP QPFLPPAAC FFATAAAAAA AAAAAAQA QQQQQQQQQ 60
 QQQQAPQLRP AADGQPSGGG HKSAPKQVQR QRSSEPELMR CKRRLNFSGF GYSLPQQQPA 120
 AVARRNERER NRVLVNLGF ATLREHVPNG AANKMMSKVE TLRSAVEYIR ALQQLLDEHD 180
 AVSAAFQAGV LSPTTSPNYS NDLNSMAGSP VSSYSSDEGS YDPLSPPEQE LLDFTNWF

Seq ID NO: 199 DNA sequence
 Nucleic Acid Accession #: NM_007015
 Coding sequence: 1-1005

1 11 21 31 41 51
 ATGACAGAGA ACTCCGACAA AGTTCCTTCC GGCCTGGTGG GACCTGATGA CGTGGAAATC 60
 TGCAGCCCCC CGGCTACGCG TACGCTGACG GTGAAGCCCT CCAGCCCCGC GCGGCTGCTC 120
 AAGGTGGGAG CCGTGGTCTT CATTTCCGGA GCTGTGCTGC TGCTCTTTGG GGCCATCGGG 180
 GCCTTCTACT TCTGGAAGGG GAGCGACAGT CACATTACCA ATGTCCATTA CACCATGAGT 240
 ATCAATGGGA AACTACAAGA TGGGTCAATG GAAATAGACG CTGGGAACAA CTTGGAGACC 300
 TTAAAAATGG GAAGTGGAGC TGAAGAAGCA ATTGCAGTTA ATGATTCCA GAATGGCATC 360
 ACAGGAATTC GTTTTGCTGG AGGAGAGAAG TGCTACATTA AAGCGCAAGT GAAGGCTCGT 420
 ATTCTGAGG TGGGCGCCGT GACCAACACG AGCATCTCCT CCAACTGGA AGGCAAGATC 480
 ATGCCAGTCA AATATGAAGA AAATTTCTCT ATCTGGGTGG CTGTAGATCA GCCTGTGAAG 540
 GACACAGACT TCTTGAATTC TAAGGTGTTA GAACTCTGCG GTGACCTTCC TATTTTCTGG 600
 CTTAAACCAA CATTATCCAG AGGAAAGAA GAGAAGTGGT AAGAAAAATT 660
 GTTCCAACCT CCACAAAAG ACCACACAGT GGACACGGA GCAACCCAGG CGCTGGAAGA 720
 CTGAATAATG AAACAGACCC CAGTGTTCAC GAGGACTCAC AAGCCTTCAA TCCTGATAAT 780

CCTATATCATC AGCAGGAAGG GGAAAGCATG ACATTGACCC CTAGACTGGA TCACGAAGGA 840
 ATCTGTTGTA TAGAATGTAG GCGGAGCTAC ACCCACTGCC AGAAGATCTG TGAACCCCTG 900
 GGGGGCTATT ACCCATGGCC TTATAATTAT CAAGGCTGCC GTTCGGCCTG CAGAGTCATC 960
 ATGCCATGTA GCTGGTGGGT GGCCCGTATC TTGGGCATGG TGTGAAATCA CTTTCATATAT 1020
 CACGTGCTGT AAAATAAGAA CTAGCTGAAG AGACAACCAA AGAAGCATTG AGGCAGGTTG 1080
 ATGCTGATGG GACCATAAAA TATTTTACAC CGCAGCCTGA GCGGTTATTC TTGACACTCT 1140
 TAACAGAAAT TTTTAAATCG TTTTCCAGAA CTTTAGTATA TGCAGATGCA CTGAAAGGGT 1200
 AGTTCAAGTC TAAATGCGA TAACCCCGTT ATTTGTTATT TTTTATTGTC ATTGATTGTC 1260
 CATAAGTCTT CCCTTGCTTG CATCTTCCAA AGCTATTTTC AAATAAACAC GAAATTTTAC 1320
 AGTTTGCC

Seq ID NO: 200 Protein sequence:
 Protein Accession #: NP_008946

1 11 21 31 41 51
 MTENSADKVPV ALVGPDDVEF CSPPAYATLT VKPSSPARLL KVGAVVLISG AVLLLFGAIG 60
 AFYFWKGSDD HIYNVHYTMS INGLQDGSME EIDAGNNLET FKMGSAGAEA IAVNDFQNGI 120
 TGIRFAGGEK CYIKAQVKAR LPEVGAVTKQ SISKLEGEKI MPVKYEENSL IWVAVDQPVK 180
 DNSFLSSKVL ELCGDLPIFW LKPTYPKEIQ RERREVRKI VPTTKRPHS GPRSNPGAGR 240
 LNNETRPSVQ EDSQAFNPDN PYHQEGESME TFDPRLDHEG ICCIECRRSY THCQKICEPL 300
 GGYYPWPYNY QGCRSACRVI MPCSWWVARI LGMV

Seq ID NO: 201 DNA sequence
 Nucleic Acid Accession #: NM_000728.2
 Coding sequence: 112..495

1 11 21 31 41 51
 GTAATAAGAG CGGGGTCTCC GCGGGGAAGG CGCCACAGC AGGTGTGGTG TTCATCCCGG 60
 GTCGACCGGC CGCTCGCGCT GCCCTGAAAC TCTAGTCGCC AGAGAGGCGG CATGGGTTTC 120
 CGGAAGTTCT CCCCTTCTCT GGCTCTCAGT ATCTTGGTCC TGTACCAGGC GGGCAGCCTC 180
 CAGGCGGCGC CATTGAGTTC TGCCCTGGAG AGCAGCCAGC ACCCGGCCAC ACTCAGTAAA 240
 GAGGACGCGC GCCTCCTGCT GGCTGCACTG GTGCAGGACT ATGTGCAGAT GAAGGCCAGT 300
 GAGCTGAAGC AGGAGCAGGA GACACAGGCG TCCAGCTCCG CTGCCAGAA GAGAGCCTGC 360
 AACACTGCCA CCTGTGTGAC TCATCGGCTG GCAGGCTTGC TGAGCAGATC AGGGGGCATG 420
 GTGAAGAGCA ACTTCGTGCC CACCAATGTG GGTTCCAAAG CCTTTGGCAG GCGCCGCGAG 480
 GACCTTCAAG CCTGAGCAGA TGAATGACTC CAGGAAGAAG GTGTGTCCTA AATCCAATGA 540
 CATATCCTTA TAAGAGATTG ACTCAGAAGA CACATGTGGA GAAGGTGACA TGACAGAGGC 600
 AAGGAGGCAC AAGCCAAGGA AGTCTGTGTC TACCAGAAGC CAGAATCACA GAACAGTCTC 660
 TGAAGAAGA GCAGCCCTGC TGACACCTAG AGTTTGGACT TCCAGCTTCC AGAACTGTGA 720
 GAGAATAAAT TCTGTGTGTT TAAGCCACAA AGTTTGTGGT AATTTGTTAT GACAGCCCTA 780
 GGAAACTAAT ACAATACATT TTCAATTTAT TTGGGTAAAT GCCTTGGAGT GGGATTGCTG 840
 GGTATTTTGG AAAGTGTGTA TTAACTCTG TAAGAACTG CCAAACTATT TTCTGAAGTG 900
 ACTGTACCA TCGCCCTTCT TGCCAGCCAC ATATGAGAGC TCTAGTATT CCACAAATAG 960
 GTATGTAGCA GTATCTCAT GCTGTTTTAA TTGTATTTC CCAATGACT AATGACGTTG 1020
 AGCATCTATT TTACCATATG TTATCACCT TTATTGAAG GTCTGTTTTA ATCTTCTGCT 1080
 AAATTTTGTG TGCTTGTGCT GCTTTATTAG TGTGAGTTT TTAGAGCTCT TTATATGTTG 1140
 TGGATGCAAG ATTTGTTTCA GATATATAGT TTGGAACACT CCTTCCCTG AATCTGCGGA 1200
 TTGCTTTTTT ATTTTCTTAG CAGTGTCTCT CACAGAGAAA AAGTTGTAAT TTGAATAAGA 1260
 TCCAATTCAT CTTTTTTTTT CTTTTATGTA TTGTGCTTTT AGTTTCATGC TAAGAACTCT 1320
 TTGCCTAAC AAGGTCACCA GGTCAATA ACCTTATTCT ATACTTCTT GTAAAAGTTT 1380
 TATAGTTTAT TATTTTATAT GTAGATTAGT GATCTATTTT GAGTTAATTT TTGTATAAGG 1440
 TGAGAGGTGT AGGTGAAAT TCATACCTGT GAATATAGAT ACCCAATTGT TTCAGTGCCA 1500
 TTTGTTAAAA AGACTGTTAT TTCACCATTT AATTGCCCTT GCACCTTTGT CAAAAGCAA 1560
 CTGATCATAT TTGTGTGGGT ATATTCTGCG GTTCTCAATT CTGCTCTCAT GATTGATTG 1620
 ACCATTCTTT TGCCAATGTC ATACTGCCTT GATTAGTGA GTGTTAAAGT GAATCTCAAA 1680
 ACCAGATAAT GTGGGTCTAC CAACATTGTT CATTCTTGT CAAAAGATT TTAGCTACAT 1740
 CTAAAATATT TTCTACATCT TTTATACATT TTAGAATCAG TGTGTTACTA TCTACAAAAT 1800
 TTCTGATGAG ATTTTAAATG GTATTGTGTT AAATCAGTGG GTTAATTTTG GGAGAATTAG 1860
 CATATTAATA ATATTAAATG GTTCAATTCA TGAACACAA ACATGTTTTT ACTTATTTAG 1920
 GTTTTCTCTG TTTTTTTTTT TTTAACAAGT TTCTCAGTTT TCAACAGAAA TATTCTACAC 1980
 ATATCTTGTG AGATTTTAA CTATTTTATT TTTTGGTGCT AATGTAAATG GTACTTAAAC 2040
 ATTTTGTGTT TTAATTGTTT ATTGCTAGTA GATAGAAATA CAATATTTAA AATATTAGGA 2100
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA

Seq ID NO: 202 Protein sequence:
 Protein Accession #: NP_000719.1

1 11 21 31 41 51
 MGRFKFSPFL ALSILVLYQA GSLQAAPFRS ALESSPDPAT LSKEDARLLL AALVQDYVQM 60
 KASELKQEQE TQSSSAAQK RACNTATCVT HRLAGLLSRS GGMVKS NFVP TNVGSKAQFR 120
 RRRDLQA

Seq ID NO: 203 DNA sequence
 Nucleic Acid Accession #: NM_001741
 Coding sequence: 71..496

1 11 21 31 41 51
 CTCTGGCTGG ACGCCGCGGC CGCGCTGCGC ACCGCTCTG ATCCAAGCCA CCTCCCGCCA 60
 GAGAGGTGTC ATGGGCTTCC AAAAGTTCTC CCCCTTCTG GCTCTCAGCA TCTTGGTCTC 120
 GTTGCGAGCA GGCAGCCTCC ATGCAGCACC ATTCAGGTCT GCCCTGGAGA GCAGCCAGC 180
 AGACCCGCGC ACGCTCAGTG AGGACGAAGC GCGCTCTCTG CTGGCTGCAC TGGTGCAGGA 240
 CTATGTGCGA ATGAAGGCCA GTGAGCTGGA GCAGGAGCAA GAGAGAGAGG GCTCCAGCCT 300

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GGACAGCCCC AGATCTAAGC GGTGCGGTAA TCTGAGTACT TGCATGCTGG GCACATACAC 360
 GCAGGACTTC AACAGTTTC ACACGTTCCC CCAAAGTGA ATTGGGGTTG GAGCACCTGG 420
 AAAGAAAAGG GATATGTCCA GCGACTTGA GAGAGACCAT CGCCCTCATG TTAGCATGCC 480
 CCAGAAATGCC AACTAACTC CTCCCTTTCC TTCTTAATTT CCCTTCTTGC ATCCTTCCTA 540
 TAACTTGATG CATGTGGTTT GGTTCCTCTC TGGTGGCTCT TTGGGCTGGT ATTGGTGGCT 600
 TTCCTTGTGG CAGAGGATGT CTCAAATTC AGATGGGAGG AAAGAGAGCA GGAATCACAG 660
 GTTGGAGAG AATCACTCG GAAATACCA GAAATGAGG GCCGCTTTGA GTCCCCCAGA 720
 GATGTCATCA GAGCTCCTCT GTCTGCTTC TGAATGTGCT GATCATTGA GGAATAAAAT 780
 TATTTTTCCT C

Seq ID NO: 204 Protein sequence:
 Protein Accession #: NP_001732

1 11 21 31 41 51
 | | | | |
 MGFKQKSPFL ALSILVLLQA GSLHAAPFRS ALESSPADPA TLSEDEARLL LAALVQDYVQ 60
 MKASELEQEQ EREGSSLDSP RSKRCGNLST CMLGTYTQDF NKFTHTFPQTA IGVGAPGKKR 120
 DMSSDLERDH RPHVSMQNA N

Seq ID NO: 205 DNA sequence
 Nucleic Acid Accession #: NM_005361
 Coding sequence: 1-945

1 11 21 31 41 51
 | | | | |
 ATGCTCTTTG AGCAGAGGAG TCAGCACTGC AAGCCTGAAG AAGGCCTTGA GGCCCGAGGA 60
 GAGGCCCTGG CCTCGGTGGG TCGCAGGGCT CCTGCTACTG AGGAGCAGCA GACCGCTTCT 120
 TCCTCTTCTA CTCTAGTGGA AGTTACCTCG GGGGAGGTGC CTGCTGCCGA CTCACCGAGT 180
 CCTCCCCACA GTCCTCAGGG AGCCTCCAGC TTCTCGACTA CCATCAACTA CACTCTTTGG 240
 AGACAATCCG ATGAGGGGTC CAGCAACCAA GAAGAGGAGG GGCCAAGAAT GTTTCCCGAC 300
 CTGGAGTCCG AGTTCCCAAG AGCAATCAGT AGGAAGATGG TTGAGTTGGT TCATTTTCTG 360
 CTCTCAAGT ATCGAGCCAG GGAGCCGGTC ACAAAGGCAG AAATGCTGGA GAGTGTCTC 420
 AGAAATTGCC AGGACTTCTT TCCCGTGATC TTCAGCAAAG CCTCCGAGTA CTTGCAGCTG 480
 GTCTTTGGCA TCGAGGTGGT GGAAGTGGTC CCCATCAGCC ACTTGTACAT CCTTGTCAAC 540
 TGCCCTGGGC TCTCTACGA TGGCTGCTG GGCAGCAATC AGGTTCATGCC CAAGACAGGC 600
 CTCCTGATAA TCGTCTTGGC CATAATCGCA ATAGAGGGCG ACTGTGCCCC TGAGGAGAAA 660
 ATCTGGGAGG AGCTGAGTAT GTTGAGGTG TTTGAGGGGA GGGAGGACAG TGTCTTCGCA 720
 CATCCAGGA AGCTGCTCAT GCAAGATCTG GTGCAGGAAA ACTACCTGGA GTACCGGCAG 780
 GTGCCCGGCA GTGATCCTGC ATGCTACGAG TTCCTGTGGG GTCCAAGGGC CTTCAATTGAA 840
 ACCAGCTATG TGAAAGTCTC GCACCATACA CTAAAGATCG GTGGAGAACC TCACATTTCC 900
 TACCCACCCC TGCATGAACG GGCTTTGAGA GAGGGAGAAG AGTGA

Seq ID NO: 206 Protein sequence:
 Protein Accession #: NP_005352

1 11 21 31 41 51
 | | | | |
 MPLEQRSQHC KPEEGLEARG EALGLVGAQA PATEEQQTAS SSSTLVEVTL GEVPAADSPS 60
 PPHSPQGASS FSTTINYTLW RQSDGSSNQ EEEGRPMFPD LESEFQAALIS RKMVELVHFL 120
 LLKYRAREPV TKAEMLESVL RNCQDFPVI FSKASEYLQL VFGIEVVEVV PISHLYILVT 180
 CLGLSYDGLL GDNQVMPKTG LLIIIVLAIIA IEGDCAPEEK IWEELSMLEV FEGREDSVFA 240
 HPRKLLMQDL VQENLYEVRQ VPGSDPACYE FLWGPRALIE TSYVKVLHHT LKIGGEPHIS 300
 YPPLHERALR EGEE

Seq ID NO: 207 DNA sequence
 Nucleic Acid Accession #: NM_021115
 Coding sequence: 743-2893

1 11 21 31 41 51
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 CCCAAACTAA CTGGTGTCTT TTCTCTCTT CCAAGATGCT CTTCCCGAGG GAGATGCTAG 180
 CCCTTTGGGT CCTTACCTCC TGCCCTCAGG AGCCCGGAG AGAGGCAGTC CTGGCAAAGA 240
 GCACCTGAA GAGAGAGTGG TAACAGCGCC CCCAGTTCC TCACAGTCGG CGGAAGTGCT 300
 GGGCGAGCTG GTGCTGGATG GGACCGCAC CTCTGCACAT CACGACATCC CAGCCCTGTC 360
 ACCGTGCTT CCAGAGGAGG CCCGCCCAA GCACGCCTTG CCCCCAAGA AGAAACTGCC 420
 TTCGCTCAAG CAGGTGAAC CTGCCAGGAA GCAGCTGAGG CCCAAGGCCA CCTCCGCAGC 480
 CACTGTCCAA AGGGCAGGT CCCAGCCAGC GTCCAGGGC CTAGATCTCC TCTCTCTC 540
 CACGGAGAAG CCTGGCCAC CGGGGAGACC GGACCCCATC GTGGCCTCCG AGGAGGCATC 600
 AGAAATGCCC CTTTGGCTGG ACCGAAAGGA GAGTGCAGTC CCTACAACAC CCGACCCCT 660
 GCAAATCTCC CCCTTCACTT CGCAGCCCTA TGTGGCCAC ACACTCCCCC AGAGGCCAGA 720
 ACCCGGGGAG CCTGGCCCTG ACATGGCCCA GGAGGCCCCC CAGGAGGACA CCAGCCCAT 780
 GGCCCTGATG GACAAAGGTG AGAATGAGCT GACTGGGTCA GCCTCAGAGG AGAGCCAGGA 840
 GACCACTACC TCCACCATTA TCACCACCAC GGTATCATCC ACCGAGCAGG CACCAGCTCT 900
 CTGCACTGTG AGCTTCTCCA ATCCTGAGGG GTACATTGAC TCCAGCGACT ACCCACTGCT 960
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 CCGAAGCCCC ACCAACACCA TCTCCGTCTA CTTCGGACC TTCCAGGACG ACGGCCTTGG 1200
 GACCTTCCAG CTTCACTACC AGGCCTTCAT GCTGAGCTGC AACTTTCCCC GCCGCGCTGA 1260
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 CTGGAGCAGC CAGGAGCCCA TCTGCTCAGC TCCTTGTGGA GGGGCACTGC ACAATGCCAC 1440
 CATCGGCCGC GTCTCTCTCC CAAGTTACCC TGAACACACA AATGGGAGCC AATTCTGCAT 1500
 CTGGACGATT GAAGCTCCAG AGGGCCAGAA GCTGCACCTG CACTTTGAGA GGCTGTGCT 1560

5 GCATGACAAG GACAGGATGA CGGTTACAG CGGGCAGACC AACAGTCAG CTCTTCTCTA 1620
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 AAGGAATGAC TCCTGCTCGG ATTTACCCGA GATCCAGAAT GGCTGGAAAA CCACCTTCTCA 2340
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 15 GGGGAGTGAC ACCCTACCT GCGAGTGGGA CCTCAGCTGG AGCAGCGACC CCCCATTTTG 2460
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 GGATCTCTGT CTGCTGGTGG GGACCAACAT CCAATACACC TGCAACCCCG GTTTTGTGCT 2580
 TGAAGGAGT TCTCTTCTGA CTGCTACAG CCGTGAACA GGGACTCCCA TCTGGACGTC 2640
 20 TCGCCTGCCC CACTGCGTTT CAGAAGCGGC AGCAGAGAGC TCGCTGGAAG GGGGGAACAT 2700
 GGCCCTGGCT ATCTTCATCC CGGTCTCAT CATCTCCTTA CTGCTGGGAG GAGCCTACAT 2760
 TTACATCACA AGTAGTCCCT ACTATTCCAA CCTCGCCTG CCTCTGATGT ACTCCACCC 2820
 CTACAGCCAG ATCACCGTGG AAACCGAGTT TGACAACCCC ATTTACGAGA CAGGGGGAAC 2880
 CCAAAAGGTT TAGGGTTTCA TTTAAAAGA GGTACCCTTT AAAAAGGGGC TTGTGAATC 2940
 25 AACCCCAATT TCCCCGAGAC ATTTATCCAA AGGCCCTGGG GGCCTTGATT TAAACCCCA 3000
 AAAGGCGGCT GTTTTGTGGT TAAACTTTT AACAAAGGT TACGGGTTT TTCCCGGGAT 3060
 TTTATAAATT TTAAAGTG

Seq ID NO: 208 Protein sequence:
 Protein Accession #: NP_066938

35 1 11 21 31 41 51
 MAQEAPOEDT SPMALMDKGE NELTGSASEE SQETTTSTII TTTVITTEQA PALCSVSFSN 60
 PBGYIDSSDY PLLPLNLFLE CTYNVTVYTG YGVELQVKSV NLSGDGELL SI RGVDGPTLTIV 120
 LANQTLLEVG QVIRSPINTI SVYFRTFQDD GLGTFQLHYQ AFMLSCNFR RPDSDGVTVM 180
 DLHSGGVAHF HCHLGYELQG AKMLTCINAS KPHWSSQEP I CSAPCGGAVH NATIGRVLSP 240
 SYPENTNGSQ FCINTIIEAPE GQKLHLHFER LLLHDKDRMT VHSQGQTNKSA LLYDSLQTES 300
 40 VFPEGLLSEG NTIRIRFTSD QARAATFNI RFEAFKGGHC YEPYIQNGNF TSDPTYNIG 360
 TIVEFTCDPG HSLEQGPAIL ECINVRDPYV NDTEPLCRAM CGGELSAVAG VVLSFNWPEP 420
 YVEGEDCIWK IHVGEERKIF LDIQFLNLSN SDILTIYDGD EVMPHILGQY LGNSGPFQKLY 480
 SSTPDLTIQF HSDPAGLIFG KGQGFIMNYI EVSRNDSUSD LPEIQNGWKT TSHTELVRGA 540
 RTTYQCDPGY DIVGSDTLTC QWDLWSSDP PFCEKIMYCT DPGEVDHSTR LISDPVLLVG 600
 45 TTIQYTCNPG FVLEGSLLT CYSREGTPTI WTSRLPHCVS EAAAEISLEG GNMALAIPIP 660
 VLIISLLLG AYYIYTRCRY YSNLRPLPMY SHPYSQITVE TEFDNPIYET GGTQKV

Seq ID NO: 209 DNA sequence
 Nucleic Acid Accession #: NM_001327.1
 Coding sequence: 89-631

50 1 11 21 31 41 51
 AGCAGGGGGC GCTGTGTGTA CCGAGAATAC GAGAATACCT CGTGGGCCCT GACCTTCTCT 60
 CTGAGAGCCG GGCAGAGGCT CCGGAGCCAT GCAGGCCGAA GGCCGGGGCA CAGGGGGTTC 120
 55 GACGGGCGAT CTGATGGCC CAGGAGGCC TGGCATTCCT GATGGCCAG GGGGCAATGC 180
 TGGCGGCCCA GGAGAGGCGG GTGCCACGGG CCGCAGAGGT CCCCAGGGCG CAGGGGCAGC 240
 AAGGGCCTCG GGGCCGGGAG GAGGCGCCCC GCGGGGTCCG CATGGCGGCG CGGCTTCAGG 300
 GGTGAATGGA TGCTGAGGAT GCGGGGCCAG GGGGCCGGAG AGCCCGCTGC TTGAGTTCTA 360
 60 CCTCGCCATG CTTTCGCGA CACCCATGGA AGCAGAGCTG GCCCGCAGGA GCCTGGCCCA 420
 GGATGCCCCA CCGCTTCCCG TGCCAGGGGT GCTTCTGAAG GAGTTCACTG TGTCCGGCAA 480
 CATACTGACT ATCCGACTGA CTGCTGCAGA CCACCGCCAA CTGCAGCTCT CCATCAGCTC 540
 CTGTCTCCAG CAGCTTTCCC TGTGTATGTG GATCACGCGA TGCTTTCTGC CCGTGTTTTT 600
 GGCTCAGCCT CCTTCAGGCG AGAGGCGCTA AGCCAGCCT GGCGCCCTT CCTAGGTCAT 660
 65 GCCTCCTCCC CTAGGGAATG GTCCAGCAC GAGTGGCCAG TTCATTGTGG GGGCCTGATT 720
 GTTTGTGCGT GGAGGAGGAC GGCTTACATG TTTGTTTCTG TAGAAAAATA AACTGAGCTA

Seq ID NO: 210 Protein sequence:
 Protein Accession #: NP_001318.1

70 1 11 21 31 41 51
 MQAEGRGTTG STGDADGPGG PGIPDGPGGN AGGPGEAGAT GGRGPRGAGA ARASGPGGGA 60
 PRGPHGGAAS GLNGCCRCGA RGPESRLLEF YLAMPFATPM EABELARRSLA QDAPPLPVPG 120
 75 VLLKEFTVSG NILTIRLTAA DHRQLQLSIS SCLQLSLLM WITQCFPLPVF LAQPPSGQRR

Seq ID NO: 211 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 52-459

80 1 11 21 31 41 51
 CCTCGTGGGC CTGACCTTC TCTCTGAGAG CCGGGCAGAG GCTCCGGAGC CATGCAGGCC 60
 GAAGGCCAGG GCACAGGGGG TTCGACGGGC GATGCTGATG GCCCAGGAGG CCCTGGCATT 120
 85 CTTGATGGCC CAGGGGGCAA TGCTGGCGGC CCAGGAGAGG CCGGTGCCAC GGGCGGCAGA 180
 GGTCCCCGGG GCGCAGGGGC AGCAAGGGCC TCGGGGCCGA GAGGAGGCGC CCGCGGGGT 240
 CCGCATGGCG GTGCCGCTTC TGCGCAGGAT GGAAGGTGCC CCTGCGGGGC CAGGAGGCCG 300

GACAGCCGCC TGCTTCAGTT CCGACTGACT GCTGCAGACC ACCGCCAACT GCAGCTCTCC 360
 ATCAGCTCCT GTCTCCAGCA GCTTCCCTG TTGATGTGGA TCACGCACTG CTTTCTGCCC 420
 GTGTTTTTGG CTCAGGCTCC CTCAGGGCAG AGGCGCTAAG CCCAGCCTGG CGCCCCCTCC 480
 TAGGTTCATGC CTCTCCCTC AGGGAATGGT CCCAGCAGCA GTGGCCAGTT CATTGTGGGG 540
 GCCTGATTGT TTGTCGTGAG AGGAGGACGG CTTACATGTT TGTTCTGTGA GAAATAAAG 600
 CTGAGCTA

Seq ID NO: 212 Protein sequence:
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MQAEGQGTGG STGDADGPGG PGIPDGPGGN AGGPGGAGAT GGRGPRGAGA ARASGPRGGA 60
 PRGPHGGAAS AQDGRCPGCA RRPDSRLQLF RLTAADHRQL QLSISSCLQQ LSLLMWITQC 120
 FLVPVFLAQAP SGQRR

Seq ID NO: 213 DNA sequence
 Nucleic Acid Accession #: NM_000555
 Coding sequence: 416..1498

1 11 21 31 41 51
 CTTATTTTTT ATGAATGTGC GATAGCTGCA CCAGCTTGGT GGGGAAAGGG TTGATGAAT 60
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 TCTGGGGGGA GGGGATGCAC ACATTAGAGT AGGAAAGAGG GCTTGGAAATA AAATGAAAAC 180
 ACTCCCCCTT CATAGTCATT GTACTGAAAT GCAAAGACTG CTTCTTAAGC TGGAGATGCT 240
 AACCTTGGGT AGCTCCTTCT GTTCTCTTCA AGGGGAATTT TGTCAGGCTA TGGATTCAAT 300
 TACAACCTGT AGTCATGTGG GCATGTGTGA GGAACAGAT GCCAGTTTAA ATGTATTTAG 360
 CCCGAAGTTC CAATTTGATA GGAGCCACTG TCAGTCTCTG AGGTTCCACC AAAATATGGA 420
 ACTTGATTTT GGACACTTTG ACGAAAGAGA TAAGACATCC AGGAACATGC GAGGCTCCCG 480
 GATGAATGGG TTGCCTAGCC CCACTCACAG CGCCCACTGT AGCTTCTACC GAACCAGAAC 540
 CTTGCAGGCA CTGAGTAATG AGAAGAAAGC CAAGAAGGTA CGTTTCTACC GCAATGGGGA 600
 CGCCTACTTC AAGGGGATGT TGTCACGTGT GTCTCTGAC CGTTTTCGCA GCTTTGACGC 660
 CTTGCTGGCT GACCTGACGC GATCTCTGTC TGACAACATC AACCTGCCTC AGGGAGTGCG 720
 TTACATTTAC ACCATTGATG GATCCAGGAA GATCGGAAGC ATGGATGAAC TGGAGGAAGG 780
 GGAAGCTATG GTCTGTCTCT CAGACAACTT CTTTAAAGAG GTGGAGTACA CCAAGAAATG 840
 CAATCCCAAC TGGTCTGTCA ACGTAAAGAC ATCTGCCAAT ATGAAAGCCC CCCAGTCCCT 900
 GGCTAGCAGC AACAGTGCAC AGGCCAGGGA GAACAAGGAC TTTGTGCGCC CCAAGCTGGT 960
 TACCATCATC CGCAGTGGGG TGAAGCCTCG GAAGGCTGTG CGTGTGCTTC TGAACAAGAA 1020
 GACAGCCCAAC TCTTTTGAGC AAGTCTCTAC TGATATCACA GAAGCCATCA AACTGGAGAC 1080
 CGGGGTGTGT AAAAACTCTC AACTCTGTGA TGGAAACAGG GTAACTGTCT TCCATGATTT 1140
 CTTTGTGTAT GATGATGTGT TTATTGCTGT TGGTCTGAA AAATTTGCGT ATGCTCAGGA 1200
 TGATTTTCTC CTGGATGAAA ATGAATGCCG AGTCATGAAG GGAAACCCAT CAGCCACAGC 1260
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 CCGAAGCAAG TCTCCAGCTG ACTCAGCAAA CGGAACCTCC AGCAGCCAGC TCTCTACCCC 1380
 CAAGTCTAAG CAGTCTCCCA TCTCTACGCC CACCAGTCTC GGCAGCTCC GGAAGCACAA 1440
 GGACCTGTAC CTGCCTCTGT CCTTGGATGA CTGGGACTCG CTTGGTGATT CCATGTAAAG 1500
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 CACTGATCCA CAGTTACCAA TTATGAGAGA TAGATTGATA ACCATCCTTT GGGGCAGCAT 1740
 TCCAGGGATG CAAAATGTGC TAGTCCATGA CTTTCAATG GAAAGCTTAG GGGCCTGGGG 1800
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 ATACAGCAAT TAAAAGTTT GTGTGGGAAA AAAAAAACT CATTGGCAGA TCCAAGAAATG 1920
 ACAAAACAAA GTGCCCTTT TCTCTGGATC TCAAGAAATG TGGAGGACCC TGAAGGACA 1980
 GCAAGGCAGC TCCCCGCTC CACTCTTCAC TCTGATTGTA GGCCCGGTT TGTGTGCCAG 2040
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 TGCTTAGGAT CCTGGTGTG GGTAGCTAA GAGAATAGAC AGAATTGGA AATACTGCAG 2160
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 TTTGGAATCA ATAAGCAATT GATAATAGTT TGGAGTAAGG GACTTCATAT ACCTGATTCC 2280
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 CATGTCTGTA TTTCAGGAGC AAACCTCTCA GGCTCCTTT TTATAAACTG GTGATTTTTC 2520
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 ATGTTATTTA GAAATTATGC TGTCACTGCC AAACAGTAAC CTCCAGGAGA AAACAGATG 2640
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 ATATTTTAA GCACTCTTTT TATCTATAAT CTAATATTT CATACTGAAG ACACAGAAAT 2820
 CTTTCACTTG TCTTTAATC TAGAAAGGAT TTCTCTTTAC TAAGGACTGA TCATTGAAA 2880
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 GCCCATAATG GCAAAAAACAA CTAATTTTAA TTGAAGGTCT TGCTTGCCAN TCTGTGTTG 3000
 GCTTTNACCA AATATAAAAA TTCCCTTATT CTTTGGTAAT GGTGCAAAAT TTTGAAAGG 3060
 CACAGCATCC AAACCAAGCT GCTGTTTGGC TACTGAATGG CTTGCAGTTG TTCTTCCACT 3120
 CTAAATGGAA TGAGCTTGCT GTGTGTGTGT GTGGTGGTGG TGGGAGGGGG TGGTGCATGT 3180
 GTGTGTGTGT GTGTGATCT GCAGCTGCTT CAAAATTAAG AAATACTACA AGACACCCCT 3240
 GTAATGGATT GGTGGCAACT GGTGGGCACT GCTGATGTGC ACTGTGTAGG GGGGAACCCA 3300
 GTGGTGGTGG GGTATCTCAA ATGCCCTAG ACAAGCTTCA GATGTCTGTA GCTACCAAAA 3360
 ACATTTTCGG TTCAAGAAAA GTGAGATGAT GGTAGTACTG GTTCTGGTG AAATTGAAAA 3420
 ACCCCAAATG ATGAGGATCT CTTTGTGCCC CTTCTCTTT TTTTGTAAAC CCATTCAAAA 3480
 CCATTAATAA GCCCAATTTT TAANCCCTCT ATTTCTTTCT AGAAGCTCAG GGTTNCTTA 3540
 GTGCCTCCCA NAACATTTTG TAGTTAATTG GGAAGAAAGT ATACTTGGAT TAGGGGGTGT 3600
 GGGCATAAAG AATGGTGGGA GGCCTGATTT TAAAATTCAG GCCAGAACCC CCAATGACTC 3660
 CACCCATAGT NTCACTTTAG GTCTCATTTA GTCCATCACC TTTATTTTAA GTTGAGGAAG 3720
 TGGAGGCTGG TAAAGAGGAG GACCAGAGGA AGAATCCAGA TTTCTTATG CTTGGGCCCTC 3780
 AACTAGCTC TGTGAGTATT TCCTTGATTG CGGTATATGT ACTACTAGAA AATACCAAT 3840
 GGATATATTT TCTTTAGGAT AACCTTTGAA CCAACAATNT TCAATAACAA TAGTACATCT 3900

	TCCATCTTAC	TTTTAATCGA	GTATAAGGAA	ATGTTTCTTT	ATGGCCATT	TGGAGGGAGC	3960
	AGGGGATGAG	GCTTGGCATA	GTCCAAAAAT	TAAGNCTCCA	ATAATTAATT	GCATTTTAAA	4020
	TTGTTTTAAA	TTGGGCCACT	TTCAAGGCAA	TTTTTTTTGT	GTGCTGTGAA	CTGAGCTCCT	4080
5	CCACCCCTGT	CATTCACTTC	CAATTTTACC	CAATCCAATT	TTAGCACTCA	AGTTCATTG	4140
	TGTTAATTTT	TGCACGGTCT	ACACACATCA	AGTCAGCAAG	CATTTGCCAC	CACTCCCTAT	4200
	ACTTCTCCCT	CTTTTTTACA	CACACACACA	CACACACACA	CACAATCCAT	CTCTTGCTTG	4260
	TTCTCTACCT	CCTGATTTTT	CTTCCCTACA	GAAATAGAAA	TAGGGACAAA	GAAGGGGAAA	4320
	ATGTATATAT	TGGGGCTGGG	CTGAACAAC	AACCTCATAA	GTAGTATTAA	CTAGGGGTAA	4380
10	ATTGAGAGAA	AAGCTCCTTT	TCTCTTCACT	GTTTTGGAAA	GGATAGCCAT	TAGCATGACT	4440
	GCTTTGTGCT	CTTATGGACT	TTAGTATTAG	CCTAGATTGA	ATTATAGCGT	TTTTCTAGCT	4500
	GAAGGAACCT	TAAGATCACA	TCATCTACTC	CTCTACTCCA	AATTTCTCAT	TCTTCAGGCC	4560
	AGGAAACCGA	GACACAGAGG	TAAAGTAATT	TCCCCAAGGT	CACACAGCTG	GCTGGGGCAG	4620
	GATTGGGT	ACAACCCACA	TCTCTGGCT	CTTATTCCAG	GGCCTTTTCC	CACTAAGTAG	4680
15	TATTGCCTTC	CATTAGGCTC	CTGAGAGTTA	TTTCTCAGGG	TCATGTTGCA	TCTTGGAGCC	4740
	ACATGCTGCT	GCCTGATCT	CAGTGGGAAA	TNCAACCAGC	AACCTAATAC	AGCCCCCTTT	4800
	CCCTGCATT	ACCTGGTTCC	CATCCACATG	GGTTGCAGAT	TCTCTGAAG	AGAGTGAGGC	4860
	ATTGAGGGCC	AATAGGAGCA	ATGGGGTCCC	TGGCCTTGTC	CATCTGATT	AGGAGATCAC	4920
	TGCTCCATCG	TGAGGAGCTC	TCTGAATAGC	CCCCCACTGA	ATGCTTGCCT	TGCCCAAATG	4980
20	GAATGGAGGA	AGATTGATTT	TCTCCATCAG	TTACCTTGT	GTCTCTCAT	AATGGTTGGT	5040
	CTTTCAGGCG	TGAGGGAAT	GTCTCTGTT	TCCANAGTAN	AAAAAAGAAA	GAGTGGAAAC	5100
	ATANCTTGT	TCATCTTAAC	TTCTGAGAT	GGCTTTTCAA	CATTTAAAAA	AAACTAGTGT	5160
	GGTACCATT	ACTGGCANGA	TTNTTTTTAG	AATATGGGAG	TAAGATGAGG	TAGAGAAAAT	5220
	AACCTGGTCT	CACCTGGGTT	GCCTCATCC	ACAATGTCCC	CAAAGCCATC	CTGCTNTGAT	5280
25	GAGGACAAAT	TCCAGTATC	AGCAAGGGGC	TTTGTGACAA	AAATGTACCC	TGGCTGATGT	5340
	TAAACATTGG	CTCCTGTGTT	TGCACCAAAA	TAGCAAGCTG	TGTGCTCTAT	ACACTCTTCC	5400
	CATCGTCTTG	TGTACACTGC	TCTGTGGGCC	TTCCACAGCA	GAACCCAGGG	CAAAAGGGTC	5460
	CAAACACATG	GTCTTCTGTT	CTGCAAGGCT	NTTCTGGGA	ACTAAGGGGG	TATTTATTAG	5520
	TTTCAGTTNTA	AGAGACCTCC	TTCTGGGCTT	ACCCCACTCC	TCAGGTACTT	CTCTCTCCTT	5580
30	CTCTCTCTC	CTCCACATG	ACAAGTAACC	AAGGAACCTG	AAAGTGGATG	TGTAGCTATT	5640
	TGAAGAAGGC	AAGGAACCTT	GAGATTCTTC	TTTGAATCCT	TTAGTCCAAG	TCTTAGACCA	5700
	GTGATTGGTG	CTTACCTTGA	ACAAAATTTT	GTCTGTGTTT	CTAATCCCTT	CAATACNTG	5760
	GGTACAAATG	TCCCAATCAC	CTGACACATT	TGATTCTAAA	TGGCTTTTAT	TTTTTAAAAA	5820
	TCCATATCCC	TAGGACAAGA	NAACAGGATG	CCTATATCCC	CAAAATGAGC	TCCAGGACAC	5880
35	TGATGGGAAT	GATCCCAANG	ATCACCCAC	CTCAGAAAAC	GTCTGTGCCA	ANAGACTTCC	5940
	CCAGATAGAA	NCACTGGGAC	AGTGGTTTGA	ACGACTTCTT	TTATGGTTGT	CCAGTTTGCT	6000
	ATGGAATAAA	AAGGCATTGA	TTTTTTAAAA	AAGATGATTG	GAACCTGTCT	TGGGCCACAT	6060
	AGGGCCACTT	GCATCTCTT	CCAGGCCTTA	CTCATATATT	GCCTTCACTG	AAGGGCTTTG	6120
	GCTTTAAGTC	CCAGACTGGT	CTCCCAAGTG	AACCATAGT	GTTTTGGAGC	TCATCTGGGG	6180
40	TGAGGCATGA	GAATGTTGCC	CCATCTATCC	CTTCAGGAAA	AGGTGCCTTC	CCTCCCTTTC	6240
	TCCTAAAGCC	TGGTCCCCAA	AAATGTTTTT	TGTCTCCAAA	AGTCTAGTAT	GGTCTTTATA	6300
	CACCCANACT	CTTAGTGTG	CGTCTGCCT	TGTTTCTTTC	TTAAGGATCT	ATGCANACCT	6360
	CCCGCTTTGG	CTTAGCTAGC	GTGACATTGG	CTATCATTTC	ACAAGACTAA	CTTTTTTTTT	6420
	TTTTTTTTTTG	ACTGAGTCTC	CCTCTGTAC	CTAGGCTGGA	GTGCGTGGC	ACAATCTTGG	6480
45	CTCGCTGCAA	CCCTCACCTC	TCACCTCCCA	GGTCGAAGCG	ATTCTCCTGC	CTCAGTCTCC	6540
	CGAGTAGCTG	GGATTACAGG	CGTGCGCCAC	CAAATCTGGC	TATTTTTTTA	TTATTATTAT	6600
	TTTTTAGTAGA	GATGGGGTTT	CACCATGTTG	GCCAGACTGG	TCTTGAACCT	TTGGCCTCAA	6660
	ATTATCTGCC	CACCTCGGCC	TCCCAAAGTG	CTGGGATTAC	AGGCATGAGC	ACCATGCCCA	6720
	GCTGACAAGA	CTAATTTTTT	ATCCCTTGGT	TTATTGGCTT	CAACATCTTC	TGGAATCAGA	6780
50	GGTGATTTTT	TCTTACCTTG	GATGCCTGAG	ACTAGGGGAG	TATAGAATTC	CAATTGGTAA	6840
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	CAACAGAAGT	CACTTTGTAA	GTAAGGCAAA	GACTTTGAAG	GCATTAGCGT	TTCTCATTAC	6960
	TAGGTCAT	AACCTTGAGG	GAATCAATGG	CTTTTTTGCC	GCTCTACCTC	TTTGTGTATC	7020
	TTCTTTGACTT	TTCTTTCTCT	GTCTAGTTTC	CTCTGTTCTC	AGTTTATATT	CTATGTTATC	7080
55	AGTCTCTCTT	TCCACAGTAC	AAACATCCAT	CCTTCTCCTT	GTGCAATTCT	GTCTCTCCCT	7140
	CTTATTATCT	TTATTGTATC	TTTTTCTTTC	CTCCCTGTCT	AGGCATTGGG	CATGTGCCTC	7200
	TTCTTAGCCT	GTGATTTTGC	CTTGGGACTG	ATGATAAATT	ATTTCCAGAT	TCAATCAGCC	7260
	CTGGTCTTAC	CCCAGTCCAA	TCAGAAATAT	GTGGTGGGG	AATCAACCTG	ATCCTGGCCC	7320
	TTTCTTCTTC	TCCATTTTCA	TTCTGAATCC	CCCTCAGCAG	ATCTTTACAA	GCAGTTTCTT	7380
60	TATAGCTCAT	GTATCTTTAG	GTCTTTGCCT	TCCAAGCACT	GTACAGAATA	CTTTGTGGTT	7440
	CCTTTTGTAGT	CTGACATTTT	GTGGAGCAGT	GAAGCGTGCT	CAGAGACATA	ATCAGCTGAA	7500
	GAGAAAAAAT	CAACCCATGG	ATTTATATCA	GCTAAATACT	AATAATTGAT	TTTGTTTGAT	7560
	GTGCCATAAA	TTTTTAAAGC	TGCAATATAA	TATAATGAGG	GACCACAGST	AATTTCTCCT	7620
	GTCAATTGTT	TTGGCTGGAT	GGGGGTGGGG	GAGTAATTGC	TTAAAGTTTT	ACCATTACAC	7680
65	ATTAACACTCT	CTATAATAAT	CTTGTTTGGG	GCTTGCTAAC	TGTTGAGCTG	TTTTAACTAA	7740
	ACTGGTAGGC	AATCGGAGTT	GATTTAAATG	AAAAGATAAT	TTAACAAATC	TATACTATAA	7800
	AAAGAGACAT	TTGCTTAATT	GACATGTATT	TTTTCTTCT	GAGTCACCTA	AACATTTACT	7860
	CTTGACACCA	ACTGTTTCAT	ATACTGAATA	GACAGTCCAT	ATAAGAGAAA	TTAGTGGACC	7920
	TAAAGAAGCC	AGATTGTAGG	TGTTAATTTA	TTAAACAGAA	TTGCAAGGCC	CTTGGAAATG	7980
70	TCAGTGGTTG	GCAATACCAT	ATGGCATGCC	AAAATTTACA	ATGACTTTTC	TTTATAAGTT	8040
	ATCCAAAAGG	GATTTGAACA	AGTAAGAGGT	TATGCCAAAA	TGTCTCCAAT	GTATGGTCTT	8100
	GTAATATATT	GCAGCTTGAA	GCCATGATC	CCTTATGACT	TGTATACAA	TAATGCATGT	8160
	TTTATTGAAT	TTTGCAATTC	CCACGTGTGG	TAAGTCTTTA	AAATGTTTTT	GATCACCTTT	8220
	NTGTGCCATT	AAACTTGTAC	AGAAAATGTT	TTTATGGCCA	TTTTCAAAGG	GAGAAAGTTT	8280
75	AAAATGGAAA	CAGCCCAACC	TTTCTGCCCT	ATAGCTGTAG	TTAGAATTGA	GTACCTGTAG	8340
	CAAAACAGCT	GTAATTGGTG	GTGTAGTGT	TAGAGGTGTT	AGCTTGCTAG	TGACTAGCTT	8400
	TGGAGAGTAA	ATGCATGGTA	TTGTACATCA	CATTTCTTAA	CTCGTTTTAA	CCTCTGAAAA	8460
	GAATATATTC	TTCTTTGTAG	TCTTCTTCC	CACCCCTTTC	CCCTCTCCCT	CTCCCTGCTC	8520
	CCAGTTGTCT	TACAGTTGTA	AATATCTGAT	TTGAGGCCCA	ATAACTCTTG	CCAAGTAAAG	8580
	TCAGCAAAAC	ACAAACAAAC	CAAAATGTGG	GGAAAAGGCA	TTTCTCAACC	ATCTCTCAGC	8640
80	AGTTATTGAT	GATTTCTTAA	GGAAACAGCAT	TGTGATCAAA	GACTCAACTT	TACGTAAAAA	8700
	TCAGTGGTAA	ATTGGGGTTG	TATTGGCCAT	TGATTACATT	CAGGATTGAA	TAGTTTTCAG	8760
	AATACATGT	AATCCAAAGA	CAGTAGGTAG	TGATGTCCTT	TATCCCTGCA	GCTGTTTTAA	8820
	GATAGAGACC	TCAGAAGACT	CTGCTTGACC	GATGACCAAT	AATTATTGTA	AAAAAAAAGA	8880
	AAAAATGAGA	AAAAATAAAC	AGATATTTAA	GAACTTTAGC	CACCTATTTA	GAATAGTTAT	8940
85	AGCCAGAAAA	AAAAACAAGG	GCATGAGTTC	AAATGCATTA	CTATCAGTGT	CCTAGGCAAT	9000
	ACCTAACCTA	CTCTGAAATT	GTGATTCAAA	AGCAGTATTT	CAAGAGGCAT	TCTCCTTTTT	9060
	TGGTTTGCTG	ACCCCACTTG	GACTGGTAGG	TTGGTGAGG	CCCCCATAAA	CCAGCTGGAG	9120

CAGACCCCTT TCATCTCCTG TGCCTGTAAC ACCCTCTCTC CCCCACCCCC TCCGCAATTC 9180
 AATGAGGGCT TTCTTGGGTC AGAGGACTTC AAGGTGTCT AGAGAAGTT GCCATGTGTG 9240
 TAAGTGTCTG TGAACGTGTA GTGCTGAAGA TTCGCAGCAT TCAATACCAG GCAGCCAAAG 9300
 AGCTGCTCTT GCAATTATTT TGGCTCTCAA GCTCTGTCTC TCATCGCATT CTCATTTCTG 9360
 TGTACATTTG CAAGATGTGT GTAATGTCAT TTTCACAAAA TAAATTTGA TTTCAT

Seq ID NO: 214 Protein sequence:
 Protein Accession #: NP_000546

1 11 21 31 41 51
 MELDFGHFDE RDKTSRNMRG SRMNGLPSP T HSAHCSFYRT RTLQALSNEK KAKKVRFYRN 60
 GDRYFKGIYV AVSSDRFRSF DALLADLTRS LSDNINLPQG VRYIYIDGS RKIGSMDELE 120
 EGESYVCSSD NFFKKVEYTK NVNPNWSVNV KTSANMKAPQ SLASSNSAQA RENKDFVRPK 180
 LVTIIRSGVK PRKAVRVLLN KKTAFSFEQV LTDITEAIKL ETGVVVKLYT LDGKQVTCILH 240
 DFFGDDDVFI ACPGPKFRYA QDDFSLDENE CRVMKGNPSA TAGPKASPTP QKTSKSPGP 300
 MRRSKSPADS ANGTSSSQLS TPKSKQSPIS TPTSPGSLRK HKDLYLPLSL DDSDSLGDMS

Seq ID NO: 215 DNA sequence
 Nucleic Acid Accession #: NM_130467
 Coding sequence: 312..644

1 11 21 31 41 51
 GGCACGAGGC AGAGCTCTGC AAGGAGAGGT TGTGTCTTCG TTCTTTCCGC CATCTTCGTT 60
 CTTTCCAACA TCCTTCGTTCT TTCTCACTGA GCCGGTAGGT CTGCAGAGTG 120
 GTCTTCCTGG TAAATTAGTT GTGAGTGAAT GTGTGGAGGA GCCAGCGGGC TTAGGACAGG 180
 TCCTGTGGCA CAGTCCGTGG CTTTGAGGGA AAAGGGCCTC GCGGTGGTCC TCCGCCTTCC 240
 CCCAGGTCGT GATGCAGGCG CCATGGGCGG GTAATCGTGG CTGGGCTGGA ACGAGGGAGG 300
 AAGTGAGAGA TATGAGTGAG CATGTAACAA GATCCCAATC CTCAGAAAGA GGAAATGACC 360
 AAGAGCTTTC CCAGCCAGTT GGACCTGTGA TTGTCCAGCA GCCCACTGAG GAAAAACGTC 420
 AAGAAGAGGA ACCACCAACT GATAATCAGG GTATTGCACC TAGTGGGGAG ATCAAAAATG 480
 AAGGAGCACC TGCTGTTCAA GGGACTGATG TGGAAAGCTTT TCAACAGGAA CTGGCTCTGC 540
 TTAAGATAGA GGATGCACCT GGAGATGGTC CTGATGTCAG GGAGGGGACT CTGCCCACTT 600
 TTGATCCAC TAAAGTGCTG GAAGCAGGTG AAGGGCAACT ATAGGTTTAA ACCAAGACAA 660
 ATAAGACTG AAACCAAGAA TATTGTTCTT ATGCTGGAAA TTGACTGCT AACATTCTCT 720
 TAATAAAGTT TTACAGTTTT CTGCAAAAAA AAAAAAAAAA AAA

Seq ID NO: 216 Protein sequence:
 Protein Accession #: NP_569734

1 11 21 31 41 51
 MSEHVTRSQS SERGNDQESS QPVGPIVQQ PTEEKREEE PPTDNQGIAP SGEIKNEGAP 60
 AVQGTDFEAF QQELALLKIE DAPGDGPDVR EGTLPFDFT KVL EAGEGQL

Seq ID NO: 217 DNA sequence
 Nucleic Acid Accession #: NM_001476.1
 Coding sequence: 82..435

1 11 21 31 41 51
 GCCAGGGAGC TGTGAGGCAG TGCTGTGTGG TTCTGCGCGT CCGGACTCTT TTCTCTCTAC 60
 TGAGATTCTAT CTGTGTGAAA TATGAGTTGG CGAGGAAGAT CGACTATTA TTGGCCTAGA 120
 CCAAGGCGCT ATGTACAGCC TCCTGAAGTG ATTGGGCCCTA TGCGGCCCGA GCAGTTCACT 180
 GATGAAGTGG AACCAGCAAC ACCTGAAGAA GGGGAACCAG CAACTCAACG TCAGGATCCT 240
 GCAGCTGCTC AGGAGGGAGA GGATGAGGGA GCATCTGCAG GTCAGGGGCC GAAGCCTGAA 300
 GCTGATAGCC AGGAACAGGG TCACCCACAG ACTGGGTGTG AGTGTGAAGA TGGTCTGAT 360
 GGGCAGGAGG TGGACCCGCC AAATCCAGAG GAGGTGAAAA CGCCTGAAGA AGGTGAAAAG 420
 CAATCACAGT GTTAAAGAA GACACGTTGA AATGATGCAG GCTGCTCCTA TGTGGAAGAT 480
 TTGTTTATTA AAATCTCTCC AATAAAGCTT TACAGCCTTC TGCAAAA

Seq ID NO: 218 Protein sequence:
 Protein Accession #: NP_001467.1

1 11 21 31 41 51
 MSWRGRSTYY WPRPRRYVQP PEVIGPMRPE QFSDEVEPAT PEEGEPATQR QDPAAQEGE 60
 DEGASAGQGP KPEADSQEQG HPQTGCECED GPDGQEVDFP NPPEVKTPPE GEKQSQC

Seq ID NO: 219 DNA sequence
 Nucleic Acid Accession #: NM_001476
 Coding sequence: 90-3671

1 11 21 31 41 51
 ACAGCGGAGC GCAGAGTGAG AACCAACCAAC CGAGGCGCCG GGCAGCGACC CCTGCAGCGG 60
 AGACAGAGAC TGAGCGGCCG GGCACCGCCA TGCCTGCGCT CTGGCTGGGC TGCTGCCTCT 120
 GCTTCTCGCT CCTCTGCCC GCAGCCCGGG CCACCTCCAG GAGGGAAGTC TGTGATTGCA 180
 ATGGGAAGTC CAGGCAGTGT ATCTTTGATC GGGAACTTCA CAGACAAACT GGTAATGGAT 240
 TCCGCTGCCT CAACTGCAAT GACAACTAG ATGGCATTCA CTGCGAGAAG TGCAAGAAAT 300
 GCTTTTACCG GCACAGAGAA AGGGACCGCT GTTTGCCCTG CAATTGTAAC TCCAAGGTT 360

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CTCCTAGTGC TCGATGTGAC AACTCTGGAC GGTGCAGCTG TAAACCAGGT GTGACAGGAG 420
 CCAGATGCGA CCGATGTCTG CCAGGCTTCC ACATGCTCAC GGATGCGGGG TGCACCCAAG 480
 ACCAGAGACT GCTAGACTCC AAGTGTGACT GTGACCCAGC TGGCATCGCA GGGCCCTGTG 540
 ACGCGGGCCG CTGTGTCTGC AAGCCAGCTG TTACTGGAGA ACGCTGTGAT AGGTGTGCGAT 600
 CAGGTTACTA TAATCTGGAT GGGGGGAACC CTGAGGGCTG TACCCAGTGT TTCTGCTATG 660
 GGCATTGAGC CAGCTGCCGC AGCTCTGCAG AATACAGTGT CCATAAGATC ACCTCTACCT 720
 TTCATCAAGA TGTGTGATGC TGGAAGGCTG TCCAACGAAA TGGGTCTCCT GCAAAGCTCC 780
 AATGGTCACA GCGCCATCAA GGTGTGTTTA GCTCAGCCCA ACGACTAGAC CCTGTCTATT 840
 TTGTGGCTCC TGCCAAATTT CTTGGGAATC AACAGGTGAG CTATGGGCAA AGCCTGTCTCT 900
 TTGACTACCG TGTGGACAGA GGAGGCAGAC ACCCATCTGC CCATGATGTG ATTCTGGAAG 960
 GTGCTGGTCT ACGGATCACA GCTCCCTTGA TGCCACTTGG CAAGACACTG CCTTGTGGGC 1020
 TCACCAAGAC TTACACATTC AGGTAAATG AGCATCCAAG CAATAATTGG AGCCCCAGC 1080
 TGAGTTACTT TGAGTATCGA AGGTACTTGC GGAATCTCAC AGCCTCCGC ATCCGAGCTA 1140
 CATATGGAGA ATACAGTACT GGGTACATTG ACAATGTGAC CCTGATTTC A GCCCGCCCTG 1200
 TCTCTGGAGC CCGACGACCC TGGGTGGAAC AGTGTATATG TCCTGTGGG TACAAGGGGC 1260
 AATCTGCCA GGATGTGCT TCTGGCTACA AGAGAGATTG AGCGAGACTG GGGCCTTTTG 1320
 GCACCTGTAT TCCTTGTAA CAGGAGGGG GAGGGGCTG TGATCCAGAC ACAGGAGATT 1380
 GTTATTGAGG GGATGAGAAT CCTGACATTG AGTGTGCTGA CTGCCCAATT GGTTCCTACA 1440
 ACGATCCGCA CGACCCCGC AGCTGCAAGC CATGTCCCTG TCATAACGGG TTCAGCTGCT 1500
 CAGTGATGCC GGAGACGAG GAGGTGGTGT GCAATAACTG CCCTCCCGGG GTCACCGGTG 1560
 CCCGCTGTGA GCTCTGTGCT GATGGCTACT TTGGGGACCC CTTTGGTGAA CATGGCCAG 1620
 TGAGGCCTTG TCAGCCCTGT CAATGCAACA CCCCAGTGCC TCTGGGAATT 1680
 GTGACCGGCT GACAGCGAGG TGTGTGAAGT GTATCCACAA CACAGCCGGC ATCTACTCGG 1740
 ACCAGTGCAA AGCAGCTTAC TTCGGGGACC CATTGGCTCC CAACCCAGCA GACAAGTGTG 1800
 GAGCTTGCAA CTGTAACCCC ATGGGCTCAG AGCCTGTAGG ATGTGGAAGT GATGGACCT 1860
 GTGTTTGCAA GCCAGGATTT GGTGGCCCA ACTGTGAGCA TGGAGCATTC AGCTGTCCAG 1920
 CTTGCTATAA TCAAGTGAAG ATTCAGATGG ATCAGTTTAT GCAGCAGCTT CAGAGAATGG 1980
 AGGCCTGAT TTCAAAGGCT CAGGCTGGTG ATGGAGTAGT ACCTGATACA GAGCTGGAAG 2040
 GCAGGATGCA GCAGGCTGAG CAGGCCCTTC AGGACATTCT GAGAGATGCC CAGATTTTCA 2100
 AAGGTGCTAG CAGATCCCTT GGTCTCCAGT TGGCCAAGGT GAGGAGCCAA GAGAACAGCT 2160
 ACCAGAGCCG CCGGATGAG CTCAAGATGA CTGTGGAAG AGTTCGGGCT CTGGGAAGTC 2220
 AGTACCAGAA CCGGATTGCG GATACTCACA GGCTCATCAC TCAGATGAGC CTGAGCCTGG 2280
 CAGAAAGTGA AGCTTCTTGG GGAACACTA ACATTCTGCT CTCAGACCAC TACGTGGGGC 2340
 CAAATGGCTT TAAAGTCTG GCTCAGGAG CCACAAGATT AGCAGAAAGC CACGTTGAGT 2400
 CAGCCAGTAA CATGGAGCAA CTGACAAAGG AACTGAGGA CTATTCCTAA CAAGCCCTCT 2460
 CACTGGTGGC CAAGGCCCTG CATGAAGGAG TCGGAAGCGG AAGCGGTAGC CCGGACGGTG 2520
 CTGTGGTGCA AGGGCTTGTG GAAAATTGG AGAAAACCAA GTCCTTGCC CAGCAGTTGA 2580
 CAAGGGAGGC CACTCAAGCG GAAATTGAAG CAGATAGGTC TTATCAGCAC AGTCTCCGCC 2640
 TCCTGGATTG AGTGTCTCGG CTTCAAGGAG TCAGTGATCA GTCCTTTTCA GTGGAAGAAG 2700
 CAAAGAGGAT CAACCAAAA GCGGATTAC TCTCAACGCT GGTAAACGAG CATATGGATG 2760
 AGTTCAAGCG TACACAAAAG AATCTGGGAA ACTGGAAAGA AGAAGCACAG CAGCTCTTAC 2820
 AGAATGGAAA AAGTGGGAGA GAGAAATCAG ATCAGCTGCT TTCCCGTGCC AATCTTGCTA 2880
 AAAGCAGAGC ACAAGAGACA CTGAGTATGG GCAATGCCAC TTTTATGAA TTGAGAGCA 2940
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 AGCAAGCAGA AAGAGCCCTG GGGAGCGCTG CTGCTGATGC ACAGAGGGCA AAGAATGGGG 3120
 CCGGGGAGGC CCTGGAATC TCCAGTGAGA TTGAACAGGA GATTGGGAGT CTGAACCTGG 3180
 AAGCCAAATG GACAGCAGAT GGAGCCTTGG CCATGGAAAA GGGACTGGCC TCTCTGAAGA 3240
 GTGAGATGAG GGAAGTGGAA GGAGAGCTGG AAAGGAAGGA GCTGGAGTTT GACACGAATA 3300
 TGGATGCACT ACAGATGGTG ATTACAGAAG CCCAGAAGGT TGATACCAGA GCCAAGAACG 3360
 CTGGGGTTAC AATCCAAGAC ACACCTAACA CATTAGACGG CCTCCTGCACT CTGATGGACC 3420
 AGCCTCTCAG TGTAGATGAA GAGGGGCTGG TCTTACTGGA GCAGAAGCTT TCCCGAGCCA 3480
 AGACCCAGAT CAACAGCCAA CTGCGGCCCA TGATGTCAGA GCTGGAAGAG AGGGCACGTC 3540
 AGCAGAGGGG CCACCTCCAT TTGCTGGAGA CAAGCATAGA TGGGATTCTG GCTGATGTGA 3600
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 AGCAACAGTG AAGCTGCCAT AAATATTTCT CAACTGAGGT TCTTGGGATA CAGATCTCAG 3720
 GGCTCGGGAG CCATGTCATG TGAGTGGGTG GGATGGGGAC ATTTGAACAT GTTTAATGGG 3780
 TATGCTCAGG TCAACTGACC TGACCCCAAT CCTGATCCCA TGGCCAGGTG GTTGTCTTAT 3840
 TGCAACATAC TCCTTGCTTG CTGATGCTGG GCAATGAGGC AGATAGCACT GGGTGTGAGA 3900
 ATGATCAAGG ATCTGGACCC CAAAGAATAG ACTGGATGGA AAGACAAACT GCACAGGCAG 3960
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 ATAGTCAACT TATTCTTTGA GTAATGTGAC TAAAGGAAAA AACTTTGACT TTGCCAGGC 4080
 ATGAAATCTT TCCTAATGTC AGAACAGAGT GCAACCCAGT CACACTGTGG CCAGTAAAT 4140
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 ACCCAGGGTG TGAACATGTT CTCCATTTTC AAGCTGGAAG AAGTGAGCAG TGTGGAGTG 4260
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 GTTCTGGACC TGGGCATGAC ATCCCTTCTT TTAATGATGC CATGGCACT TAGAGATTGC 4380
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 GTTTCAAAGT GATAGAAAAG TGTGGCTTGG GCATTGAAAAG AGGTAAATTT CTCTAGATT 4500
 ATTAGTCCTA ATTCAATCCT ACTTTTCGAA CACCAAAAT GATGCGCATC AATGTATTTT 4560
 ATCTTATTTT CTCAATCTCC TCTCTCTTC CTCCACCCAT AATAAGAGAA TGTTCTTACT 4620
 CACACTCAG CTGGGTACA TCCATCCCTC CATTCATCCT TCCATCCATC TTTCATCCA 4680
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 GTGGGACAGT GGTGACATAG TCTCTGCCCT CATAGAGTTG ATGTCTAGT GAGGAAGACA 4800
 AGCAATTTTA AAAAATAAAT TTAACCTTAC AAACCTTTGT TGTCACAAGT GGTGTTTATT 4860
 GCAATAACCG CTGTGTTTGC AACCTCTTTC CTCAACAGAA CATATGTTGC AAGACCCCTC 4920
 CATGGGGGCA CTGAGTTTGT GGCAAGGCTG ACAGAGCTCT GGGTTGTGCA CATTCTTTG 4980
 CATTCCAGCT GTCACTCTGT GCCTTTCTAC AACTGATTGC AACAGACTGT TGAGTTATGA 5040
 TAACACCAGT GGAATTTGCT GGAGGAACCA GAGGCACTTC CACCTTGGCT GGGAAAGACTA 5100
 TGGTGTGCTC TTGCTTCTGT ATTTCTCTGG ATTTTCTGTA AAGTGTTTTT AAATAAAGAA 5160
 CAATTGTTAG ATGCC

Seq ID NO: 220 Protein sequence:
 Protein Accession #: NP_005553

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1 11 21 31 41 51
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	MPALWLGCC	CFSLLLPAA	ATSRREVCD	NGKSRCQIFD	RELHRQTGNG	FRCLNCNDNT	60
	DGIHCEKCKN	GFYRHRERDR	CLPCNCNSKG	SLSARCDNSG	RCSCPKGVTV	ARCDRLCPGF	120
	HMLTDAGCTQ	DQRLLDKSCD	CDPAGIAGPC	DAGRCKVCKPA	VTGERCDRCR	SGYYNLDDGN	180
5	PEGCTQCFCY	GHSASCRSSA	EYSVHKITST	FHQDVGWKA	VQRNGSPAKL	QWSQRHQDVF	240
	SSAQRIDPVY	FVAPAKFLGN	QQVSYGQSL	FDYRVDRGGR	HPSAHDVILE	GAGLRITAPL	300
	MPLGKTLPCG	LTKTYTFRLN	EHPSPNNWSPQ	LSYFERYRLL	RNLTLALRIRA	TYGEYSTGYI	360
	DNVTILISAR	VSGAPAPWVE	QCICPVGYKG	QFCQDCASGY	KRDSARLGP	GTCIPCNCOG	420
	GGACDPDTGD	CYSGDENPDI	ECADCPIGFY	NDPHDPRSC	PCPCHNGFSC	SVMPEEEVV	480
10	CNNCPGVTV	ARCELCADGY	FGDPFGEHGP	VRPCQPCQCN	NNVDPSPASGN	CDRLTGRCLK	540
	CIHNTAGIYC	DQCKAGYFGD	PLAPNPADKC	RACNCNPMGS	EPVGCERSDGT	CVCKPGFGGP	600
	NCEHGAFSCP	ACYNQVIQIM	DQFMQQLQRM	EALISKAQGG	DGVVPDTELE	GRMQQAQAL	660
	QDILRDAQIS	EGASRSGLQL	LAKVRSQENS	YQSRLLDDLM	TVERVRALGS	QYQNRVRDTH	720
	RLITQMLSL	AESEASLGNT	NIPASDHYVG	PNGFKSLAQE	ATRLAESHVE	SASNMEQLTR	780
15	ETEDYSKQAL	SLVRKALHEG	VSGSGSPDQ	AVVQGLVEKL	EKTKSLAQQL	TREATQAEIE	840
	ADRSYQHSRL	LLDSVSRLLQ	VSDQSFQVEE	AKRIKQKADS	LSTLVTRHMD	EFKRTQKNLG	900
	NWKEEAQQLL	QNGKSGREKS	DQLLSRANLA	KSRAQEALSM	GNATFYEVES	ILKNLREFDL	960
	QVDNRKAEE	EAMKRLSYIS	QKVSDASDKT	QQAERALGSA	AADAQRAKNG	AGEALEISSE	1020
	IEQEIGSLNL	ENAVTADGAL	AMEKGLASLK	SEMREVEGEL	ERKELEFDTN	MDAVQMVITE	1080
20	AQKVDTRAKN	AGVTIQDTLN	TLDGLHLMD	QPLSVDEEGL	VLEEQKLSRA	KTQINSQRLP	1140
	MMSELEERAR	QQRGHLHLE	TSIDGILADV	KNLENIRDNL	PPGCVNTQAL	EQQ	

Seq ID NO: 221 DNA sequence
Nucleic Acid Accession #: NM_016529
Coding sequence: 13-1854

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30	AAAGGGGCTG	ATAATGTGAT	TTTTAGAGA	CTTTCAAAG	ACTCAAATA	TATGGAGGAA	120
	ACATTATGCC	ATCTGGAATA	CTTTGCCACG	GAAGGCTTGC	GGACTCTCTG	TGTGGCTTAT	180
	CTGTATCTCT	CTGAGAATGA	GTATGAGGAG	TGGCTGAAAG	TCTATCAGGA	AGCCAGCACC	240
	ATATTGAAGG	ACAGAGCTCA	ACGGTTGGAA	GAGTGTTCAG	AGATCATTGA	GAAGAATTTG	300
	CTGCTACTTG	GAGCCACAGC	CATAGAAGAT	CGCCTTCAAG	CAGGAGTTCC	AGAAACCATC	360
	GCAACACTGT	TGAAGGCAGA	AATTAAATA	TGGGTGTGGA	CAGGAGACAA	ACAAGAAACT	420
35	GCGATTAAATA	TAGGGTATTC	CTGCCGATTG	GTATCGCAGA	ATATGGCCCT	TATCCTATTG	480
	AAGGAGGACT	CTTTGGATGC	CACAAGGGCA	GCCATTACTC	AGCACTGCAC	TGACCTTGGG	540
	AATTTGCTGG	GCAAGGAAAA	TGACGTGGCC	CTCATCATCG	ATGGCCACAC	CCTGAAGTAC	600
	CGCGCTCTCT	TGGAAGTCCG	GAGGAGTTTC	CTGGATTGCG	CACTCTCTGT	CAAAGCGGTC	660
	ATATGCTGCA	GAGTGTCTCC	TCTGCAGAA	TCTGAGATAG	TGGATGTGGT	GAAGAAGCGG	720
40	GTGAAGGCCA	TCACCTTCGC	CATCGGAGAC	GGCGCCAACG	ATGTCGGGAT	GATCCAGACA	780
	GCCCCAGTGG	GTGTGGGAAT	CAGTGGGAAT	GAAGGCATGC	AGGCCACCAA	CAACTCGGAT	840
	TACGCCATCG	CACAGTTTTC	CTACTTAGAG	AAGCTTCTGT	TGGTTCATGG	AGCCTGGAGC	900
	TACAACCGGG	TGACCAAGTG	CATCTTGATC	TGCTTCTATA	AGAACGTGGT	CCTGTATATT	960
	ATTGAGCTTT	GGTTCGCTTT	TGTTAATGGA	TTTTCTGGGC	AGATTTTATT	TGAACGTTGG	1020
45	TGCATCGGCC	TGTACAAATG	GATTTTCACC	GCTTTGCCCG	CCTTCACTCT	GGGAATCTTT	1080
	GAGAGGTCTT	GCACTCAGGA	GAGCATGCTC	AGGTTTCCCC	AGCTCTACAA	AATCACCAGG	1140
	AATGGCGAAG	GCTTCAACAC	AAAGGTTTTC	TGGGGTCACT	GCATCAACGC	CTTGGTCCAC	1200
	TCCCTCATCC	TCTTCTGTTT	TCCCATGAAA	GCTCTGGAGC	ATGATACTGT	GTTTGACAGT	1260
50	GGTCATGCTA	CCGACTATTT	ATTTGTTGGA	AAATATTGTT	ACACATATGT	TGTTGTTACT	1320
	GTTTGTCTGA	AAGCTGGTTT	GGAGACCACA	GCTTGGACTA	AATTCACTGA	CTTGGCTGTC	1380
	TGGGGAAGCA	TGCTGACCTG	GCTGGTGTTC	TTTGGCATCT	ACTCGACCAT	CTGGCCACCC	1440
	ATTCCCATTT	CTCCAGATAT	GAGAGGACAG	GCAACTATGG	TCCTGAGCTC	CGCACACTTC	1500
	TGTTTGGGAT	TATTTCTGGT	TCCTACTGCC	TGTTTGATTG	AAGATGTGGC	ATGGAGAGCA	1560
55	GCCAAGCACA	CTGCAAAAA	GACATTGCTG	GAGGAGGTGC	AGGAGCTGGA	AACCAAGTCT	1620
	CGAGTCTCTG	GAAAAGCGGT	GCTGCGGGAT	AGCAATGGAA	AGAGGCTGAA	CGAGCGCGAC	1680
	CGCCTGATCA	AGAGGCTGGG	CCGGAAGACG	CCCCCGACGC	TGTTCCGGGG	CAGCTCCCTG	1740
	CAGCAGGGCG	TCCCGCATGG	GTATGCTTTT	TCTCAAGAAG	AACACGGAGC	TGTTAGTCAG	1800
	GAAGAAGTCA	TCCGTGCTTA	TGACACCACC	AAAAAGAAAT	CCAGGAAGAA	ATAAGACATG	1860
60	AAATTTCTCT	ACTGATCTTA	GGAAAGAGAT	TCAGTTTGTT	GCACCCAGTG	TTAACACATC	1920
	TTTGTGAGAG	AAGACTGGCG	TCCAAGGCCA	AAACACCAGG	AAACACATTT	CTGTGGCCTT	1980
	AGTTAAGCAG	TTTGTAGTGT	ACATATTCCC	TCGCAAACTT	GGAGTGCAGA	CCACAGGGGA	2040
	AGCTATCTTT	GCCTCCCAA	CTCGTCTGCA	GTGCTTAGCC	TAACTTTTGT	TTATGTCGTT	2100
	ATGAAGCATT	CAACTGTGCT	CTGTGAGGTC	TCAAATTAAA	AACATTATGT	TTACCAATA	2160
65	AGAAAAA	AAAAAA					

Seq ID NO: 222 Protein sequence:
Protein Accession #: NP_057613

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	MSVIVRTPSG	RLRLYCKGAD	NVIFERLSKD	SKYMEETLCH	LEYFATEGLR	TLCVAYADLS	60
	ENEYEELWKV	YQEAETILKD	RAQRLEECYE	IEKNLLELLG	ATAIEDRLQA	GVPETIATLL	120
	KAEIKIWLVT	GDKQETAINI	GYSCRLVSQN	MALILLKEDS	LDATRAAITQ	HCTDLNLLG	180
75	KENDVALIID	GHTLKYALSF	EVRRSFLDLA	LSCKAVICCR	VSPLOKSEIV	DVVKRVRKAI	240
	TLAIGDGAND	VGMIOQTAHV	VGISGNEGMO	ATNNSDYAIA	QFSYLEKLLL	VHGAWSYNRV	300
	TKCILYCFYK	NUVLYIIELV	PAFVNGFSGQ	ILFERWCIGL	YNVIFTALPP	FTLGIFERS	360
	TQESMLRFPQ	LYKITQNGEG	FNTKVPWGH	INALVHSLIL	FWFPMKALEH	DTVFDSGHAT	420
	DYLFVGNIVY	TVVVVTVCLK	AGLETTAWTK	FSHLAVWGSM	LTWLVFVFGY	STIWPITPIA	480
80	PDMRGQATMV	LSSAHFWLGL	FLVPTACLIE	DVAWRAAKHT	CKKTLLEEVQ	ELETKSRVLG	540
	KAVLRDSNGK	RLNERDRLIK	RLGRKTPPTL	FRGSSLQQGV	PHGYAFSQEE	HGAVSQEEVI	600
	RAYDTTKKKS	RKK					

Seq ID NO: 223 DNA sequence
Nucleic Acid Accession #: BC017001
Coding sequence: 1-394

85	1	11	21	31	41	51
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	1	11	21	31	41	51	
	AACGCTGGGC	AGGGCCGGCG	CGGGTCGGGG	GGCGCCCGAG	GGGCCCCGGC	CGAGCGGCGG	60
	CGCGCAGGGC	GGCAGCATCC	ACTCGGGCCG	CATCGCCGCG	GTGCACAACG	TGCCGCTGAG	120
5	CGTGCTCATC	CGGCCGCTGC	CGTCCGTGTT	GGACCCCGCC	AAGGTGCAGA	GCCTCGTGGA	180
	CACGATCCGG	GAGGACCCAG	ACAGCGTGCC	CCCCATCGAT	GTCTCTGGA	TCAAAGGGGC	240
	CCAGGGAGGT	GACTACTTCT	ACTCCTTTGG	GGGCTGCCAC	CGGTACGCGG	CCTACCAGCA	300
	ACTGCAGCGA	GAGACCATCC	CCGCCAAGCT	TGTCCAGTCC	ACTCTCTCAG	ACCTAAGGGT	360
	GTACCTGGGA	GCATCCACAC	CAGACTTGCA	GTAGCAGCCT	CCTTGGCACC	TGCTGCCACC	420
10	TTCAAGAGCC	CAGAAGACAC	ACCTGGCCTC	CAGCAGGCTG	GGCCATGCAG	AAGGGATAGC	480
	AGGGGTGCAT	TCTCTTTGCA	CCTGGCGAGA	GGGTCTGACT	CTGGGCACCC	CTCTCACCCG	540
	CTACAAGGCC	TTGGACTCAC	TGTACAGTGT	GGGAGCCCCA	GTTCCACCTT	CTGTGACAA	600
	AGGATCATGG	CCTTACCCTT	GAAGCATTAC	CGAGAAGGAG	AACAGAGATG	GGCTTGAAGA	660
	GCCACGTGCT	GCCGGCTCCA	AATTCCCAAG	GACAAGGATC	CCTCTGCATT	TTTGTCTATG	720
15	TAACTCTTTA	TATGGAATAC	ATTGAGCTGC	AAGGAAAGGA	AAACCTTGAT	TGCAGTGGTT	780
	TAAACAAACA	GAAAGATTGT	TTTCCACATA	GCATGGATTG	TGGAGATGGG	TGGCTAATGG	840
	TATTGGTTCA	ACAACCTCAC	GGAGGTAGGG	GTACGCTCTT	GGATCCTTTT	GCCTTAATCT	900
	CAGTGCTCGT	TACTTCATGG	TCCCAAGATG	GCTGCTGTAT	CCCCAAGAAT	CATGTCTGCG	960
	TTCAAGGAAG	GAGGGGTGGA	GGAAGAGGAA	GGGCCAAACT	AGCTGGACCC	GTACACCTTCT	1020
20	ATCAGAAAGT	AAAACCTCGT	CAGAAGTCTG	TTTCTGCTC	TCTCCCTCTG	CATATCTTCA	1080
	CTTAGATGCC	CTTGGCCCGA	GCCAGCTACC	ATTGCACCTC	TAGCTGCAAA	CAAAGCTAAG	1140
	ACAGCAGGGA	ACAGAATTGT	CATGGCTGAA	TAGACCAATC	GTGTTCCATC	TACTGAGACT	1200
	GGCACACTGC	CTCCTGCAAT	AAAACCTGGG	TCCCATTACC	AAGAGAGAAA	TGCAGAATTG	1260
	TGTACCAGTT	AGCTTTTGCT	GTGTAACAAA	CCATCCCCAA	ACTTGGCAGC	TAGAAAACAAA	1320
	CCCTGTATTT	TCCACACAAT	CTATGGGTTG	GCAATTTGGG	CTGGGCTCAA	CAGGGCAGTT	1380
25	CTGCTGCTCA	CACCTGGGAT	CCCTCATGGA	GCTAAGGTCA	GCTGTTACCT	CAGCTGGGCC	1440
	TGGATGGTCT	AGGATAGCCT	TACTCACTTG	CCTGGCAGGT	GACAGGCTGT	TGGCTGGAAT	1500
	TGCTTGGTTC	TCCCTCATGT	GGCCTCTCCA	GCAGGCTAGC	TCAGGCTTAT	TCACATGATG	1560
	GCTTCAGGAT	TCCAAAGAGA	GTGAGAGTAG	AAGCTGAAAG	ACTTCTTGAG	TTCTTGGCCT	1620
	GGAACTGGGA	CTAGGACAGT	GTCACCTCTG	CTAAGTCTTT	TTGGTCAGAG	CAATCACAA	1680
30	GGCTTTACCC	AGATTCAAGG	GATGAGAAAC	AGACTACATG	TCTTGATGAG	GGGAACCACA	1740
	AAGAGCTTGT	GGCCATTTT	CACCTATCAC	AAATAATTTT	GGATGGGTAT	TTATTTGGAT	1800
	AAAGGTATTT	CCCTCTTCCC	CCTTCTCTC	TGTCTCATGG	GGCCTCACTC	TGCCAAGTTG	1860
	GAAGGCCTA	AGACATTGTC	CTGGCCCTCA	GGGTCTAGGG	GAAGAGGTGT	TGGGGCAGGA	1920
35	AGTGAGTCTC	TCCATGGGCT	GGACCCACTG	TAGTAGGAGT	GCCTCCTTGT	CTGCACTGCT	1980
	GGTATGGGGT	TAGGCCAGGT	AGGACATTCC	AGAGGGGCTT	CTGAAAACCA	AGAGTCCCTG	2040
	GGGAAAGGGA	ACAGAGTAAG	GCAGGCCTTG	TTCTCACTGC	CCTCTAAGGG	AACTTGGTCA	2100
	CTCGGCATT	TTAAGCCTCA	GTTTCTCCAG	TTCAATAATA	AGGACAAGAG	CTTTTCCCAT	2160
	GCATTCTCTT	TCCCGGGGAA	AGTTGACTGA	GGTGACCGAT	AATAGAATTG	AAAAGGGAGA	2220
40	GTGTCTTCAG	TGCAATGTGG	CATCCTGGAT	TGGGTCTTGG	AACAAAAACA	GGACATTAGT	2280
	GGGAAATTTG	GAAATCTGAA	AAAAGTCTGA	ATTTTAGTTA	ATATACCAAT	TTCACTCTCT	2340
	TGGTTTGGAC	AGATGTACCA	TGGTGATGTA	AGATGTTGAC	CTTGGGGTAG	GCTGGGTGAA	2400
	GGGTATACAG	GAACCTTTTG	TACTATCTCT	GCAACTTCTC	TGTAATATCTA	GTATCATTTCC	2460
	AAAATAAAAG	TTTATTTAAT	TTAAAAAATA	AAAAAATAAA	AA		

Seq ID NO: 224 Protein sequence:
Protein Accession #: AAH17001.1

	1	11	21	31	41	51	
50	TLGRAGAGRG	APEGPSPSGG	AQGGSIHSGR	IAAVHNVPLS	VLIRPLPSVL	DPKQVQSLVD	60
	TIREDPDSVP	PIDVLWIKGA	QGGDYFYSFG	GCHRYAAYQQ	LQRETIPAKL	VQSTLSDLRV	120
	YLGASTPDLQ						

Seq ID NO: 225 DNA sequence
Nucleic Acid Accession #: NM_021048
Coding sequence: 1..1110

	1	11	21	31	41	51	
60	ATGCCTCGAG	CTCCAAAGCG	TCAGCGCTGC	ATGCCTGAAG	AAGATCTTCA	ATCCCAAAGT	60
	GAGACACAGG	GCCTCGAGGG	TGCACAGGCT	CCCCTGGCTG	TGGAGGAGGA	TGCTTCATCA	120
	TCCACTTCCA	CCAGCTCCTC	TTTTCATCC	TCTTTTCCCT	CCTCCTCCTC	TTCCCTCTCC	180
65	TCCTCCTGCT	ATCCTCTAAT	ACCAAGCACC	CCAGAGGAGG	TTTCTGCTGA	TGATGAGACA	240
	CCAAATCCTC	CCCAGAGTGC	TCAGATAGCC	TGCTCCTCCC	CCTCGGTCTG	TGCTTCCCTT	300
	CCATTAGATC	AATCTGATGA	GGGCTCCAGC	AGCCAAAAGG	AGGAGAGTCC	AAGCACCCCTA	360
	CAGGTCTCTC	CAGACAGTGA	GTCTTTACCC	AGAAGTGAGA	TAGATGAAAA	GGTGACTGAT	420
70	TTGGTGCAGT	TTCTGCTCTT	CAAGTATCAA	ATGAAGGAGC	CGATCACAAA	GGCAGAAATA	480
	CTGGAGAGTG	TCATAAAAAA	TTATGAAGAC	CACCTTCCCTT	TGTTGTTTAG	TGAAGCCTCC	540
	GAGTGATATG	TGCTGTGCTT	TGGCATTGAT	GTAAAGGAAG	TGGATCCCAC	TGGCCACTCC	600
	TTTGTCTCTT	TCACCTCCCT	GGGCTTCACC	TATGATGGGA	TGCTGAGTGA	TGTCCAGAGC	660
	ATGCCCAAGA	CTGGCATTCT	CATACITATC	CTAAGCATAA	TCTTCATAGA	GGGCTACTGC	720
	ACCCCTGAGG	AGGTCTATCT	GGGAAGCACTG	AATATGATGG	GGCTGTATGA	TGGGATGGAG	780
75	CACCTCATTT	ATGGGGAGCC	CAGGAAGCTG	CTCACCCAAG	ATTGGGTGCA	GGAAAACTAC	840
	CTGGAGTACC	GGCAGGTGCC	TGGCAGTGTG	CCTGCACGGT	ATGAGTTTCT	GTGGGGTCCA	900
	AGGGCTCATG	CTGAAATTAG	GAAGATGAGT	CTCCTGAAAT	TTTTGGCCAA	GGTAAATGGG	960
	AGTGATCCAA	GATCCTTCCC	ACTGTGGTAT	GAGGAGGCTT	TGAAAGATGA	GGAAGAGAGA	1020
80	GCCCAGGACA	GAATTGCCAC	CACAGATGAT	ACTACTGCCA	TGGCCAGTGC	AAGTTCTAGC	1080
	GCTACAGGTA	GCTTCTCCTA	CCCTGAATAA				

Seq ID NO: 226 Protein sequence:
Protein Accession #: NP_066386

	1	11	21	31	41	51	
85	MPRAPKRQRC	MPPEEDLQSQS	ETQGLEGAQA	PLAVEEDASS	STSTSSSFPS	SFPPSSSSSSS	60

SSCYPLIPST PEEVSADDET PNPPQSAQIA CSSPSVVASL PLDQSDDEGSS SQKEESPSTL 120
 QVLPDSESLP RSEIDEKVT LQVFLFLFKYQ MKEPITKABI LESVIKNYED HFPLLFSEAS 180
 EEMLLVFGID VKEVDPTGHS FVLVTSLSGLT YDGMLSDVQS MPKTGILILI LSIIPIEGYC 240
 TPEEVIWEAL NMMGLYDGM EHLIYGEPRKL LTQDWVQENY LEYRQVPGSD PARYEFLWGP 300
 RAHAERKMS LKFLAKVNG SDRSFPLWY EEALKDEEER AQDRIATTD TTMASASSS 360
 ATGSFSYPE

Seq ID NO: 227 DNA sequence
 Nucleic Acid Accession #: NM_005025.1
 Coding sequence: 82-1314

1 11 21 31 41 51
 | | | | | |
 GCGGAGCACA GTCCGCCGAG CACAAGCTCC AGCATCCCCT CAGGGGTTCG AGGTGTGTGG 60
 GAGGCTTGAA ACTGTTACAA TATGGCTTTC CTGGGACTCT TCTCTTTGCT GGTTCGTCAA 120
 AGTATGGCTA CAGGGGCCAC TTTCCTGAG GAAGCCATTG CTGACTTGTC AGTGAATATG 180
 TATAATCGTC TTAGAGCCAC TGGTGAAGAT GAAAATATTC TCTTCTCTCC ATTGAGTATT 240
 GCTCTTGCAA TGGGAATGAT GGAACCTGGG GCCCAAGGAT CTACCCAGAA AGAAAATCCGC 300
 CACTCAATGG GATATGACAG CCTAAAAAAT GGTGAAGAAT TTTCTTTCTT GAAGGAGTTT 360
 TCAAAACATGG TAACTGCTAA AGAGAGCCAA TATGTGATGA AAATTGCCAA TTCCTTGTTT 420
 GTGCAAAATG GATTTTCATGT CAATGAGGAG TTTTTCGAAA TGATGAAAAA ATATTTTAAT 480
 GCAGCAGTAA ATCATGTGGA CTTCAGTCAA AATGTAGCCG TGGCCAACTA CATCAATAAG 540
 TGGGTGGAGA ATAACACAAA CAATCTGGTG AAAGATTGGG TATCCCCAAG GGATTTTGAT 600
 GCTGCCACTT ATCTGGCCCT CATTAAATGCT GTCTATTTCA AGGGGAACTG GAAGTCGCAG 660
 TTTAGCCCTG AAAAATACTAG AACCTTTTCT TTCACTAAAG ATGATGAAAG TGAAGTCCAA 720
 ATTCCAATGA TGTATCAGCA AGGAGAATT TATTATGGGG AATTTAGTGA TGGCTCCAAT 780
 GAAGCTGGTG GTATCTACCA AGTCCTAGAA ATACCATATG AAGGAGATGA AATAAGCATG 840
 ATGCTGGTGC TGTCCAGACA GGAAGTTCCT CTGTCTACTC TGGAGCCATT AGTCAAAGCA 900
 CAGCTGGTTG AAGAATGGGC AAACCTGTGT AAGAAGCAAA AAGTAGAAGT ATACCTGCC 960
 AGGTTACAG TGAACAGGA AATTGATTTA AAAGATGTTT TGAAGGCTCT TGAATAAAT 1020
 GAAATTTTCA TCAAAGATGC AAATTGACA GGCTCTCTG ATAATAAGGA GATTTTCTT 1080
 TCCAAAGCAA TTCACAAGTC CTTCCTAGAG GTTAATGAAG AAGGCTCAGA AGCTGCTGCT 1140
 GTCTCAGGAA TGTCTCAAT TAGTAGGATG GCTGTGCTGT ATCTTCAAGT TATTGTGAC 1200
 CATCCATTTT TCTTTCTTAT CAGAAACAGG AGAACTGGTA CAATTCTATT CATGGGACGA 1260
 GTCATGCATC CTGAAACAAT GAACACAAGT GGACATGATT TCGAAGAACT TTAAGTTACT 1320
 TTATTTGAAT AACAGGAAA ACAGTAACTA AGCACAATTAT GTTTGCAACT GGTATATATT 1380
 TAGGATTTGT GTTTTACAGT ATATCTTAAG ATAATATTTA AAATAGTTCC AGATAAAAAC 1440
 AATATATGTA AATTATAAGT AACTTGTCAA GGAATGTTAT CAGTATTAAG CTAATGGTCC 1500
 TGTATGTGTA TTGTGTTTGT GTGCTGTTGT TTAAATATAA AGTACCTATT GAACATGTG

Seq ID NO: 228 Protein sequence:
 Protein Accession #: NP_005016.1

1 11 21 31 41 51
 | | | | | |
 MAFLGLFSL VLSMATGAT FPPEAIADLS VNMYNRLRAT GEDENILFSP LSIALAMGMM 60
 ELGAQGSTQK EIRHSMGYDS LKNGEBSFSL KEFSNMVTAK ESQYVMKIAN SLFVQNGFHV 120
 NEEFLQMMKK YFNAAVNVHD FSQNVAVANY INKWVENNTN NLVKDLVSPR DFDAATYLAL 180
 INAVFYKGNW KSQFPENR TFSFTKDD EVOIPMMYQQ GEFYVGEFSD GSNEAGGIYQ 240
 VLEIPEYEGDE ISMMVLVLSRQ EVPLATLEPL VKAQLVEENA NSVKKQKVEV YLPRTVEQE 300
 IDLKDVLKAL GITEIFIKDA NLTLGLSDNKE IFLSKAIHKS FLEVNEEGSE AAASVGMIAI 360
 SRMAVLYPQV IVDHPPFFLI RNRRTGTILF MGRVMHPETM NTSGHDFFEL

Seq ID NO: 229 DNA sequence
 Nucleic Acid Accession #: NM_003695
 Coding sequence: 12-398

1 11 21 31 41 51
 | | | | | |
 CGACATCAGA GATGAGGACA GCATTGCTGC TCCTTGACAGC CCTGGCTGTG GCTACAGGGC 60
 CAGCCCTTAC CCTGGCTGC CACGTGTGCA CCAGCTCCAG CAACTGCAAG CATTCTGTGG 120
 TCTGCCCGGC CAGCTCTCGC TTCTGCAAGA CCACGAACAC AGTGGAGCCT CTGAGGGGGA 180
 ATCTGGTGAA GAAGGACTGT GCGGAGTCTG GCACACCCAG CTACACCCCTG CAAGGCCAGG 240
 TCAGCAGCGG CACCAGCTCC ACCCAGTGTG GCCAGGAGGA CCTGTGCAAT GAGAAGCTGC 300
 ACAACGCTGC ACCCAGCCGC ACCGCTCTCG CCCACAGTGC CCTCAGCCTG GGGCTGGCCC 360
 TGAGCCTCCT GGCCTCATC TTAGCCCCCA GCCTGTGACC TTCCCCCAG GGAAGGCCCC 420
 TCATGCCCTT CCTTCCCTTT CTCTGGGGAT TCCACACCTC TCTTCCCCAG CCGGCAACGG 480
 GGGTGCCAGG AGCCCCAGGC TGAGGGCTTC CCCGAAAGTC TGGGACCAGG TCCAGGTGGG 540
 CATGGAATGC TGATGACTTG GAGCAGGCC CACAGACCCC ACAGAGGATG AAGCCACCCC 600
 ACAGAGGATG CAGCCCCAG CTGCATGGAA GGTGGAGGAC AGAAGCCCTG TGGATCCCCG 660
 GATTTTCACAC TCCTTCTGTT TTGTTGCCGT TTATTTTGTA CTCAAATCTC TACATGGAGA 720
 TAAATGATTT AAAC

Seq ID NO: 230 Protein sequence:
 Protein Accession #: NP_003686

1 11 21 31 41 51
 | | | | | |
 MRTALLLLAA LAVATGPALT LRCHVCTSSS NCKHSVVCFA SSRFCKTTNT VEPLRGNLVK 60
 KDCAESCTPS YTLQGQVSSG TSSTQCCQED LCNEKLHNAA PTRTALAHS LSLGLALSL 120
 AVILAPSL

Seq ID NO: 231 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 126-752

	1	11	21	31	41	51	
	CCGGGCGAGGT	GGCTCATGCT	CGGGAGCGTG	GTTGAGCGGC	TGGCGCGGTT	GTCTTGGAGC	60
5	AGGGGCGCAG	GAATTCTGAT	GTGAAACTAA	CAGTCTGTGA	GCCCTGGAAC	CTCCACTCAG	120
	AGGAAGATGAA	GGATATCGAC	ATAGGAAAAG	AGTATATCAT	CCCCAGTCCT	GGGTATAGAA	180
	GTGTGAGGGA	GAGAACCCAGC	ACTTCTGGGA	CGCACAGAGA	CCGTGAAGAT	TCCAAGTTCA	240
	GGAGAAGCTCG	ACCGTTGGAA	TGCCAAGATG	CCTTGGAAAC	AGCAGCCCGA	GCCGAGGGCC	300
	TCTCTCTTGA	TGCCCTCCATG	CATTCTCAGC	TCAGAATCCT	GGATGAGGAG	CATCCCAAGG	360
10	GAAAGTACCA	TCATGGCTTG	AGTGCTCTGA	AGCCCATCCG	GACTACTTCC	AAACACCAGC	420
	ACCCAGTGGA	CAATGCTGGG	CTTTTTCTCT	GTATGACTTT	TTGCTGGCTT	TCTTCTCTGG	480
	CCCGTGTGGC	CCACAAGAAG	GGGGAGCTCT	CAATGGAAGA	CGTGTGGTCT	CTGTCCAAGC	540
	ACGAGTCTTC	TGACGTGAAC	TGCAGAAGAC	TAGAGAGACT	GTGGCAAGAA	GAGCTGAATG	600
	AAGTTGGGCC	AGACGCTGCT	TCCCTCGGAA	GGGTTGTGTG	GATCTTCTGC	CGCACCAGGC	660
15	TCATCTGTGC	CATCGTGTGC	CTGATGATCA	CGCAGCTGGC	TGGCTTCAGT	GGACCAAAAT	720
	TTCAGGATGG	CTGTATTCTG	CGGTGAGAA	GAGAGAGTCA	AGCTGGGCAG	AATCTCTCGC	780
	CAAGAGTTCA	GCCTTCCTTT	GGAGACTGCT	CCATCAGTGC	CGAGGTGTGT	GGGAACAGGC	840
	TTCAGTGCAC	CGCCATCTTA	CTGAGTTGCT	TCACGTGAGG	AAAAGGGGGC	TTTGGCCCTG	900
	TGACTCAGTT	CCACATTTTG	GATTGCATAC	TGGAAAAGAA	GCCAACTCTC	TTGCTAGTAA	960
20	ACCAGCAACC	CGGCTGTATA	CAGTGGTGAC	CCAAGCAATG	GATATAAACC	TAAAAATCTG	1020
	AGGGAGGGGA	GAGGTGGAAT	ACAGTAGTTC	TTGGAATCTG	AAGTCTCCTA	TTTGATCAGG	1080
	TTATTTCTCTG	GGACTTGGCA	AAAATCTGAT	TGGTGGGGAT	CTCCTAGGAC	CTAGTGGACA	1140
	TCGTGTATTA	ATTTAATCTC	AGGAAAAACA	AGAAATTAAC	CCAGAGAGAG	TCTGGGTTTT	1200
	GGAAATCAGC	GTAGCTACCT	CCAGACCGTG	GTGTCTGGCC	TCCATTTTTG	TCTGTCAATC	1260
25	AGCTCTGACT	TACAGCTGCA	GTCACCTTTG	CTATAAGGCA	CCTGGGTAGA	AGGGTGGATG	1320
	GGCTTCACAT	CAATTTTTTT	CTTCTTTTAG	GGTGGGGGAT	TGGTTTGGCT	TTCTTTTGT	1380
	TGGGTTTTTT	GTATTATTTT	TGTCAGATT	GATTTTTAGA	TGCAAGGACT	TGAAAAGACC	1440
	CAGAAGGATG	CCACCAAGTT	TTCCTTGAGG	CCTAGGATTT	TTTATCTCTG	CCCGAGCAGA	1500
	GGTAATTCCT	CACAACTTAG	TGCACCAGTA	GCACCAGCCA	TTTTGAGCAG	AGTACCTCTT	1560
30	TGGGGAGACT	TTCTGTTTGT	TTTGTTTTGA	ATTCTCTTTC	CTTAGCAGCA	AGGTCTTTTT	1620
	TCCTAGAGAA	TCTACTCCGT	TGCAGAAACA	TTGCAACCTC	AGGAGCCCTC	ACTGATTGAG	1680
	TGCTGTCTAG	CTGATATACT	ACTTTGGACT	CTGGAACACG	ATATGGGTTT	TATTCTCTAT	1740
	TTCTACTGTG	TGTCGTAAAC	CAACCGTCGG	AGACCAGATG	ACCTGTGTAG	TGGCTAGTCC	1800
35	TGTATAAATC	GACTCTGTAT	GTTTCAATGT	ATGTTACTGC	AATGCTTCAC	CTGCTGTACA	1860
	GTGTTTGTGA	GATGCTCTTT	GAAGATGGTA	CTTTTATATT	T		

Seq ID NO: 232 Protein sequence:
Protein Accession #: Eos sequence

	1	11	21	31	41	51	
40	MKDIDIGKEY	IIPSPGYRSV	RERTSTSGTH	RDREDSKFRR	TRPLECQDAL	ETAARAEGLS	60
	LDASMSQLR	ILDEEHPKVK	YHGLSALKP	IRTTSKHQHP	VDNAGLFSCM	TFSWLSLAR	120
	VAHKKGELSM	EDVWSLSKHE	SSDVNCRRL	RLWQEELNEV	GPDAASLRRV	VWIFCRTRLI	180
45	LSIVCLMITQ	LAGFSQPNFQ	DGCILRSE				

Seq ID NO: 233 DNA sequence
Nucleic Acid Accession #: CAT cluster

	1	11	21	31	41	51	
50	TTTAAATGGT	GCTCATATAT	ACTGTATTTT	TTGTTGTTTA	GTTTTACTTA	TTGAGAGTGT	60
	CACAAATGGA	ATCACATAAT	CATGATTTTT	TTTTTTTACT	TTTACTCCCC	AAATTATTCA	120
	TGTTTCTTAG	ATCGTAGTCA	TTGAGAAGTC	CCAATAACTC	TAAACTTTTG	AGTTATAACG	180
55	TAGTAACATCT	CTCTTTCATC	TTTGTGTTAG	CTCTGTAGTC	TTAACCTGGA	TTTAAATTTT	240
	TTTGTTTCCA	AAGTCACAA	TGAATTATTC	TTAGATACCT	TAAAGCACTG	AATTCAAGTT	300
	TGTTTGACTG	AAAGCAAAAC	AACGTGACAG	TTTATTTTCA	AACACTAACT	TCTTGATATT	360
	TGTTTATGGT	ATATCTTTTT	ATTAAATATT	TATTTTGACT	AAGCTTTTCA	AAAATATTTG	420
	AAGCTATTTT	AATCATCAAG	TATGGAAAAC	AAATTACTAT	TGCATTTTCC	TATATATGCA	480
60	TATATTATGG	ATTAACCAGA	ATTGTATCAT	TTTTGGCCTA	ATGCTGGGAT	ATAAAAGATA	540
	ATTAGCCTAC	TATAGTATTA	ATAAAATTTT	CAGTTGGTTT	GGGCAAAATT	AAACCTGAAA	600
	AATAGGTTAA	AAAGTAGTTA	CAAATTAAAC	TTACTAATTT	ATACCTGATT	TTTTTCTTGG	660
	AATTAAAGTA	CATTTTAAAT	GAGCTTTATA	ATACCTTAAA	AAGTTGGTTC	TAATTTAAAA	720
	TATGAAAGCT	CTGGCTATCA	TCTTGGGATA	GTAATTCTTA	ATTATATAGT	ATTTCAAAC	780
65	TATATATTTT	TTAGTTCCCT	TGAGATAACT	AATTTCTAAT	TATATATGTT	TCAAAAACCA	840
	TATCTGTGAT	TTTTTTTAA	AATTTGTTTA	TAAATAGGTC	ATAAGATACA	AGGTCTGCAT	900
	TAGAAAGACCC	ACTCTTACTA	GGTTCCCTAA	GGATCTGCCA	TAGATTTTTT	TTTTTTTTTT	960
	TTTTTTTTTAG	GATGTTTAAA	GCAAGCACTG	ATACCAGTGG	GAGTTGGTCT	TGATCTAGGA	1020
	GATTCGTGTTA	AGCATCCAAA	AACAATGCCT	AATTTTCAAT	CTTAGGTTAT	GGCTTGTGAC	1080
70	TCCAGATAAA	AGATGGAGAA	TACCTCATGT	ACTGTGACTT	GAAAATGAAT	TCTTAAAAAT	1140
	CTTAGGCTCT	CTCCATGTAT	CTTCTTAAAG	GAAAAGTTTC	TGAGTGTGAT	CTCTCTTTTG	1200
	CCATAGTATC	AAGTGGAGGG	TAGTTTCAGAA	AAGTTAATAG	GAAATCTTTT	GTGACAGCAG	1260
	ACTATAATAG	AAGTTTGAGT	AATATTTTAA	TAAATTTTAA	TAATTCAAAT	GATAAAAATG	1320
	TATCAATGTT	ATCCAATGAT	TTTTATTAAA	AAATTACCTT	ATTATTAGAA	CTGTGCCTAT	1380
75	TACATAAAAA	GTGCTCATGT	ATTGGAATTT	TAAATAATTT	ATTAAATCA	AGACCAACAT	1440
	AAGTCATTAA	TAATTTAATA	ATTGTTTAAA	ATCAGTGGTT	TTCAACCTCT	ACTTCATATT	1500
	AGAATCATCT	GAGGACTTTT	AATATGGAAT	CCACCTCATA	ACAATTAAGT	CTAAATTTCT	1560
	GGGAAGATGGA	GCCATCTTG	TTTTTCCAAA	AGCTCTTTGA	GTGATTTTCA	TTTGTAGTCA	1620
	GAGTTGAAGA	CCACTGCTCT	AAATTAGTGC	AGGAAAATGC	TTTTATTCTT	CCCATGTTAA	1680
80	CTTTTAAAC	TAGTAATGTA	CCAGTTAAG	TTTTGATGGT	TTAAATTTCA	CTAAAGAAC	1740
	TATTCTTCTA	ATAACTAGCA	TTTATTACAT	GAAATTTAAG	AGTTTAAGTT	CCATCAAAC	1800
	AGCCCTGTGT	TAAGATTATT	ATTTCTTCTC	TATAACTTCA	AAATAGATAT	TTCAATCAAA	1860
85	CTGTTCAAGT	GAGAAAACAT	AATGGATTTT	TTTTTTTTTC	CTCTGGAGCT	GCCTGTTCAG	1920
	TGAGATGGAG	GAGGTGGGCA	CATTTAAGGT	CAGTTCACTA	ACCTATGGTT	CAGAGTTCTG	1980
	ATCATATGGA	AGTTTGGAAA	AGAGAGCTTA	TCACAGGTTT	GTATGCTGGT	GAATGGATAG	2040
	TTTAAATCTC	CACGTCTTCA	AAAGAGAAAT	AGCTCTCCAG	CAGTTCTAGA	AAAGCTTTGA	2100
	CAATCCCCAA	GGGGCAGTGT	TACCTTACTC	CTTCACTGCT	TCTTAGAAGG	TAGAAATTAAG	2160
	TTTCTGGAAT	TGCACCTACA	TGTTTTCTTA	TTAACATTCA	GAATTTGGAA	TATTAATTTT	2220

TCCAGTGAAGT AGTTTTCTGA AATTGGTAAC TTGGAGAGTA AAATAACGTA TTTTGCTTTT 2280
 CAATTTTGTG TTTGTTTACT TTTATGTAAG AATTGGATAT GTGAATTACA CAGTTCTAAT 2340
 AAAACCTCAT GCCTTTTCAT TACATCTAAT TTGAACCTCT AACTTCAGTG CCAGAAGTGC 2400
 TTTAAAGATG CTTTAATGAA AAGTATTAAAG AAAATATATA GATTTGTATG TCAGTTTATA 2460
 CTTCAGAAAT CCATATATTT GTCATATTTA TTTTCTTAGA AACCTCCTAA TTGGATAACT 2520
 AGATGGTATT TAAATGAAT GCCCAAAAT ATCTTGTAAC TTTGTCCAAA AGTTTATCTG 2580
 TTGGAAGCCG CCAGCCATTC ATGTAGAGAG TTTATAAGAA AATAATTATA AATTGTATGC 2640
 ATTTTATATT ACTATGGTAT CTGTGTACCA TATTCTAAG TATTCTATAT TAAATTGGTA 2700
 CTTCTTAAAA CCATAACCTG CTTGCTCTTT TAGTGTAAAA CACAAAATCC AACATTGTAT 2760
 ATAGAGATTC TTCTTTTATG AAGAAGAGCT GACGTAATTT ATTACCACTG CATCTGCACA 2820
 AAGACATTAA CATAAGTCTC TGAGCAGTGA TACATTTTCA AACATGAAGA GTGACAACCA 2880
 CCACATTAAA CAACCCAGGC AACACTCAGA CTTGGCACTT TCCTACGAAT CCATCCTATA 2940
 TGTGCTTGGT ATGCGCTCTG GCATAACTTA CACGAATCGT CCTCCCTACT TGTCTAGCT 3000
 CCTTCATCAA GCACTTGCCA ACACATTAC CTCTAAGTTG TACAACCTTA CCAACTCACC 3060
 ACAACCTCTG CAACTCTACC CTATCAACTG CCAACCTAAA GACCCCAAC ACAACACAC 3120
 CCCCACACAC AAAACCATTA AATCATAACC ACCACACACG CCAACACCA CACACCCACC 3180
 CACACAACCA ACACACACG ACCAAACACC CCACCACAAA CAAGCTAACA ACCACAACA 3240
 GACAACACAT CACATACACT CACTACCCCC CCATACTCCC ACCCACCA

Seq ID NO: 234 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 27-281

1 11 21 31 41 51
 AGCAGGAGGA GAGCTGGCGG GAAGACATGC ACCCCTTGAA GACCCAGAGA GAGGCCGTCT 60
 GTCTACCGCG TAGCAGTTAC ATCAGACTGA GACACTTCCT GTTTACAGGA GACTATAAAA 120
 TTCTGCCCC GTGCTCATTT GGGGCTGACG CCATTTTAGG CCTCAGCCCA TCTGCACCCA 180
 GGCCTCTACT GAAAACAGTG GTTGCTCCAC ACCGCTTGT TTTGCTTGT GCGCGCTCT 240
 CAGGGTTCCG ACCAATCCAA GAGCCTTGCA GAAAGCATT ACGTGCTTTT CTCTTTGGCA 300
 GAGTTTTTCT TTGCTCTGAT CTTGGAGACA TCCTCTGCTC TAGTGGAAAC ATAAGGAATA 360
 CAGAAAGAAAT GCAAGGAGAT AGACCAACGT GAGATTCTCC TTCTATGCACT CAAGAGAAAG 420
 ATGTTGCAGG AAGAGCTAGT CTTTCAGGCT GGGCTGGTGA CCTGAGAAAG AATGTCACGC 480
 TTTTCTTCTC CACTTGGCAT ATCAAGAGCC AGGCGTGGAA GACTAAAAA GGAATGTTT 540
 ATAAAAAAGT TTACGCGGTT CGCCAAACAAG AAGTGGTAAA GTAGCAAAAA TGGGGATGGA 600
 GATGCCAGGA GGAAGATGCG CAGGGGTAAA GTGGGAAAAT GGGAACCTGA AGCCAGGAGG 660
 TCAAGCCAAG CCAACAGTGT TTTCTTTT CATCACAGAA CTAATAAGTG GTGCTGAGGA 720
 CTCAAAACCG GGAAGGCCA CTCTAGAACC CATGCTGGTC ATCCATATCC CCAAGGCCCT 780
 GGTGAGAAC CAGCTAAGCA GATGGCTTGG GTCATCAGGA CGTCCATTAC ATCCAAAGGA 840
 AGACAGCCTG TGACGTTTCA AAAGCAAAAAG TCCCCTACCA GCCAGTGAAG CTACCTGATT 900
 TCTCAGTATC TTACGCCAG TGACACGATC TACCCTCAA ACTTAAAAA AAAAGGGAAA 960
 CATAAACACA TAACAGCAGC AGCAATAATT AAAGATGAGA TGAGAACAA TAAGAAAAA 1020
 GGAAGGCTCT CCTGTGACTG TTTTATTTT AGGGAACAG AGAGGAAGAA GAATGATTTT 1080
 TCTTTTGATG ACTCTATATC CAACTCTGAG GTTTGATTAA AGAAATGACC TTGAACACA 1140
 GCAAGAAAAA ATAAAGACA ATTTCCAGTA AGTATGCCAG TTGCAATTAA TGATTTACTT 1200
 TTTATTTTTA AACTGAATTC AGCAGAGATT TACATGCATT ACGATGATTA ACATCTGAAA 1260
 TTTGACCTTG AAATAATCTT TACATTGTAA ATTCTTAATG ATCAAAACAA GGTCTCTCAGT 1320
 GATTAAACA TATTAGTAAT TAATTATTAA AGGAGAATAA TTGCAAAATC AACATTCTTA 1380
 AAATCTCAAG GCTTTTAAAG CATTGTGACA AATGACTGGA CATTTTATA ATTGAAAAA 1440
 AAAAAAAGC CCTCCATCTG ATTCTCATTT TCATTGTGAG TGCAACAACA AAAAAGGTAT 1500
 GCACCTTCTCT TCTCATTTTC CACTGTCTCG CAAGCTAGAA ATTCTCACGA CTACCTTTGA 1560
 TCCCATCAAA GCCAAAGAAA GAAAAGAAAA TTGTTCTGTA CAGATATATG ACATTAAAAA 1620
 ATAATCCC

Seq ID NO: 235 Protein sequence:
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MHPLKQREA VCLPRSSYIR LRHFLFTGDY KIPAPCSFGA DAILGLSPSA PRRSLKQCV 60
 PHRLVLLVGA LSGFRPIQEP CRKH

Seq ID NO: 236 DNA sequence
 Nucleic Acid Accession #: NM_002075
 Coding sequence: 406..1428

1 11 21 31 41 51
 CCACAATAGG GGCAGACCTG TCCATCCTTC TCTGTGGGTC CCCTGTACCT TTCTCCCCA 60
 ACAGGATCAG ACCCAGAGGC AGCTGGTTGG GGTTTGTGCA GAAGAAGGAT TATCCAGATC 120
 AGTCCTTTCT AATCTCAGCT CCTGCCTGTA CCTCCCATTA CTCACCAAC CCTCTTCCC 180
 ACCACCTGGA GCTGAGGAGC ACAGTTTGAG GCCCCCCCAA CCCCCCGCCG GTCGGGGCCA 240
 GGCCAGGCCA GGCCAGCTCC TCTGGCAGCA GAGCCTGGGC AGGTGACGGG CGGGCGCGGG 300
 CGTCGCAAGT GAGGGAGTAA GGAGGCTCCC AGGAACCGGA GCTGGAACCC CGGCGGAGGT 360
 CCAGCCAGAG CCAAGAGGCC AGATGACCCC CTCGACCTGT CAGCCATGGG GGAGATGGAG 420
 CAACTGCGTC AGGAAGCCGA GCAGCTCAAG AAGCAGATTG CAGATGCCAG GAAAGCCTGT 480
 GCTGACGTTA CTCTGGCAGA GCTGGTGTCT GGCCTAGAGG TGGTGGGACG AGTCCAGATG 540
 CGGACGCGGC GGACGTTAAG GGGACACCTG GCCAAGATTT ACGCCATGCA CTGGGCCACT 600
 GATTCTAAGC TGTGTTAAG TGCCTCGCAA GATGGGAAGC TGATCGTGTG GGACAGCTAC 660
 ACCACCAACA AGGTGCAGCG CATCCCATG CGCTCCTCCT GGGTCATGAC CTGTGCCCTAT 720
 GCCCCATCAG GGAACCTTGT GGCATGTGGG GGGCTGGACA ACATGTGTTC CATCTACAC 780
 CTCAAATCCC GTGAGGGCAA TGTCAAGGTC AGCCGGGAGC TTTCTGCTCA CACAGGTTAT 840
 CTCTCCTGCT GCCGCTTCTT GGATGACAAC AATATTGTGA CCAGCTCGGG GGACACACG 900
 TGTGCTTGT GGGACATTGA GACTGGGACG CAGAAGACTG TATTGTGGG ACACACGGGT 960
 GACTGCATGA GCCTGGCTGT GTCTCCTGAC TTCAATCTCT TCATTTCGGG GGCTGTGTAT 1020
 GCCAGTGCCA AGCTCTGGGA TGTGCGAGAG GGGACCTGCC GTCAGACTTT CACTGGCCAC 1080

GAGTCGGACA TCAACGCCAT CTGTTTCTTC CCCAATGGAG AGGCCATCTG CACGGGCTCG 1140
 GATGACGCTT CCTGCCGCTT GTTTGACCTG CGGGCAGACC AGGAGCTGAT CTGCTTCTCC 1200
 CACGAGAGCA TCATCTGCGG CATCACGTCC GTGGCCTTCT CCCTCAGTGG CCGCCTACTA 1260
 TTCGCTGGCT ACGACGACTT CAACTGCAAT GTCTGGGACT CCATGAAGTC TGAGCGTGTG 1320
 GGCATCTCTT CTGGCCACGA TAACAGGGTG AGCTGCCTGG GAGTCACAGC TGACGGGATG 1380
 GCTGTGGCCA CAGGTTCTTG GGACAGCTTC CTCAAAATCT GGAAGCTGAGG AGGCTGGAGA 1440
 AAGGGAAGTG GAAGGCAGTG AACACACTCA GCAGCCCCCT GCCCGACCCC ATCTCATTTA 1500
 GGTGTTCTCT TCTATATTCC GGGTGCCATT CCCACTAAGC TTTCTCTTTT GAGGGCAGTG 1560
 GGGAGCATGG GACTGTGCCTT TTGGGAGGCA GCATCAGGGA CACAGGGGCA AAGAACTGCC 1620
 CCATCTCTCT CCATGGCCTT CCCCTCCACC AGTCCTCACA GCCTCTCCCT TAATGAGCAA 1680
 GGACAACTCG CCCCTCCCA GCCCTTTGCA GGCCAGCAG ACTTGAGTCT GAGGCCCCAG 1740
 GCCCTAGGAT TCCTCCCA GAGCCACTAC CTTTGTCCAG GCCTGGGTGG TATAGGGCGT 1800
 TTGGCCCTGT GACTATGGCT CTGGCACCAC TAGGGTCCTG GCCCTCTTCT TATTCATGCT 1860
 TTCTCCTTTT TCTACCTTTT TTTCTCTCT AAGACACCTG CAATAAAGTG TAGCACCTGT 1920
 GT

Seq ID NO: 237 Protein sequence:
 Protein Accession #: NP_002066

1 11 21 31 41 51
 MGEMEQLRQE AEQLKKQIAD ARKACADVTI AELVSGLEV V GRVQMRTRRT LRGLHLAKIYA 60
 MHWATDSKLL VSASQDGLLI VMDSYTTNKV HAIPLRSSWV MTCAYAPSGN FVACGGGLDNM 120
 CSIYNLKSRE GNVKVSRELS AHTGYLSCCR FLDDNNIVTS SGDITCALWD IETGQKQTVF 180
 VGHTGDCMSL AVSPDFNLFI SGACDASAKL WDVREGTCRQ TFTGHESDIN AICFFPNGEA 240
 ICTGSDDASC RLFDLRADQE LICFSHESII CGITSVAFSL SGRLLFAGYD DFNENNVDSM 300
 KSERVGILSG HDNRVSLGV TADGMAVATG SWDSFLKIWN

Seq ID NO: 238 DNA sequence
 Nucleic Acid Accession #: CAT cluster

1 11 21 31 41 51
 TCCCAATGTG TNGAACCTAC CATAAATTCT TTTCTTACNG GACAATCTTA TNCTAANCAA 60
 TACCAATTGC TTTTAAGGCA GATAATCCTC CAAGTTTCT AATGATATCT GAAACTATTA 120
 ACTGATCTCG TGAATATAGA AATCTGAAAA GGAAATGGAA GTTGCTAAAA ATCTATCATT 180
 TGCATTGACC AGTGTGAAGC ACAGTGAAGT GAGAATGCGT GCCCTGACAC CAAAGAAAAA 240
 TAAGTGACTG GAAAGCTGAA GAATCACCGG CTCAGTGAC ATGGAACCCA GTGATTTGAT 300
 TTTTGACGAG TATCGGGTGA CTTTGAGGTG GTCAAGAAAC CACACTTTAA GAACAATGTC 360
 AAAAAAGGGG AAAAAAAGA GCAACCAAAG AAAAAAATC CATAAAATG CACAGAAGAA 420
 AAGAAAGAAA AATAAATAC ACAATATGGA CGATGGAGAA AAACAGTTAC ATTTCTTTAT 480
 GGATCAAGAA GTTTGTGTAC ACATAATCTC ATTTTGAGAT ATATAACTAT TTTTGTCTTT 540
 CAGAAGTGAA TCAAAATATT TCAAAATGCT GTCTTATGAA ACTACAATAT TCTCACAGAT 600
 TAGAAAAGTT TTTCTGTAA AGTCAGATAG TAAATATTTT AGGTTTTCGA GTGTCTTTTG 660
 CAACTACTCA ACTTTCCTAC TGTAGCACAA GAGTAGCTGT GGTACTGTGC AAATAAATG 720
 CTTGTGTTCC AATAAGCTT CATTACAAA AACATGCCAT GGGCCATATT TGGCCTGTAC 780
 ACTGTTGTTT GCCAAGTCTT AATATAGTTG CTTAGCAAGT ATTGTGAGCT ATTTGAGGAA 840
 GACATGAAAG TCTATTGGGT TGCTAAAAAG TATGTAGAAA TTCAAAGGAA AATTAAATTT 900
 TAGGCTAAGT TATAATACAC TGTTTTAACA ATTGTAAAT GTAAGAGAAA TTTACAAATA 960
 AAAATCCCAA ATAAAA

Seq ID NO: 239 DNA sequence
 Nucleic Acid Accession #: NM_001786.1
 Coding sequence: 130-1023

1 11 21 31 41 51
 GGGGGGGGGG GGCACCTTGGC TTCAAAGCTG GCTCTTGGA ATTGAGCGGA GAGCGACGCG 60
 GTTGTGTAG CTGCCGCTGC GGCCGCCGCG GAATAATAAG CCGGGATCTA CCATACCCAT 120
 TGAATACTA TGGAAGATTA TACCAAAATA GAGAAAATTG GAGAAAGTAC CTATGGAGTT 180
 GTGTATAAGG GTAGACACAA AACTACAGGT CAAGTGGTAG CCATGAAAAA AATCAGACTA 240
 GAAAGTGAAG AGGAAGGGGT TCCTAGTACT GCAATTCGGG AATTTCTCT ATTAAAGSAA 300
 CTTGCTCATC CAAATATAGT CAGTCTTCAG GATGTGCTTA TGCAAGATTC CAGGTATAT 360
 CTCATCTTTG AGTTTCTTTC CATGGATCTG AAGAAATACT TGGATTCTAT CCTCCTGGT 420
 CAGTACATGG ATTCTTCACT TGTTAAGAGT TATTTATACC AAATCCTACA GGGGATTGTG 480
 TTTTGTCACT CTAGAAGAGT TCCTTACAGA GACTTAAAC CTCAAAATCT CTTGATTGAT 540
 GACAAAGGAA CAATTAAACT GGCTGATTTT GGCCTTGCCA GAGCTTTTGG AATACCTATC 600
 AGAGTATATA CACATGAGGT AGTAACACTC TGGTACAGAT CTCCAGAAAT ATTGCTGGGG 660
 TCAGCTCGTT ACTCAACTCC AGTTGACATT TGGAGTATAG GCACCATATT TGCTGAACCTA 720
 GCAACTAAGA AACCACTTTT CCATGGGGAT TCAGAAATTG ATCAACTCTT CAGGATTTTC 780
 AGAGCTTTGG GCATCCCA TAATGAAGTG TGGCCAGAA TGAATCTTT ACAGGACTAT 840
 AAGAATACAT TTCCCAATG GAAACCAGGA AGCCTAGCAT CCCATGTCAA AAACCTGGAT 900
 GAAAAATGGCT TGGATTGTCT CTCGAAAATG TTAATCTATG ATCCAGCCAA ACGAATTTCT 960
 GGCAAAATGG CACTGAATCA TCCATATTTT AATGATTGAG ACAATCAGAT TAAGAAGATG 1020
 TAGCTTTCTG ACAAAAGTT TCCATATGTT ATGTCAACAG ATAGTTGTGT TTTTATTGTT 1080
 AACTCTTGTC TATTTTGTCT TTTATATAT TTTCTTTGTA TCAAACTTCA GCTGTACTTC 1140
 GTCTTCTAAT TTCAAAAATA TAACTTAAAA ATGTAAATAT TCTATATGAA TTTAAATATA 1200
 ATTCTGTAAA TGTGAAAAA AAAAAAATA AAAAA

Seq ID NO: 240 Protein sequence:
 Protein Accession #: NP_001777.1

1 11 21 31 41 51
 MEDYTKIEKI GEGTYGVVYK GRHKTGTQVV AMKKIRLESE EEGVPSTAIR EISLLKELRH 60
 PNIVSLQDVL MQDSRLYLIF EFLSMDLKKY LDSIPPGQYM DSSLVKSPLY QILQGIVFCH 120

SRRVLHRDLK PQNLLIDDKG TIKLADFGLA RAFGIPIRVY THEVVTWLWYR SPEVLLGSAR 180
 YSTPVDIWSI GTIFABELATK KPLFHGDSEI DQLFRIFRAL GTPNNEVWPE VESLQDYKNT 240
 FPKWKPGSLA SHVKNLDENG LDLLSKMLIY DPAKRISGKM ALNHPYFNDL DNQIKKM

5

Seq ID NO: 241 DNA sequence
 Nucleic Acid Accession #: NM_033379.1
 Coding sequence: 132-854

10 1 11 21 31 41 51
 CGCCCGCGCG CGGGCTCAAC TTTGTAGAGC GAGGGGCCAA CTTGGCAGAG CGCGCGGCCA 60
 GCTTTGCAGA GAGCGCCCTC CAGGGACTAT GCGTGCAGGG ACACGGGATC TACCCATACC 120
 15 ATTGACTAAC TATGGAAGAT TATACCAAAA TAGAGAAAAT TGGAGAAGGT ACCTATGGAG 180
 TTGTGTATAA GGGTAGACAC AAAACTACAG GTCAAGTGGT AGCCATGAAA AAAATCAGAC 240
 TAGAAAGTGA AGAGGAAGGG GTTCCTAGTA CTGCAATTCT GGAAATTTCT CTATTAAAGG 300
 AACTTCCTCA TCCAAATATA GTCACTCTTC AGGATGTGCT TATGCAGGAT TCCAGGTTAT 360
 ATCTCATCTT TGAGTTTCTT TCCATGGATC TGAAGAAAATA CTTGGATTCT ATCCCTCCTG 420
 20 GTCACTACAT GGATTCCTCA CTTGTTAAGG TAGTAACACT CTGGTACAGA TCTCCAGAAG 480
 TATGTCTGGG GTCACTCTGT TACTCAACTC CAGTTGACAT TTGGAGTATA GGCACCATAT 540
 TTGCTGAAC AGCAACTAAG AAACCACTT TCCATGGGGA TTCAGAAAT GATCAACTCT 600
 TCAGGATTTT CAGAGCTTTG GGCACCTCCA ATAATGAAGT GTGGCCAGAA GTGGAATCTT 660
 TACAGGACTA TAAGAAATACA TTTCCCAAAAT GGAACACAGG AAGCCTAGCA TCCCATGTCA 720
 25 AAAACTTGA TAAGAAATGGC TTGGATTGCT TCTCGAAAAA GTTAATCTAT GATCCAGCCA 780
 AACGAATTC TGGCAAAATG GCACTGAATC ATCCATATTT TAATGATTG GACAATCAGA 840
 TTAAGAAAGT GTAGCTTTCT GACAAAAAGT TTCCATATGT TATGTCAACA GATAGTTGTG 900
 TTTTATTGT TAACCTCTGT CTATTTTGT CTATATATA TTTCTTTGT ATCAAACCTC 960
 AGCTGTACTT CGTCTTCTAA TTTCAAAAAT ATAACCTAAA AATGTAAATA TTCTATATGA 1020
 30 ATTTAAATAT AATTCTGTAA ATGTGAAAAA AAAAAAATA AAAAAA

Seq ID NO: 242 Protein sequence:
 Protein Accession #: NP_203698.1

35 1 11 21 31 41 51
 MEDYTKIEKI GEGTYGVVYK GRHKTTGQVV AMKKIRLESE EEGVPSTAIR EISLLKELRH 60
 PNIVSLQDVL MQDSRLYLIF EFLSMDLKKY LDSIPPGQYM DSSLVKVVTL WYRSPVLLG 120
 SARYSTPVDI WSLGTIFAEL ATKKPLPHGD SEIDQLFRIF RALGTPNNEV WPEVESLQDY 180
 40 KNTFPKWPG SLASHVNLD ENGLDLLSKM LIYDPAKRIS GKMLNHPYP NDLNQNKKM

Seq ID NO: 243 DNA sequence
 Nucleic Acid Accession #: AF101051.1
 Coding sequence: 221-856

45 1 11 21 31 41 51
 GAGCAACCTC AGCTTCTAGT ATCCAGACTC CAGCGCCGCC CCGGGCGCGG ACCCCAACCC 60
 CGACCCAGAG CTTCTCCAGC GCGGGCGCAG CGAGCAGGGC TCCCGGCCTT AACTTCTCTC 120
 50 GCGGGGCCCA GCCACCTTCG GGAGTCCGGG TTGCCACCTC GCAAACTCTC CGCCTTCTGC 180
 ACCTGCCACC CTTGAGCCAG CGCGGGCGGCC CGAGCGAGTC ATGGCCAACG CGGGGCTGCA 240
 GCTGTGTGGG TTAATCTCTG CCTTCTCTGG ATGGATCGGC GCCATCGTCA GCACTGCCCT 300
 GCCCCAGTGG AGGATTACTT CCTATGCCGG CGACAACATC GTGACCGCCC AGGCCATGTA 360
 CGAGGGGCTG TGAGTGTCTT GCGTGTGCGA GAGCACCAGG CAGATCCAGT GCAAACTCTT 420
 55 TGACTCCTTG CTGAATCTGA GCAGCACATT GCAAGCAACC CGTGCCTTGA TGGTGGTTGG 480
 CATCCTCTCG GAGTGTATAG CAATCTTTGT GGCACCGCTT GGCATGAAGT GTATGAAGTG 540
 CTTGGAAGAG GATGAGGTGC AGAAGATGAG GATGGCTGTC ATTGGGGGTG CGATATTCTT 600
 TCTTGCAAGT CTGGCTATTT TAGTTGCCAC AGCATGGTAT GGCATAGATA TCGTTCAAGA 660
 ATTCTATGAC CCTATGACCC CAGTCAATGC CAGGTACGAA TTTGGTCAGG CTCTCTTCAC 720
 60 TGGCTGGGCT CTGCTCTCTC TCTGCCCTCT GGGAGGTGCC CTACTTTGCT GTTCCTGTCC 780
 CCGAAAAACA ACTCTTACC CAACACCAAG GCCCTATCCA AAACCTGCAC CTTCACGCGG 840
 GAAAGACTAC GTGTGACACA GAGCAAAAAG GAGAAAATCA TGTGTAAACA AACCAGAAAT 900
 GGACATTGAG ATACTATCAT TAACATTAGG ACCTTAGAAT TTTGGGTATT GTAATCTGAA 960
 GTATGGTATT AAAAAACAAA CAAACAAACA AAAAACCCAT GTGTAAAAAT ACTCAGTGCT 1020
 65 AAACATGGCT TAATCTTATT TTATCTTCTT TCCTCAATAT AGGAGGGAAG ATTTTACCAT 1080
 TTGTATTACT GCTTCCCATT GAGTAATCAT ACTCAAATGG GGGAGGGGGT GCTCCTTAAA 1140
 TATATATAGA TATGTATATA TACATGTTTT TCTATTAAAA ATAGACAGTA AAATACTATT 1200
 CTCATTATGT TGATACTAGC ATACTTAAAA TATCTCTAAA ATAGGTAAAT GTATTTAATT 1260
 CCATATTGAT GAAGATGTTT ATTGGTATAT TTTCTTTTTC GTCCCTATAT ACATATGTAA 1320
 70 CAGTCAATA TCATTTACTT TTCTTCATTA GCTTGGGTG CTTTGCCAC AAGACCTAGC 1380
 CTAATTTACC AAGGATGAAT TCTTTCAATT CTTTCATGCGT GCCCTTTTCA TATACTTATT 1440
 TTATTTTTTA CCATAATCTT ATAGCACTTG CATCGTTATT AAGCCCTTAT TTGTTTTGTG 1500
 TTTTATGGT CTCTATCTGC TGAATCTAAC ACATTTTATA GCCTACATTT TAGTTTCTAA 1560
 75 AGCCAAAGAAG AATTTATTAC AAATCAGAAC TTTGGAGGCA AATCTTTCTG CATGACCAA 1620
 GTGATAAATT CTGTTTGACC TTCCACACACA ATCCCTGTAC TCTGACCCAT AGCACTCTTG 1680
 TTTGCTTTGA AATATTGTG CCAATTGAGT AGCTGCATGC TGTTCGCCCA GGTGTTGTAA 1740
 CACAACCTTA TTGATTGAAT TTTTAAGCTA CTTATTATAT GTTTTATATC CCCCTAAACT 1800
 80 ACCTTTTGTG TCCCATCTCC TTAATTGTAT TGTTTTCCCA AGTGTAATTA TCATGCGTTT 1860
 TATATCTTCC TAATAAGGTG TGGTCTGTTT GTCTGAACAA AGTGCTAGAC TTTCTGGAGT 1920
 GATAATCTGG TGACAAATAT TCTCTCTGTA GCTGTAAGCA AGTCACCTAA TCTTTCTACC 1980
 TCTTTTCTCT ATCTGCCAAA TTGAGATAAT GATACTTAAC CAGTTAGAAG AGGTAGTGTG 2040
 AATATTAATT AGTTTATATT ACTCTCATTC TTTGAACATG AACTATGCCT ATGTAGTGTC 2100
 TTTATTTGCT CAGCTGGCTG AGACACTGAA GAAGTCACTG AACAAAACCT ACACACGTAC 2160
 85 TTTCTATGTA TCTACTGCTT TCCTCTCTCT ACCAGTCTAT TTCCACTGAA CAAAACCTAC 2220
 ACACACTACCT TCATGTGGTT CAGTGCCTTC CTCTCTCTAC CAGTCTATTT CCATGAACA 2280
 AAACCTACGC ACATACCTTC ATGTGGCTCA GTGCCTTCCT CTCTCTACCA GTCTATTTC 2340
 ATTCTTTTCA CTGTGCTGTA CATGTTTGTG CTCTGTTCCA TTTTAAACAA TGCTCTTACT 2400
 TTTCCAGTCT GTACAGAAAT CTATTTCACT TGAGCAAGAT GATGTATGGA AAGGGTGTG 2460

GCACTGGTGT CTGGAGACCT GGATTGAGT CTTGGTGCTA TCAATCACCG TCTGTGTTTG 2520
 AGCAAGGCAT TTGGCTGCTG TAAGCTTATT GCTTCATCTG TAAGCGGTGG TTTGTAATTC 2580
 CTGATCTTCC CACCTCACAG TGATGTTGTG GGGATCCAGT GAGATAGAAT ACATGTAAGT 2640
 GTGGTTTTGT AATTGAAAAA GTGCTATACT AAGGGAAAAG ATTGAGGAAT TAACTGCATA 2700
 CGTTTTGGTG TTGCTTTTCA AATGTTTGAA AATAAAAAAA TGTTAAGAAA TGGGTTTCTT 2760
 GCCTTAACCA GTCCTCAAG TGATGAGACA GTGAAGTAAA ATTGAGTGCA CTAAACGAAT 2820
 AAGATTCTGA GGAAGTCTTA TCTTCTGCAG TGAGTATGGC CCAATGCTTT CTGTGGCTAA 2880
 ACAGATGTAA TGGGAAGAAA TAAAGCCCTA CGTGTGGTA AATCCAACAG CAAGGGAGAT 2940
 TTTTGAATCA TAATAACTCA TAAGGTGCTA TCTGTTCACT GATGCCCTCA GAGCTCTTGC 3000
 TGTTAGCTGG CAGCTGACGC TGCTAGGATA GTTAGTTTGG AAATGGTACT TCATAATAAA 3060
 CTACACAAGG AAGTCAAGC ACCGTGCTT ATGAGGAATT GGACCTAATA AATTTTAGTG 3120
 TGCCTCCAA ACCTGAGAAT ATATGCTTTT GGAAGTTAAA ATTTAAATGG CTTTGGCCAC 3180
 ATACATAGAT CTTTATGATG TGTGAGTGTA ATTCCATGTG GATATCAGTT ACCAAACATT 3240
 AAAAAAAAT TTTATGGCCC AAAATGACCA ACGAAATTGT TACAATAGAA TTTATCCAAT 3300
 TTTGATCTTT TTATATTCTT CTACCACACC TGGAAACAGA CCAATAGACA TTTTGGGGTT 3360
 TTATAATGGG AATTGTGATA AAGCATTACT CTTTTCATAT AAATGTTTTT TTAATTTAAA 3420
 AAAAGGAAAA AAAAAAAA AAA

Seq ID NO: 244 Protein sequence:
 Protein Accession #: AAD16433.1

1 11 21 31 41 51
 | | | | |
 MANAGLQLLG FILAFLGWIG AIVSTALPQW RIYSYAGDNI VTAQAMYEGL WMSCVSQSTG 60
 QIQCKVFDLS LNLSSLTQAT RALMVVGILL GVIAIFVATV GMKCMKLED DEVQKMRMAV 120
 IGGAILLLAG LAILVATAWY GNRIVQEFYD PMTPVNARYE FGQALFTGWA AASLCLLGGA 180
 LLCSCPRKT TSYTPRPYP KPAPSSGKDY V

Seq ID NO: 245 DNA sequence
 Nucleic Acid Accession #: CAT cluster

1 11 21 31 41 51
 | | | | |
 TTTTTTTTTT TTTTTTTTTT TTTTCAAGG AGAGCACAAAG GAACCTTTATT AATGACTTTC 60
 TTAATGGTTA AATGCTGTTT ACCAAGTGAC CCAGAGGCAG CGTGGTTTAG TGGTTTCAAC 120
 AGCATGGTCC CGAGAGTCTG ACAAACCTCA GTTCAAATCC TTCTTTTGTC TTCACCTAGT 180
 TTTTCTTCTT GAGATTTAGT TTCCTCATCG TTAACAATGA GGATATTAAAT ATGTTTCACA 240
 CAGTTGTTAT GAAGAATGCA TATATTAGAA TGCCTGTAGT CTCAGCTACT CAGGAGGCTA 300
 AGGTGGGGAG GTCCCTCAAG CCCAGGAATT CAAAGCTGCA ATGCATTATG ATTACAGCTG 360
 TTAATAGCCA CTGCACTTCA GCCTGGGCAA TGTAGTAAGA TCCCATCTCT GGCTCGGAGG 420
 GTCCTACGCC CACGGAGTCT CGCTGATTGC TAGCACAGCA GTCGTGAGATC AAACCTGCA

Seq ID NO: 246 DNA sequence
 Nucleic Acid Accession #: XM_058553.2
 Coding sequence: 897-1400

1 11 21 31 41 51
 | | | | |
 AATTTTCAGA AGTTTCGTAT GGGGATGGTT TTATATAAAT TCAGGTTTTT CCCACAATAA 60
 TAAATGTATT TAGTCTCAGT GCTCAATAGA AGAGATTCTT AATAGAAAAG GATTCAAAC 120
 GTGAAACCAT TTCTCTTTTAT ATGTTTCACA TTCCTGTAC AGATTGTTC TCTTGTGACT 180
 CTGTTATCCA TAATATGAC AGTTCTTGAG TCCTAACATT GAGAGGTTTT CCCTTAGTGC 240
 ATAGAGGGAA TGAGTATTAA TTGGAGAAGC TTAAGTATT GCCACTTTAG CACTGAAGAT 300
 TGGGATGAGA GAGGGTGAAA CCTCACTAGA AAAAGGGACA ATGTTAGTGT GGCCCTTCCT 360
 GATCATGTTT AAGAAAAATG ATGAAAAATG TGAAGTAGTG TTTCCAAGCA TATTGGAAGG 420
 GTTGAGTGTA TACTGTCTGT CAAAGACTTC CAGCATTTC AGGTCCCTAGA GAGGAACAAG 480
 ACTGGTAACC TGCCTATCTG TATTTTTAAG AACCCAGGAG GAAAGCTTTA TAATAGAACA 540
 TTATTTCTGT GTTTATGTAT AAGGGGTTTT TTGTTTTTTT AAAGACAGGA TCTCACTCCA 600
 TTGTCAGGCG CAAGTGCAAT GGCACGAACC TCATAGCTCC TGGACTTAAG TGATCTGCCT 660
 GCCTTTGCCT CCTGAGTAGC TGGGACTACA GGCATGAGCC CCCATGCCTG GCTAAGTTTG 720
 TTTTTTTGTT TGTGTTGTTG TTTGTTTTTG GGGGGGGTTG TTTTGTTTTT TGTAGAGACG 780
 TAGTCTTGCT TTGTTGCCAG GCTAGTCTCA AACTCCTGGC TTCAGTGAT CCTCCTGCCT 840
 CAGCTCCCA GAGTGCTAGG ATTACAGCAC TTGGATTGAG CTTCTTCATT TCCAACATGG 900
 AAGAACTTA CACCGACTCC CTGGACCCCTG AGAAGCTATT GCAATGCCCC TATGACAAAA 960
 ACCATCAAA CAGGGCTTGC AGTTTCCTT ATCATCTTAT CAAGTGCAGA AAGAATCATC 1020
 CTGATGTTGC AAGCAAAATTG GCTACTTGTC CCTTCAATGC TCGCCACCAG GTTCTCTGAG 1080
 CTGAAATTAG TCATCATATC TCAAGCTGTG ATGACAGAAG TTGTATTGAG CAGATGTTG 1140
 TCAACCAAAC CAGGAGCCTT AGACAAGAGA CTCTGGCTGA GAGCACTTGG CAGTGCCCTC 1200
 CTTGCGATGA AGACTGGGAT AAAGATTGTT GGGAGCAGAC CAGCACCCCA TTTGTCTGGG 1260
 GCACAACCTA CTACTCTGAC AACACAGGCC CTGCGAGCAA CATAGTTACA GAACATAAGA 1320
 ATAACCTGGC TTCAGGCATG CGAGTTCCCA AATCTCTGCC GTATGTTCTG CCATGGAAAA 1380
 ACAATGGAAA TGCACAGTAA CTGAATACCT ATCTCATCAA ATGCCAGACC CTAGAAGACT 1440
 GTTGCTTCTT CTTCTACCAG TGGGTTCTCA TTTTCTCCT AATCTAATTA TAGAATGGTA 1500
 AACTCCCTGT GACTTCCAA ACTGACAAGC ACACCTTTTT CCTCCCCCT TGAATCTCTA 1560
 TTTAATGCAA GAACCTCAT ACTCAGAAGC TTCCAAATAA ACCTTTGATA CAGATTG

Seq ID NO: 247 Protein sequence:
 Protein Accession #: XP_058553.1

1 11 21 31 41 51
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 RAEISHHISS CDDRSCEIQD VVNQTRSLRQ ETLEASTWQC PPCDEDDWKO LWEQTSSTFFV 120
 WGTTHYSNN SPASNIVTEH KNNLASGMRV PKSLPYVLPW KNNGNAQ

Seq ID NO: 248 DNA sequence
Nucleic Acid Accession #: NM_003392
Coding sequence: 758..1855

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10    CGCGCTGGTC CCGGGGGCCT CGCCCCCCAC CCCCTGCCCT TCCCTCCCGC GTCCTGCCCC 180
CATCTCCAC CCCCCGCGT GGCCACCCCG CCTCCTTGGC AGCCTCTGGC GGCAGCGCGC 240
TCCACTCGCC TCCCGTGCTC CTCTCGCCCA TGGAAATTAAT TCTGGCTCCA CTGTGTGCTC 300
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GAGGGACTGA GCACAGCACC AACTAGAGAG GGGTCAGGGG GTGCGGGACT CGAGCGAGCA 420
15    GGAAGGAGGC AGCGCTTGGC ACCAGGGCTT TGACTCAACA GAATTGAGAC ACGTTTGTAA 480
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GAGAAGCGCA GTCAATCAAC AGTAACTTA AGAGACCCCC GATGCTCCCC TGGTTAACT 660
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CAAGTTCTTC CTAGTGGCTT TGGCCATATT TTTCTCTTTC GCCCAGGTTG TAATTGAAGC 840
CAATTCTTGG TGGTCGCTAG GTATGAATAA CCTGTTCAG ATGTCAGAAG TATATATTAT 900
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25    CCACTTGTAT CAGGACCACA TGCAGTACAT CGGAGAAGGC GCGAAGACAG GCATCAAGA 1020
ATGCCAGTAT CAATTCGAC ATCGACGGTG GAACTGCAGC ACTGTGGATA ACACCTCTGT 1080
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30    GCGCATCCAC GCCAAGGGCT CCTACGAGAG TGCTCGCATC CTATGAACC TGCAACAACA 1380
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45    CTGTGTGGGA CATGGTACAC ATCCAGAAGG TAAAGAAATA CATTTCTTT TTCTCAATA 2220
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50    GGTATATCAC ATGTCTCATT CTCCTCAAA ATTTCCATTG CAGACAGACC GTCATATTCT 2520
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60    TGGAAAAAG TTTCACTACT AGGGATTTT GTTTCCTAAA ACTTTTATTT TGAGGAGCAG 3060
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CACTACATAG ATAGCTTTT TTTTTTTTT TTTTTTTTTA TAAGGACACC TCTTTCCAAA 3840
75    CAGGCCATCA AATATGTTCT TATCTCAGAC TTACGTTGTT TTAAGAGTTT GGAAAGATAC 3900
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TACTTTTTTT ATTTGCTAAA TCAGATTGTT CCTTTTATAGT GACTCATGTT TATGAAGAGA 4200
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CATTCAGATA TTATGTATAT CTCTAGCCCT TTATTCTGTA CTTTAAATGT ACATATTCT 4320
85    GTCTTGCGTG ATTTGTATAT TTCCTGGTT TAAAAAAACA ACATCGAAGG GCTTATTCCA 4380
AATGAAGAT AGAATATAAA ATAAAACGTT ACTTGTAATA AAAAAAAA

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Seq ID NO: 249 Protein sequence:
Protein Accession #: NP_003383

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 AFTYAVSAAG VVNAMSRACR EGELSTCGCS RAARPKDLPR DWLWGGCGDN IDYGYRFAKE 180
 FVDARERERI HAKGSYBSAR ILMNLHNEEA GRRTVYNLAD VACKCHGVSG SCSLKTCWLQ 240
 LADFRKVGDA LKEKYDSAAA MRLNSRGKLV QVNSRFNSPT TQDLVYIDPS PDYCVRNEST 300
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Seq ID NO: 250 DNA sequence
 Nucleic Acid Accession #: NM_014058
 Coding sequence: 56..1324

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 CGTCATCTTC ATATCCCTGA TTGCTCTGGC AGTGTGCATT GGACTCACTG TTCATTATGT 180
 GAGATATAAT CAAAAGAAGA CCTACAATTA CTATAGCACA TTGTCATTTA CAACTGACAA 240
 ACTATATGCT GAGTTTGGCA GAGAGGCTTC TAACAATTTT ACAGAAATGA GCCAGAGACT 300
 20 TGAATCAATG GTGAAAAATG CATTTTATAA ATCTCCATTA AGGGAAGAAT TTGTCAAGTC 360
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 TGAAGAGCTG CAAGATGCTG TAGGACCCCC TAAAGTAGAT CCTCACTCAG TTAATAATTAA 540
 AAAAATCAAC AAGACAGAAA CAGACAGCTA TCTAAACCAT TGCTGCGGAA CACGAAGAAG 600
 25 TAAACTCTA GGTGAGAGTC TCAGGATCGT TGGTGGGACA GAAGTAGAAG AGGGTGAATG 660
 GCCCTGGCAG GCTAGCCTGC AGTGGGATGG GAGTCATCGC TGTGGAGCAA CCTAATTAA 720
 TGCCACATGG CTTGTGAGTG CTGCTCACTG TTTTACAACA TATAAGAAC CTGCCAGATG 780
 GACTGCTTCC TTTGGAGTAA CAATAAAACC TTCGAAAATG AAACGGGGTC TCCGGAGAAT 840
 AATGTCTCAT GAAAAATACA AACACCCATC ACATGACTAT GATATTTCTC TTGCAGAGCT 900
 30 TTCTAGCCCT GTTCCCTACA CAAATGCAGT ACATAGAGTT TGCTCCCTG ATGCATCCTA 960
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 35 AGATATCTGG TACCTTGCTG GAATAGTGAG CTGGGGAGAT GAATGTGCGA AACCCAAACA 1260
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 CTAAGAGAGA AAGCCCTCAT GGAACAGATA ACATTTTTTT TTGTTTTTTG GGTGTGGAGG 1380
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 40 AATAAACTGT TTGCTTGATG CAAAAAAA A

Seq ID NO: 251 Protein sequence:
 Protein Accession #: NP_054777

1 11 21 31 41 51
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 45 MYRPDVVRAR KRVCWEPWVI GLVIFISLIV LAVCIGLTVH YVRYNQKQTY NYYSTLSFTT 60
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 50 ICRFHSTEDP ETVDKIQVLV LHEKLQDAVG PPKVDPHSVK IKKINKTETD SYLNHCCGTR 180
 RSKTLGQSLR IVGGTEVEEG BWPWQASLQW DGSHRCGATL INATWLVSAA HCFTTYKNPA 240
 RWTASFGVTI KPSKMKRGLR RIIVHEKYKH PSHDYDISLA ELSSPVPTYN AVHRVCLPDA 300
 SYEQPGDVM FVTGFGALKN DGYSQNLHRQ AQVTLIDATT CNEPQAYNDA ITPRMLCAGS 360
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Seq ID NO: 252 DNA sequence
 Nucleic Acid Accession #: NM_003504.2
 Coding sequence: 71-1771

1 11 21 31 41 51
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 65 GAGGGTCCTT CTCTTCGTGG CCTCGGACGT GGTGCTCTG TGTGCGTGCA AGATCCTTCA 180
 GGCCTGTGTC CAGTGTGACC ACGTGCAATA TACGCTGGTT CCAGTTTCTG GGTGGCAAGA 240
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 70 ACTCATTAAA CAAGATGATG ACCTTGAAGT TCCGCGCTAT GAAGACATCT TCAGGGATGA 480
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 75 GTCAGCCATG GTGATGTTTG AGCTGGCTTG GATGCTGTCC AAGGACCTGA ATGACATGCT 720
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 CCTGGTGCTC TACCAGCACT GGTCCCTCCA TGACAGCCTG TGCAACACCA GCTATACCGC 960
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 80 CATGGGTCTT CCCCTGAAGC AGGTGAAGCA GAAGTTCAG GCCATGGACA TCTCTTTGAA 1080
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 85 CATCCAGGCT CTGGACAGCC TCTCCAGGAG TAACCTGGAC AAGCTGTACC ATGGCCTGGA 1320
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 CATGCTGTTT TCTAGGCCGG CATCCCTAAG CCTGCTCAGC AAACACCTGC TCAAGTCTTT 1500
 TGTGTGTTTC ACAAGAAGCC GGCCTGCAA ACTGCTGCCC CTGGTGATGG CTGCCCCCTT 1560

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 GCTGCACAAC CATTTTGACC TCTCAGTAAT TGAGCTGAAA GCTGAGGATC GGAGCAAGTT 1740
 TCTGGACGCA CTATTTCCTC TCCTGTCTTA GGAATTTGAT TCTTCCAGAA TGACCTTCTT 1800
 ATTTATGTAA CTGGCTTTCA TTTAGATTGT AAGTTATGGA CATGATTGA GATGTAGAAG 1860
 CCATTTTFTA TTAAATAAAA TGCTTATTTT AGGCTCCGTC CCCAAAAAAA AAAAAAAA 1920
 AAAAAAAA AA

Seq ID NO: 253 Protein sequence:
 Protein Accession #: NP_003495.1

1 11 21 31 41 51
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 AFLEHKEQFH YFILINCGAN VDILLDILQPD EDTIFFVCDT HRPVNVVNVY NDTQIKLLIK 120
 QDDLEVPAY EDIFRDEED EHSNDSGDG SEPSEKTRRL EEEIVEQTMR RRQRREWEAR 180
 RRDILDFEYQ YEYHGTSSAM VMFELAWMLS KDLNDMLNWA IVGLTDQWVQ DKITQMKYVT 240
 DVGVLQRHVS RHNHRNEDEE NTLSDVCTRI SFHEYDLRLVL YQHWSLHDSL CNTSYTAARF 300
 KLWSVHGQKR LQEFPLADMGL PLKQVKQKQFQ AMDISLKENL REMIEESANK FGMDMRVQT 360
 FSIHFQKHK FLASDVVFAV MSLMESPEKD GSGTDHFIQA LDSLSRSNLD KLYHGLELAK 420
 KQLRATQQTI ASCLCTNLVI SQGFPLYCSL MEGTPDVMLF SRPASLSLLS KHLKSFVCS 480
 TKNRRCKLLP LVMAAPLSME HGTVTVVGIP PETDSSDRKN FFGRAFEKAA ESTSSRMLHN 540
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Seq ID NO: 254 DNA sequence
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 CACATGTGGC AAGCCAAAGA TCTATGCCCT TGTTTTTTCA ATGAGAGAGA AATAGCAAAT 840
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Seq ID NO: 255 Protein sequence:
 Protein Accession #: NP_071732

1 11 21 31 41 51
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 SVVLLANKCD QGKDVLMNNG LKMDQFCKEH GFVGVWFETSA KENINIDEAS RCLVKHILAN 180
 ECDLMESIEP DVVVKPHLTST KVASCSCGCAK S

Seq ID NO: 256 DNA sequence
 Nucleic Acid Accession #: NM_016321
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 GGTGTTCTGG CGCTACGACT TCGAGGCCGA CGCCCACTGG TGGTCAGAGA GGACGCACAA 180
 GAACCTGAGC GACATGGAGA ACGAATTCTA CTATCGCTAC CCAAGCTTCC AGGACGTGCA 240
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 5 TGGCATCATA GGGCGCATCG TGGGTGCTGT GACAGCGGCC TCCGCCAGCC TTGAAGTCTA 1140
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 10 GAAGTGTCTT GAGGATGCGG TCTACTGGGA GATGCCTGAA GGGAACAGCA CTGTCTACAT 1380
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 CCTCCCTTC ATCCAGGGG GTCTGCTGA GAATGGAGAA GGAGAAGCTA CAAAGTGGGC 1680
 15 ATCCAAGCCG GGTCTGGCT GCAGAAGTTC TGCTCTGCTG TGGGGTCTTG GCCACATTGG 1740
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 ACAACTTAGC TGCCAGTCAC CACCTATGAG GCTCTTCTAC CCCGTGCCTG CACCTCGGCC 1860
 AGCATCTCCT ATGCTCCCTG GGTCCCCAG ACCTCTCTGT GTTGTGTGCG TGGCAGCCTC 1920
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Seq ID NO: 257 Protein sequence:
 Protein Accession #: NP_057405

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 GVENLINADF CVASVCVAFG AVLKQVSPIQ LLIMTFQVTF LFAVNEFILL NLLKVKDAGG 180
 30 SMTHTFGAY FGLTVTRILY RRLNLSQSKER QNSVYQSDLF AMIGTLFLWM YWPSFNSAIS 240
 YHGD SQHRAA INTYCSLAAC VLTSVAISSA LHKKGKLDMMV HIQNTATLGG VAVGTAAEMM 300
 LMPYGALIIG FVCGIISTLG FVYLTPFLES RLHIQDTCGI NNHIGIPGII GGIIVGAVTAA 360
 SASLEVYKGE GLVHSFDFQG FNGDWTARTQ GKFFQIYGLLV TLAMALMGSI IVGLILRLPF 420
 WGQPSDENC F EDAVWEMPE GNSTVYIPED PTFKPSGSPV PSVPMVSLP MASSVPLVP

Seq ID NO: 258 DNA sequence
 Nucleic Acid Accession #: NM_002358.2
 Coding sequence: 75..692

1 11 21 31 41 51
 GGGAAAGTGCT GTTGGAGCCG CTGTGGTTGC TGTCCGCGGA GTGGAAGCGC GTGCTTTTGT 60
 TTGTGTCCCT GGCCATGGCG CTGCAGCTCT CCCGGGAGCA GGGAAATCACC CTGCGCGGGA 120
 GCGCCGAAAT CGTGGCCGAG TTCTTCTCAT TCGGCATCAA CAGCATTTTA TATCAGCGTG 180
 45 GCATATATCC ATCTGAAACC TTTACTCGAG TGCAGAAATA CGGACTCACC TTGCTTTGTA 240
 CTACTGATCT TGAGCTCATA AAATACCTAA ATAATGTGGT GGAACAACATG AAAGATTGGT 300
 TATACAAGTG TTCAGTTCAG AAACCTGGTTG TAGTTATCTC AAATATTGAA AGTGGTGAGG 360
 TCCTGGAAAG ATGGCAGTTT GATATTGAGT GTGACAAGAC TGCAAAAGAT GACAGTGCAC 420
 50 CCAGAGAAAA GTCTCAGAAA GCTATCCAGG ATGAAATCCG TTCAGTGATC AGACAGATCA 480
 CAGCTACGGT GACATTTCTG CCACTGTTGG AAGTTTCTTG TTCATTTGAT CTGCTGATT 540
 ATACAGACAA AGATTGGTT GTACCTGAAA AATGGGAAGA GTCGGGACCA CAGTTTATTA 600
 CCAATCTCTA GGAAGTCCGC CTTCTGTCAT TTAATACTAC AATCCACAAA GTAATAGCA 660
 TGGTGGCCTA CAAATTTCTT GTCAATGACT GAGGATGACA TGAGGAAAT AATGTAATTG 720
 55 TAATTTTGAA ATGTGGTTTT CCTGAAATCA GGTATCTAT AGTTGATATG TTTTATTTC 780
 TTGTTTAATT TTTACATGGA GAAAACCAAA ATGATACTTA CTGAATGTG TGTAATTGTT 840
 CCTTTATTTT TTTGGTACCT ATTTGACTTA CCATGGAGT AACATCATGA ATTTATTGCA 900
 CATTGTTCNA AAGGAACCA GAGGTTTTTT TGTCAACATT GTGATGTATA TTCCTTTGAA 960
 GATAGTAAC TATAGTGGAA AAACCTGTGC TATAAAGCTA GATGCTTTCC TAAATCAGAT 1020
 60 GTTTTGGTCA AGTAGTTTGA CTCAGTATAG GTAGGGAGAT ATTTAAGTAT AAAATACAAC 1080
 AAAGGAAGTC TAAATATTCA GAATCTTTGT TAAGTCCCTG AAAGTAACTC ATAATCTATA 1140
 AACAAATGAA TATTGCTGTA TAGCTCTTTT TGACCTTCAT TTCATGTATA GTTTTCCCTA 1200
 TTGAATCAGT TTCCAATTAT TTGACTTTAA TTTATGTAAC TTGAACCTAT GAAGCAATGG 1260
 ATATTGTATC TGTTTAATGT TCTGTGATAC AGAACTCTTA AAAATGTTTT TTCATGTGTT 1320
 65 TTATAAATC AAGTTTAAAG TGAAAGTGAG GAAATAAAGT TAAGTTTGTT TTAATAAATA 1380
 AAAAAA

Seq ID NO: 259 Protein sequence:
 Protein Accession #: NP_002349.1

1 11 21 31 41 51
 MALQLSREQG ITRGSABIV AEFFSFGINS ILYQGIYPS ETFTRVQKYG LTLVTTDLE 60
 75 LIKYLNNVVE QKDWLYKCS VQKLVVVISN IESGEVLERW QFDIECDKTA KDDSAPREKS 120
 QKAIQDEIRS VIRQTATVT FLPLLEVSCS FDLIIYTDKD LVVPEKWEES GPQFITNSEE 180
 VRLRSFTTTI HKVNSMVAIK IPVND

Seq ID NO: 260 DNA sequence
 Nucleic Acid Accession #: NM_001211
 Coding sequence: 43..3195

1 11 21 31 41 51
 AAAGGCCTGC AGCAGGACGA GGACCTGAGC CAGGAATGCA GGATGGCGGC GGTGAAGAAG 60
 85 GAAGGGGGTG CTCTGATGA AGCCATGTCC CTGGAGGGAG ATGAATGGGA ACTGAGTAAA 120
 GAAAATGTAC AACCTTTAAG GCAAGGGCGG ATCATGTCCA CGCTTCAGGG AGCACTGGCA 180
 CAAGAATCTG CCTGTAACAA TACTCTTCAG CAGCAGAAAC GGGCATTTGA ATATGAAATT 240

	CGATTTTACA	CTGGAAATGA	CCCTCTGGAT	GTTTGGGATA	GGTATATCAG	CTGGACAGAG	300
	CAGAACTATC	CTCAAGGTGG	GAAAGAGAGT	AATATGTCAA	CGTTATTAGA	AAGAGCTGTA	360
	GAAGCACTAC	AAGGAGAAAA	ACGATATTAT	AGTGATCCTC	GATTTCTCAA	TCTCTGGCTT	420
5	AAATTAGGGC	GTTTATGCAA	TGAGCCCTTG	GATATGTACA	GTTACTTGCA	CAACCAAGGG	480
	ATTGGTGT	CACCTGTCTA	GTTCTATATC	TCATGGGCAG	AAGAATATGA	AGCTAGAGAA	540
	AACTTTAGGA	AAGCAGATGC	GATATTTTCAG	GAAGGGATTG	AACAGAAGGC	TGAACCACTA	600
	GAAAGACTAC	AGTCCCAGCA	CCGACAATTC	CAAGCTCGAG	TGTCTCGGCA	AACTCTGTTG	660
	GCACCTGAGA	AAGAAGAGAA	GGAGGAAGTT	TTTGAGTCTT	CTGTACCACA	ACGAAGCACA	720
10	CTAGCTGAAC	TAAAGAGCAA	AGGGAAAAAG	ACAGCAAGAG	CTCCAATCAT	CCGTGTAGGA	780
	GGTGCTCTCA	AGGCTCCAAG	CCAGAACAGA	GGACTCCAAA	ATCCATTTC	TCAACAGATG	840
	CAAAATAATA	GTAGAATTAC	TGTTTTTGAT	GAAAATGCTG	ATGAGGCTTC	TACAGCAGAG	900
	TTGTCTAAGC	CTACAGTCCA	GCCATGGATA	GCACCCCCCA	TGCCCAGGGC	CAAAGAGAAT	960
	GAGCTGCAAG	CAGGCCCTTG	GAAACACAGC	AGGTCTTGG	AACACAGGCC	TCGTGGCAAT	1020
15	ACAGCTTCAC	TGATAGCTGT	ACCCGCTGTG	CTTCCCAGTT	TCACTCCATA	TGTGGAAGAG	1080
	ACTGCACAAC	AGGCCAGTAT	GACACCATGT	AAAATTGAAC	CTAGTATAAA	CCACATCCTA	1140
	AGCACCAAG	AGCCTGAGAA	GGAGAAGGA	GATCCTCTAC	AAAGGGTTCA	GAGCCATCAG	1200
	CAAGCGTCTG	AGGAGAAGAA	AGAGAAGATG	ATGTATTGTA	AGGAGAAGAT	TTATGCAGGA	1260
	GTAGGGGAAT	TCTCCTTTGA	AGAAATTCGG	GCTGAAGTTT	TCCGGAAGAA	ATTAAAAGAG	1320
20	CAAAGGGAAG	CCGAGCTGCA	GACCAAGTGA	GAGAAGAGAG	CAGAAATGCA	GAAACAGATT	1380
	GAAGAGATGG	AGAGAAGCTG	AAAAGAAATC	CAAACTACTC	AGCAAGAAAG	AACAGGTGAT	1440
	CAGCAAGAAG	AGACGATGCC	TACAAAAGGAG	ACAACTAAAC	TGCAAAATGC	TCCGAGTCT	1500
	CAGAAAATAC	CAGGAATGAC	TCTATCCAGT	TCTGTTTGTC	AAGTAAACTG	TTGTGCCAGA	1560
	GAAACTTCAC	TTGCGGAGAA	CATTGTGGCAG	GAACAACCTC	ATTCTAAAGG	TCCAGTGTGA	1620
25	CCTTTCTCCA	TTTTTGATGA	GTTTCTTCTT	TCAGAAAAGA	AGAATAAAAG	TCCTCCTGCA	1680
	GATCCCCCAC	GAGTTTTAGC	TCAACGAAGA	CCCCTTGCG	TTCTCAAAC	CTCAGAAAGC	1740
	ATCACCTCAA	ATGAAGATGT	GTCTCCAGAT	GTTTGTGATG	AATTTACAGG	AATTGAACCC	1800
	TTGAGCGAGG	ATGCCATAT	CACAGGCTTC	AGAAATGTAA	CAATTTGTCC	TAACCCAGAA	1860
	GACACTTGTG	ACTTTGCCAG	AGCAGCTCGT	TTTGTATCCA	CTCCTTTTCA	TGAGATAATG	1920
30	TCCTTGAAGG	ATCTCCCTTG	TGATCCTGAG	AGACTGTTAC	CGGAAGAAGA	TCTAGATGTA	1980
	AAGACCTCTG	AGGACCAGCA	GACAGCTTGT	GGCACTATCT	ACAGTCAGAC	TCTCAGCATC	2040
	AAGAAGCTGA	GCCCAATAT	TGAAGACAGT	CGTGAAGCCA	CACACTCCTC	TGGCTTCTCT	2100
	GGTTCTTCTG	CCTCGGTTGC	AAGCACCTCC	TCCATCAAAT	GTCTTCAAAT	TCCTGAGAAA	2160
	CTAGAACTTA	CTAATGAGAC	TTCAAGAAAC	CCTACTCAGT	CACCATGGTG	TTACAGTAT	2220
35	CGCAGACAGC	TACTGAAGTC	CCTACCAGAG	TTAAGTGCC	CTGCAGAGTT	GTGTATAGAA	2280
	GACAGACCAA	TGCCTAAGTT	GGAAATTGAG	AAGGAAATTG	AATTAGGTAA	TGAGGATTAC	2340
	TGCATTAAC	GAGAAATCCT	AATATGTGAA	GATTACAAGT	TATTTCTGGT	GGCGCCCAAG	2400
	AACCTCTGAG	AATTAACAGT	AATAAAGGTA	TCTTCTCAAC	CTGTCCCATG	GGACTTTTAT	2460
	ATCAACCTCA	AGTTAAAGGA	ACGTTTAAAT	GAAGATTTTG	ATCATTTTTG	CAGCTGTTAT	2520
40	CAATATCAAG	ATGGCTGTAT	TGTTTGGCAC	CAATATATAA	ACTGCTTCAC	CCTTCAGGAT	2580
	CTTCTCCAAC	ACAGTGAATA	TATTACCCAT	GAAATAACAG	TGTTGATTAT	TTATAACCTT	2640
	TTGACAATAG	TGGAGATGCT	ACACAAAGCA	GAAATAGTCC	ATGGTGACTT	GAGTCCAAGG	2700
	TGCTGATTC	TCAGAAACAG	AATCCACGAT	CCCTATGATT	GTAACAAGAA	CAATCAAGCT	2760
45	TTGAAGATAG	TGGACTTTTC	CTACAGTGT	GACCTTAGGG	TGCAGCTGGA	TGTTTTTACC	2820
	CTCAGCGGCT	TTGCGAGCTG	ACAGATCCTG	GAAGGACAAA	AGATCCTGGC	TAAGTGTCT	2880
	TCTCCCTACC	AGGTAGCTGT	GTTTGGTATA	GCAGATTAG	CACATTACT	ATTGTTCAAG	2940
	GAACACCTAC	AGGTCTTCTG	GGATGGGTC	TTCTGGAAC	TTAGCCAAAA	TATTTCTGAG	3000
	CTAAAGATG	TGTAATTTG	GAATAAATTC	TTTGTGCGGA	TTCTGAATGC	CAATGATGAG	3060
50	GCCACAGTGT	CTGTTCTTGG	GGAGCTTGCA	GCAGAAATGA	ATGGGGTTTT	TGACACTACA	3120
	TTCCAAGATC	ACCTGAACAA	AGCCTTATGG	AAGGTAGGGA	AGTTAACTAG	TCCTGGGGCT	3180
	TTGCTCTTTC	AGTGAGCTAG	GCAATCAAGT	CTCACAGATT	GCTGCCTCAG	AGCAATGGTT	3240
	GTATTGTGGA	ACACTGAAAC	TGTATGTGCT	GTAATTTAAT	TTAGGACACA	TTTAGATGCA	3300
	CTACCATGTC	TGTTCTACTT	TTTGGTACAG	GTAATTTTGT	ACGTCACCTG	TATTTTCTAT	3360
	ACAGTGATAT	CTTACTACTT	GGCCTTGCT	AACTTTTGTG	AAGAATCTAT	TTATTCTAAA	3420
55	GCACTCATT	ACAAATGGTT	ACCTTGTAT	TTAACCATT	TGCTCTACT	TTTCCCTGTA	3480
	CTTTTCCCAT	TTGTAATTTG	TAAATGTTC	TCTTATGATC	ACCATGTATT	TTGTAATAA	3540
	TAAATAGTA	TCTGTTAAAA	AAAAAATAAA	AAAAAATAAA	AAA		

Seq ID NO: 261 Protein sequence:

Protein Accession #: NP_001202

	1	11	21	31	41	51	
	MAAVKKEGGA	LSEAMSLGEG	EWELSKENVQ	PLRQGRIMST	LQGALAQESA	CNNTLQQQKR	60
	AFEYEIRFYT	GNDPLDVWDR	YISWTEQNY	QGGKESNMST	LLERAVEALQ	GEKRYYSDDP	120
65	FLNLWLKLGR	LCNEPLDMYS	YLHNQIGIVS	LAQFYISWAE	EYEARENFRK	ADAFQEGIQ	180
	QKAEPFLERLQ	SQHRQFOARV	SRQTLLEAK	EEEEVFESS	VPQRSTLAE	KSKGKKTARA	240
	PIIRVGGALK	APSNRGLQ	PPQMQNNNS	RITVFDENAD	EASTAELSKP	TVQPWIAPPM	300
	PRAKENELQA	GPWNTGRSL	HRPRGNTASL	IAPVAVLPSF	TPYVEETAQQ	PVMTFCKIEP	360
	SINHILSTRK	PGKEEGDPLQ	RVQSHQQA	EKKEKMMYCK	EKIYAGVGEF	SFEIRAEV	420
70	RKKLKEQREA	ELLTSAEKRA	EMQKQIEEME	KKLKEIQTQ	QERTGDQEE	TMPTKETTKL	480
	QIASESQIP	GMLTSSSVQC	VNCCARETSL	AENIWQEQPH	SKGPSVPFSI	FDEFLLSEKK	540
	NKSPADPPR	VLAQRRLAV	LKTSSESITS	EDVSPDVCE	FTGIEPLSED	AIITGFRNVT	600
	ICPNPEDTCD	FARAARFVST	PFHEIMSLKD	LPSDPERLLP	EEDLDVKTSE	DQQTACGTIY	660
75	SQTLSEIKLS	PIIEDSREAT	HSSGFGSSA	SVASTSSIKC	LQIPEKLELT	NETSENPTQS	720
	PWCSQYRRQL	LKSLPELSAS	AELCIEDRPM	PKLEIEKEIE	LGNEIDYCIK	EYLICEDYKL	780
	FWVAPRNSAE	LTVLKVSQ	VPWFYINLK	LKERLNEDFD	HFCSQYQD	GCIVVWHQYIN	840
	CFTLQDLQ	SEYITHEITV	LIIYNLLTIV	EMLHKAIEIV	GDLSRCLIL	RNRHIDPYDC	900
	NKNNQALKIV	DFSYSVDLRV	QLDVFTLSGF	RTVQILEGQK	ILANCSPPYQ	VDLFGIADLA	960
80	HLLEFKEHLQ	VFWDSFWKL	SNISSELKDG	ELWNKFFVRI	LNANDEATVS	VLGELAAEMN	1020
	GVFDTTFSQ	LKALWVKVGL	LTSPGALLFQ				

Seq ID NO: 262 DNA sequence

Nucleic Acid Accession #: NM_003784

Coding sequence: 365..1507

	1	11	21	31	41	51
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	1	11	21	31	41	51	
	GTCTACTTAT	CAATAAGCAG	CTGCCTGTGC	AGAGTGCAGG	CTGCACCTTT	GGACAGCCTT	60
	TAAAACTGAA	TTCTCAGAA	TTTAGAACAA	ATTTTGTCT	AGAAATGCTG	ACTTTGGTTC	120
5	ATTAGGTAGT	GGTAAACAG	GCTCCCTTCG	AAGCTCTCCT	TCATCACCTT	CCTAAGTGCA	180
	TGTACAGGGA	AGCTCTCCTT	CATCACCTTC	CTAAGTGCAT	GGGGGAAAAT	ACCTAGGGCT	240
	CAACAGTCTT	GAGAAGTGTG	GAAACATTTT	CTTTGTGAGT	GAGAACAGAT	CACCTAGAGA	300
	AAGGAAACCA	GATTTCCCAT	ACTGCTTCTG	GGTATCAGAT	GCTAGCGCTG	CACCTCCATT	360
	TGCAATGGCC	TCCCTTGCTG	CAGCAAAATG	AGAGTTTGTG	TTCAACCTGT	TCAGAGAGAT	420
10	GGATGACAA	CAAGGAAATG	GAAATGTGTT	CTTTTCCCTC	CTGAGCCTCT	TCGCTGCCCT	480
	GGCCCTGGTC	CGCTTGGGCG	CTCAAGATGA	CTCCCTCTCT	CAGATTGATA	AGTTGCTTCA	540
	TGTTAACACT	GCCTCAGGAT	ATGGAACTC	TTCTAATAGT	CAGTCAGGGC	TCCAGTCTCA	600
	ACTGAAAAGA	TTTTTTTCTG	ATATAAATGC	ATCCACACAAG	GATTATGATC	TCAGCATTGT	660
	GAATGGGCTT	TTTGTCTAAA	AAGTGTATGG	CTTTCATAAG	GACTACATTG	AGTGTGCCGA	720
15	AAAAATTATAC	GATGCCAAAG	TGGAGCGAGT	TGACTTTACG	AATCATTTAG	AAGACACTAG	780
	ACGTAAATAT	AATAAGTGGG	TTGAAAATGA	AACACATGGC	AAAATCAAGA	ACGTGATTTG	840
	TGAAGGTGGC	ATAAGTCTAT	CTGCTGTAAT	GGTGTGGTGT	AATGCTGTGT	ACTTCAAAGG	900
	CAAGTGGCAA	TCAGCCTTCA	CCAAGAGCGA	AACCATAAAT	TGCCATTTC	AATCTCCCAA	960
	GTGCTCTGGG	AAGGCAGTCG	CCATGATGCA	TCAGGAACGG	AAGTTCAATT	TGCTGTATT	1020
20	TGAGGACCCA	TCAATGAAGA	TTCTTGAGCT	CAGATACAA	GGTGGCATAA	ACATGTACGT	1080
	TCTGTGCTCT	GAGATGACCC	TCTCTGAAAT	TGAAAACAAA	CTGACCTTTC	AGAATCTAAT	1140
	GGAATGGACC	ATCCCAAGGC	GAATGACCTC	TAAGTATGTT	GAGGTATTTT	TTCTCAGTTT	1200
	CAAGATAGAG	AAGAATTATG	AAATGAAACA	ATATTGAGA	GCCCTAGGGC	TGAAAGATAT	1260
	CTTTGATGAA	TCCAAAGCAG	ATCTCTCTGG	GATTGCTTCG	GGGGTCTGTC	TGTATATATC	1320
25	AAGGATGATG	CACAAATCTT	ACATAGAGGT	CACTGAGGAG	GGCACCCGAG	CTACTGCTGC	1380
	CACAGGAAGT	AATATTGTAG	AAAAGCAACT	CCCTCAGTCC	ACGCTGTGTT	GAGCTGACCA	1440
	CCCATTCTTA	TTTGTATCA	GGAAGGATGA	CATCATCTTA	TTCAGTGGCA	AAGTTTCTTG	1500
	CCCTTGAAAA	TCCAAATGGT	TTCTGTTATA	GCAGTCCCCA	CAACATCAAA	GRACCACCAC	1560
	AAGTCAATAG	ATYTGRTT	AATTGGAAAA	ATGTGGTGT	TCCTTTGAGT	TTATTTCTTC	1620
30	CTAACATTGG	TCAGCAGATG	ACACTGGTGA	CTTGACCTTT	CCTAGACACC	TGTTTGATTG	1680
	TCCTGATCCC	TGCTCTTAGC	ATTCTACCAC	CATGTGTCTC	ACCCATTCTT	AATTTTATTG	1740
	TCTTTCTTCC	CACGCTCATT	TCTATCATTC	TCCCCCATGA	CCCGTCTGGA	AATTATGGAG	1800
	RGTTGCTAAC	TGGTAAGGAG	AACGTAGAAG	TAGCCCTAGG	GATCCTTTTT	GAAACTCTAC	1860
	AGTTATCGCA	GATATTCTAG	CTTCATTGTA	AGCAATCTAG	GAAATAAGCC	CTGCTGCTTT	1920
35	CTAGAAATAA	GTGTGAAGGA	TAAATTTTCT	TTGTTGACCT	ATGAAGATT	TAGAGTTTAC	1980
	CTTCATATGT	TTGATTTTAA	ATCAGTGTAT	AATCTAGATG	GTAATAAATG	TGAAATTTGG	2040
	ATTAGGGACC	TACCAAAATA	TTTCATTAAT	GCTTTCAATT	GACAAATTTT	GGCCTTTCTT	2100
	TGATAAGACA	ATATGTACAT	GTTTTTTCAA	ATATTAAAGA	TCTTTTAACT	GTTGGCAGTT	2160
40	GTTATCTACA	GAATCATATT	TCATATGCTG	TGTAGTTTAT	AAGTTTTTCC	TCTATTTATC	2220
	AGAAATAAGA	AATACAACAT	ACCTGTAAA				

Seq ID NO: 263 Protein sequence:
Protein Accession #: NP_003775

45	1	11	21	31	41	51	
	MASLAAANAE	FCFNLFREMD	DNQNGNVFF	SSLSLFAALA	LVRLLGAQDDS	LSQIDKLLHV	60
	NTASGYGNSS	NSQSLQSQL	KRVFSDINAS	HKDYDLISVN	GLFAEKVYGF	HKDYIECAEK	120
50	LYDAKVERVD	FTNHLEDTTR	NINKVENET	HGKIKNVIGE	GGISSAVMV	LVNAVYFKGK	180
	WQSAFTKSET	INCHFKSPKC	SGKAVAMMHQ	ERKFNLVIE	DPSMKILELR	YNGGINMYVL	240
	LEPNLSEIE	NKLTQNLME	WTNPRRMTSK	YVEVFPQFK	IEKNYEMKQY	LRLGLKIDIF	300
	DESKADLSGI	ASGGRLYISR	MMHKSYLEVT	EEGTEATAAT	GSNIVEKQLP	QSTLFRADHP	360
	FLFVIRKDDI	ILFSKGVSCP					

Seq ID NO: 264 DNA sequence
Nucleic Acid Accession #: AB052906
Coding sequence: 74-814

60	1	11	21	31	41	51	
	AAAACCTTGA	GGTGATTCAT	CTTCCAGGCT	CTCCTTCCAT	CAAGTCTCTC	CTCCCTAGCG	60
	CTCTGGGTCC	TTAATGGCAG	CAGCCGCCGC	TACCAAGATC	CTTCTGTGCC	TCCCGCTTCT	120
	GCTCTGCTG	TCCGCTGTGT	CCCGGGCTGG	GCGAGCCGAC	CCTCACTCTC	TTTGCTATGA	180
65	CATCACCGTC	ATCCCTAAGT	TCAGACCTGG	ACCACGGTGG	TGTGCGGTTC	AAGGCCAGGT	240
	GGATGAAAAG	ACTTTTCTTC	ACTATGACTG	TGGCAACAAG	ACAGTCACAC	CTGTCACTCC	300
	CCTGGGGAAG	AACTAAATG	TCACAACGCG	CTGGAAGACA	CAGAACCCAG	TACTGAGAGA	360
	GGTGGTGGAC	ATACTTACAG	AGCAACTGCG	TGACATTGAG	CTGGAGAATT	ACACACCCAA	420
	GGAACCCCTC	ACCCTGACAG	CCAGGATGTC	TTGTGAGCAG	AAAGCTGAAG	GACACAGCAG	480
70	TGGATCTTGG	CAGTTTCAGT	TCGATGGGCA	GATCTTCCTC	CTCTTTGACT	CAGAGAAGAG	540
	AATGTGGACA	ACGGTTCATC	CTGGAGCCAG	AAAGATGAAA	GAAAAGTGGG	AGAATGACAA	600
	GGTTGTGGCC	ATGTCCTTCC	ATTACTTCTC	AATGGGAGAC	TGTATAGGAT	GGCTTGAGGA	660
	CTTCTTGATG	GGCATGGACA	GCACCTTGGA	GCCAAGTGCA	GGAGCACACC	TCGCCATGTC	720
	CTCAGGCACA	ACCAACTCA	GGGCCACAGC	CACCACCTTC	ATCCTTTGCT	GCCTCCTCAT	780
75	CATCTCTCCC	TGCTTCATCC	TCCCTGGCAT	CTGAGGAGAG	TCCTTTAGAG	TGACAGGTTA	840
	AAGCTGATAC	CAAAAGGCTC	CTGTGAGCAC	GGTCTTGATC	AAACTCGCCC	TTCTGTCTGG	900
	CCAGCTGCCC	ACGACCTACG	GTGTATGTCC	AGTGGCCTCC	AGCAGATCAT	GATGACATCA	960
	TGGACCAAT	AGCTCATTTA	CTGCCCTTGAT	TCCTTTTGCC	AACAATTTTA	CCAGCAGTTA	1020
	TACCTAACAT	ATTATGCAAT	TTTCTCTTGG	TGCTACCTGA	TGGAATTCCT	GCACTTAAAG	1080
80	TTCTGGCTGA	CTAAACAAGA	TATATCATTT	TCTTTCTTCT	CTTTTGTGTT	GGAAAATCAA	1140
	GTACTTCTTT	GAATGATGAT	CTCTTCTTGG	CAAAATGATAT	TGTCAGTAAA	ATAATCACGT	1200
	TAGACTTCAG	ACCTCTGGGG	ATTCTTCCG	TGTCCTGAAA	GAGAAATTTT	AAATTATTTA	1260
	ATAAGAAAAA	ATTTATATTA	ATGATTGTTT	CCTTTAGTAA	TTTATTGTTC	TGTACTGATA	1320
85	TTTAAATAAA	GAGTTCTATT	TCCCAAAAAA	AAAAAATAAA	A		

Seq ID NO: 265 Protein sequence:
Protein Accession #: BAB61048.1

1 11 21 31 41 51
| | | | |
MAAAAATKIL LCLPLLLLS GWSRAGRADP HSLCYDITVI PKFRPGPRWC AVQGGVDEKT 60
FLHYDCGNKT VTPVSPLGKK LNVTTAWKAQ NPVLREVVDI LTEQLRDIQL ENYTPKEPLT 120
LQARMSCEQK AEGHSSGSWQ FSFDGQIFLL FDSEKRMWTT VHPGARKMKE KWENDKVVM 180
SFHYFSMGDC IGWLEDFLMG MDSTLEPSAG APLAMSSGTT QLRATATTLI LCCLLIILPC 240
FILPGI

Seq ID NO: 266 DNA sequence
Nucleic Acid Accession #: XM_084853.1
Coding sequence: 127-444

1 11 21 31 41 51
| | | | |
ATTGATGATA TATTTAACGA AATCAAAATTT GGTGAATATG TGGACACTGG AAAGCTAATC 60
GACAAGATCA ACTTACCAGA TTTCTAAAA GTGTACCTTA ACCACAAGCC ACCTTTTGGT 120
AACACCATGA GTGGCATCCA CAAGAGCTTT GAGGTGCTCG GTTATACCAA CTCCAAAGGG 180
AAAAAGGCCA TTCGAAGAGA GGACTTCCTG AGACTGCTCG TTAATAAAGG TGAGCATATG 240
ACGGAGGAGG AGATGTTTGA TTGCTTTGCT TCACTGTTTG GCCTGAATCC CGAGGGATGG 300
AAATCCGAGC CTGCAACCTG CTCCTGCAAA GGTTCAGAAA TTTGCCTTGA AGAAGAACTT 360
CCAGACGAAA TCACATGAGA AATATTCGCG ACTGAAATTC TTGGCTTAAC CATTCAGAA 420
GATTCCGGCC AGGATGGTCA GTGAAGTTAC CAGGAATGTT TAAAGCACAA AGGACTTTGG 480
GTGTGTGTGC ATGCACATGT GTGTGTTTTC CATGAGGCAC TGCTTTTAT GCATTTCCCT 540
CCCCCTCTC ATCTTTAGAA CATTAGACA TTAAAGCAAG TTTCTGGTGA GCAATG

Seq ID NO: 267 Protein sequence:
Protein Accession #: XP_084853.1

1 11 21 31 41 51
| | | | |
MSGIHKSEFV LGYNSKGKK AIRREDFRL LVTKEHMT EEMLD CFASL FGLNPEGWKS 60
EPATCSVKGS EICLEELPD EITAEIFATE ILGLTISEDS GQDQ

Seq ID NO: 268 DNA sequence
Nucleic Acid Accession #: NM_001898
Coding sequence: 57-482

1 11 21 31 41 51
| | | | |
GGCTCTCACC CTCCTCTCCT GCAGCTCCAG CTTTGTGCTC TGCCCTCTGAG GAGACCATGG 60
CCCAGTATCT GAGTACCCTG CTGCTCCTGC TGGCCACCCT AGCTGTGGCC CTGGCCTGGA 120
GCCCAAGGA GGAGGATAGG ATAATCCCGG GTGGCATCTA TAACGAGAC CTCAATGATG 180
AGTGGGTACA GCGTGCCCTT CACTTCGCCA TCAGCGAGTA TAACAAGGCC ACCAAAGATG 240
ACTACTACAG ACGTCCGCTG CGGGTACTAA GAGCCAGGCA ACAGACCGTT GGGGGGGTGA 300
ATTACTTCTT CGACGTAGAG GTGGGCCGCA CCATATGTAC CAAGTCCAG CCCAACTTGG 360
ACACCTGTGC CTTCCATGAA CAGCCAGAAC TGCAGAAGAA ACAGTTGTGC TCTTTCGAGA 420
TCTACGAAGT TCCCTGGGAG AACAGAAAGT CCCTGGTGAA ATCCAGGTGT CAAGAATCCT 480
AGGGATCTGT GCCAGCCAT TCGCACCAGC CACCACCCAC TCCCACCCCT TGTAGTGTCT 540
CCACCCCTGG ACTGGTGGCC CCCACCCCTG GGGAGGCCCT CCCATGTGCC TGCGCCAAGA 600
GACAGACAGA GAAGGCTGCA GGAGTCTCTT GTTGCTCAGC AGGGCGCTCT GCCCTCCCTC 660
CTTCCTTCTT GCTTCTAATA GCCCTGTGAC ATGGTACACA CCCCCCACC TCCTGCAATT 720
AAACAGTAGC ATCGCC

Seq ID NO: 269 Protein sequence:
Protein Accession #: NP_001889.1

1 11 21 31 41 51
| | | | |
MAQYLSTLLL LLATLAVALA WSPKEEDRII PGGIYNADLN DEWVQRALHF AISEYNKATK 60
DDYVRRPLRV LRARQTVGG VNYFDVEVG RTICTKSQFN LDTCAFHEQP ELQKKQLCSF 120
EIEYVPWENR RSLVSRQCE S

Seq ID NO: 270 DNA sequence
Nucleic Acid Accession #: XM_093210
Coding sequence: 13-1854

1 11 21 31 41 51
| | | | |
ATGGCAAGCG CCGGAATCTC CTCAGCTGCC GTTTCACAAA AGAGGTACCA GGTCCGCACC 60
AAACGAGCAC ACAAGCAGCA CCAGGAGCTG CAGAAGAAGG AGGCGGCAGC GATGGACCAG 120
GGCAGAGGGA ATGGGGAGGG GGCACTCCTAC CCCATATCTG AGGTGCGACT GCGGGACGTA 180
GAGCGGACTG GGCCTTTCCC GTTGGCGCGT GGCCTCAATC AGGACTTCTT GCCCAGTGC 240
GCCTTCAAAA CGGTAAGAGC TGCAACTGAA CGTGTGAGAC ATGGTGAGA TAGGCTGAGA 300
GGCGGGCGGA GAGATGCCCA TGAACCTCAAG TACCCGGACA CGCCCTCCAC TTCTACCACC 360
ACGAGTAACA CCGCCCCCAG GGGACCGCTC TCGAGGTCCC CCAAGCCAA GACGCAAGGA 420
GGAACGCCCC GCGCGCGGCG CAGCAGCGGC GGGCACCGGC CCAATGGCCA CGGAACCTCAG 480
CACTGGCAGT CCGCCCTCCT CACACCGCAG GCGTGCAGTG TGGCCGACGG AGCCTCCCGG 540
GCCGAGGACC CAGCTAGGCC GTCACCCCGG TTGCTCCAC GGGAGGGGGC ACCAGGCAAA 600
CTGCCAAGG CCCCAGGCC AGGCTCCCTG GCGGAGGCCT CCGCTGTGCC CGCCAGATC 660
ATGGCCGCCA CCAGGCTCCC GAGCCATGCG TTCTGTGTCG GGAACGGCCC GCGCTCTCTG 720
CTGTCCAGCT AG

Seq ID NO: 271 Protein sequence:
Protein Accession #: XP_093210

1 11 21 31 41 51

MLRHGEQKRK RARKKWDFLP TCAFKTVRAA TERVRHGADR LRGGGRDAHE LKYPDTPSTS 60
TTTSNTAPTG PLSRSPKPRP QGGTPRRRPA AAGTRANGHG TQHWQSALLT PQACSVADGA 120
SRAEDPARPS PRLLPREGAP GKLPKAPSPG SLAEASAGLL AHVRLQNADA QRVSIQALP 180
5 PNSSVGRKEE RPPGAGQRRR PAMPATELST GSRPSSHRRR AVWPTEPPGP RTQLEPSRRL 240
LPREGAPGKL PKAPSPGSLA EASAGPAQIM AATRLPSRGF LSGNGPASWL SS

Seq ID NO: 272 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..732

1 11 21 31 41 51
GGATACTGTG TCACTCAAAG TAATGGGAGG GAGAGAGAAC AGGGAGGGTA GGGATGCTTT 60
15 TGAAAAAGCT TTTTTCCTCA CTTTAACTT GCTTTAGCGT TAAGAGTACT TACCAGCTAA 120
TAATGTGGAG GAAATTATTC TTTCTCATTG GAGATTACAG AATATATCTA TTCATCTTGA 180
ATACCCACTT GAAGCCTCTG TAGAAATGTC TCGTCTCTCG GTTGTATTTC TAAACCTTAC 240
ATGATTTTGT CTTGTTTCTG CAGTGAGAAA TTACATCCAT AGCAAAGACA AAAGTCTTTT 300
20 TAAATTATTT TTATTATCTT TTCATATAGT TCTTACAATT TCTAAAAAAT TAACACTCAT 360
TTAGTATCAC AATTATATGG AGAGGGTTT TTGTATTTT AAGCATATGT GGCTTATATA 420
AAAATTGCAG AAGTCATAGG ACTGTCATGT ATTGCAGCTC TGAGAACCAA TGCCGTGAAC 480
TTAAGCC

Seq ID NO: 273 Protein sequence:
Protein Accession #: Eos sequence

1 11 21 31 41 51
MGGRENREGR DAFEKAFFPT FNLL

Seq ID NO: 274 DNA sequence
Nucleic Acid Accession #: NM_003976.2
Coding sequence: 299-961

1 11 21 31 41 51
CTCTGAGCTT CTCTGAGCCT TGTTTGCTCA TCTGGAAAAA GGGGATTAAA CCATTACCT 60
40 CATGGAGTTG TGAAGAATA GCTGCAAAGC ACCTAACACA TAGTAAGGTT CCCAGTGCAG 120
CTACTTCTGC TGGGTGTAGT CTAGCTGTGT AGGCCCTTGT TTCTCACCT GGAGAAACTG 180
GGGTGGCAGG CCGTCCCTCC ACAAAAGATA ACTCATCTCT TAAATTGCAA GCTGCCTCAA 240
CAGGAGGTG GGGGAACAGC TCAACAATGG CTGATGGGCG CTCCTGGTGT TGATAGAGAT 300
GGAACCTTGA CTTGGAGGCC TCTCCACGCT GTCCCACTGC CCCTGGCCTA GCGGCGAGCC 360
45 TGCCCTGTGG CCCACCTTGG CCGCTCTGGC TCTGCTGAGC AGCGTCCGAG AGGCCTCCCT 420
GGGCTCCGCG CCCCGCAGCC CTGCCCTCCG CGAAGGCCCC CCGCTGTCTC TGGGCTCCCT 480
CGCCGCGCAC CTGCCGGGGG GACGCACGGC CCGTGGTGTG AGTGAAGAG CCGGCGGGCC 540
GCCGCGCGCAG CCTTCTCGGC CCGCGCCCCC GCCGCTGCA CCCCACCTG CTCTTCCCTG 600
CGGGGGCGCG GCGGCGCGGG CTGGGGGCCC GGGCAGCCGC GCTCGGGCAG CGGGGGCGCG 660
GGGCTGCCGC CTGCCCTCGC AGCTGGTGCC GGTGCGCGCG CTCGGCCTGG GCCACCGCTC 720
50 CGACGAGCTG GTGGGTTTCC GCTTCTGCAG CGGCTCCTGC CGCGCGCGCG GCTCTCCACA 780
CGACCTCAGC CTGGCCAGCC TACTGGGCGC CGGGGCCCTG CGACCGCCCC CGGGCTCCCG 840
GCCGTCAGC CAGCCCTGCT GCCGACCCAC GCGCTACGAA GCGGTCTCCT TCATGGACGT 900
CAACAGCACCT TGGAGAACCG TGGACCGCCT CTCGCCACCC GCCTGCGGCT GCCTGGGCTG 960
55 AGGGCTCGCT CCAGGGCTTT GCAGACTGGA CCCTTACCGG TGGCTCTTCC TGCCTGGGAC 1020
CCTCCCGCAG AGTCCCACTA GCCAGCGGCC TCAGCCAGGG ACGAAGGCCT CAAAGCTGAG 1080
AGGCCCTTAC CCGTGGGTGA TGGATATCAT CCCCAGACAG GTGAAGGGAC AACTGACTAG 1140
CAGCCCCAGA GCCCTACCCC TGCGGATCCC AGCCTAAAG ACACCAGAGA CCTCAGCTAT 1200
GGAGCCCTTC GGACCCACTT CTCACAGACT CTGGCACTGG CCAGGCCTCG AACCTGGGAG 1260
60 CCCTCCTCTG ATGAACACTA CAGTGGCTGA GGCATCAGCC CCCGCCAGG CCCTGTAGGG 1320
ACAGCATTTG AAGGACACAT ATTGCAGTTG CTTGGTTGAA AGTGCTGTG CTGGAACCTG 1380
CCTGTACTCA CTCATGGGAG CTGGCCCC

Seq ID NO: 275 Protein sequence:
Protein Accession #: NP_003967.1

1 11 21 31 41 51
MELGLGGLST LSHCPWPRRQ PALWPTLAAL ALLSSVAEAS LGSAPRSPAP REGPPPVLAS 60
70 PAGHLPGGRT ARWCSGRARR PPPQPSRPAP PPPAPPSALP RGGRAARAGG PGSRARAAGA 120
RGCLRLSQLV PVRALGLGHR SDELVRFRFC SGSCRARSF HDLRLASLLG AGALRPPPGS 180
RPVSQPCCRP TRYEAVSFMD VNSTWRTVDR LSATACGCLG

Seq ID NO: 276 DNA sequence
Nucleic Acid Accession #: NM_057091.1
Coding sequence: 783-1445

1 11 21 31 41 51
ACTGGCCGCT GAGAGAAGAA TCGGGTGGAG CAGAGAGCAG CTGCTGCAGG GCAGACAGCC 60
80 GGACCCCAAA ATCTGCACGT ACCAGCAGTC AGCCGCCCA CGCAGGGACC GGCTTACCCC 120
TCGCTCCCGC CCCTCACTCA CTTTCTCCCG CCCTCGGCC GGCCTCCAG CTCTCTACTT 180
CGGTGTCTTA CAACTCAAC TCCCGTTTC CGTGCCTCTC CACCGCTCGA GTTCTCTACT 240
CTCCATATCC GAGGGGCCCC TCCAGCATC TACCCCTCTC CCAACCTCGG GGGACCTAGC 300
CAAGCTAGGG GGGACTGGAT CCGACGGGTG GAGCAGCCAG GTGAGCCCGG AAAGGTGGGG 360
85 CGGGGAGGG GCGCTCCAGC CCCACCCCG GGCATCTGGT ACGCTGGGCG TGAATTGA 420
CACCAGACGG CTGCGCGGGC GGGCAGGAGG CTGCTGAGGG ATGGAGTTGG GCCCGGCCCC 480
CAGACAAGGC CCGGGGGCTC CGCCAGCAGC AGGTCCCTCG GGGCCAGCC CTCGCTGCCA 540

CCCCCGGCCTG GAGCCCCACA CCCGAGGGTG CAGACTGGCT GCCAAGGCCA CACTTTTGGC 600
 TAAAGAGAGC ACTGCCAGGT GTACAGTCCT GGGCATGCGC TGTTTGAGCT TCGGGGGAGA 660
 GCCCAGCACT GGTCCCCGGA AAGGTGCCCTA GAAGAACAAG GTGCAGGACC CCGTGTCTGCC 720
 TCAACAGGAG GGTGGGGGAA CAGCTCAACA ATGGCTGATG GGGCGCTCTG GTGTGTATAG 780
 5 AGATGGAACCT TGGACTTGA GGCCTCTCCA CGCTGTCCCA CTGCCCTGG CCTAGGCGGC 840
 AGCCTGCCCT TGGGCCACCC CTGGCCGCTC TGGCTCTGCT GAGCAGCGTC GCAGAGGCCT 900
 CCCTGGGCTC CGCGCCCGC AGCCCTGCCC CCCGCGAAGG CCCCCCGCT GTCTTGGCGT 960
 CCCCAGCGCG CCACCTGCCG GGGGACGCA CGGCCCGCTG GTGCAGTGA AGAGCCCGGC 1020
 10 GGCAGCGGCC GCAGCCTTCT CGGCCCGCGC CCCCAGCGCC TGCACCCCA TCTGCTCTTC 1080
 CCCCAGGGGG CCGCGCGCGC CGGGCTGGGG GCCCGGGCAG CCGCGCTCGG GCAGCGGGGG 1140
 CGCGGGGCTG CCGCTTGGC TCGCAGCTGG TGGCGGTGCG CGCGCTCGGC CTGGGCCACC 1200
 GCTCCGACGA GCTGGTGGT TCCGCTTCT GCAGCGGCTC CTGCCCGCGC GCGCGCTCTC 1260
 CACACGACCT CAGCCTGGCC AGCCTACTGG GCGCCGGGGC CTTGCGACCG CCCCCGGGCT 1320
 15 CCCCAGCGCT CAGCCAGCCC TGCTGCCGAC CCACGCGCTA CGAAGCGGTC TCCTTCATGG 1380
 ACCTCAACAG CACCTGGAGA ACCGTGGACC GCCTCTCCGC CACCGCTGCG GGCTGCGCTG 1440
 GCTGAGGGCT CGCTCCAGG CTTTGCAGAC TGGACCCCTA CCGGTGGCTC TTCTGCTGCT 1500
 GGACCTCTCC GCAGAGTCCC ACTAGCCAGC GGCCTCAGCC AGGGACGAAG GCCTCAAGC 1560
 TGAGAGGCCC CTACCGGTGG GTGATGGATA TCATCCCCGA ACAGGTGAAG GGACAAGTGA 1620
 20 CTAGCAGCCC CAGAGCCCTC ACCCTGCGGA TCCAGCCTA AAAGACCCA GAGACCTCAG 1680
 CTATGGAGCC CTTGCGAGCC ACTTCTCACA GACTCTGGCA CTGGCCAGGC CTCGAACCTG 1740
 GGACCCCTCC TCTGATGAAC ACTACAGTGG CTGAGGCATC AGCCCCCGCC CAGGCCCTGT 1800
 AGGGACAGCA TTTGAAGGAC ACATATTGCA GTTGCTTGGT TGAAAGTGCC TGTGCTGGAA 1860
 CTGGCCTGTA CTCCTCATG GAGCTGGCC CC

Seq ID NO: 277 Protein sequence:
 Protein Accession #: NP_003967.1
 1 11 21 31 41 51
 MELGLGLST LSHCPWPRRQ PALWPTLAAL ALLSSVAEAS LGSAPRSPAP REGPPPVLAS 60
 30 PAGHLPGGRT ARWCSGRARR PPPQPSRPAP PPPAPPSALP RGGRAARAGG PGSRRARAAGA 120
 RGCRLRSQLV PVRALGLGHR SDELVRFRFC SGSCRRRASP HDLSLASLLG AGALRPPPGS 180
 REVSPQCCRP TRYEAVSFMD VNSTWRTVDR LSATACGCLG

Seq ID NO: 278 DNA sequence
 Nucleic Acid Accession #: NM_057160.1
 Coding sequence: 1-714
 1 11 21 31 41 51
 40 ATGCCCGGCC TGATCTCAGC CCGAGGACAG CCCCTCCTTG AGGTCTTCC TCCCCAAGCC 60
 CACCTGGGTG CCCTCTTCT CCCTGAGGCT CCACTTGGTC TCTCCGCGCA GCCTGCCCTG 120
 TGGCCACCCC TGGCCGCTCT GGCTCTGCTG AGCAGCGTCG CAGAGGCCTC CCTGGGCTCC 180
 45 GCGCCCGGCA GCCCTGCCCC CCGCGAAGGC CCCCAGCCTG TCCTGGCGTC CCCCAGCGGC 240
 CACCTGCGCG GGGGACGACG GGCCTGCTGG TGCACTGGAA GAGCCCGCGC GCCGCGCGCG 300
 CAGCCTTCTC GGCCTGCGCC CCGCGCGCTT GCACCCCAT CTGCTCTTCC CCGCGGGGGC 360
 CGCGCGCGCG GGGCTGGGGG CCGGGGAGC CGCGCTCGGG CAGCGGGGGC GCGGGGCTGC 420
 CGCCTGCGCT CGCAGCTGGT GCCGCTGCGC GCGCTCGGCC TGGGCCACCG CTCGACGAG 480
 CTGCTGCGTT TCCGCTTCTG CAGCGGCTCC TGCCGCGCGC CGCGCTCTCC ACACGACCTC 540
 50 AGCCTGGCCA GCCTACTGGG CGCCGCGGCC CTGCGACCGC CCCCAGGCTC CCGGCCCGTC 600
 AGCCAGCCCT GCTGCCGACC CACGCGCTAC GAAGCGGTCT CCTTCATGGA CGTCAACAGC 660
 ACCTGGAGAA CCGTGGACCG CCTCTCCGCC ACCGCTGGT GCTGCTGGG CTGAGGGCTC 720
 GCTCCAGGGC TTTGAGAGT GGACCTTAC CGGTGGCTCT TCCTGCCTGG GACCTCCCG 780
 CAGAGTCCCA TAGCAGAGG GCCTCAGCCA GGGACGAAGG CCTCAAAGCT GAGAGGGCCC 840
 55 TACCGGTGGG TGATGGATAT CATCCCCGAA CAGGTGAAGG GACAAGTAC TAGCAGCCCC 900
 AGAGCCCTCA CCCTGCGGAT CCCAGCCTAA AAGACACCAG AGACCTCAGC TATGGAGCCC 960
 TTCGACCCA CTTCTACAG ACTCTGGCAC TGGCCAGGCC TCGAACCTGG GACCCCTCT 1020
 CTGATGAACA CTACAGTGGC TGAGGCATCA GCCCCGCCC AGGCCCTGTA GGGACAGCAT 1080
 TTGAAGGACA CATATTGCAG TTGCTTGGTT GAAAGTGCCT GTGCTGGAAC TGGCCTGTAC 1140
 TCACTCATGG GAGCTGGCCC C

Seq ID NO: 279 Protein sequence:
 Protein Accession #: NP_476501.1
 1 11 21 31 41 51
 65 MPGLISARGQ PLLEVLPPQA HLGALFLPEA PLGLSAQPAL WPTLAALALL SSVAEASLGS 60
 APRSPAPREG PPPVLASPAH HLPGGRTARW CSGRARRPPP QPSRPAPPPP APPSALPRGG 120
 RAARAGGPGS RARAAGARGC RLRSQLVFVR ALGLGHRSD E LVRFRFCGSG CRRARSPHDL 180
 70 SLASLLGAGA LRPPPGSRPV SQPCCRPTRY EAVSFMDVNS TWRTVDRLSA TACGCLG

Seq ID NO: 280 DNA sequence
 Nucleic Acid Accession #: NM_057090.1
 Coding sequence: 29-715
 1 11 21 31 41 51
 75 CTGATGGGCG CTCTGGTGT TGATAGAGAT GGAAGTGA CTTGGAGGCC TCTCCACGCT 60
 GTCCCACTGC CCCTGGCCTA GCGCGCAGGC TCCACTTGGT CTCTCCGCGC AGCCTGCCCT 120
 GTGGCCACCC CTGGCCGCTC TGGCTCTGCT GAGCAGCGTC GCAGAGGCCT CCCTGGGCTC 180
 80 GCGCCCGCGC AGCCCTGCCC CCGCGAAGG CCCCAGCCTG GTCTGGCGT CCCCAGCGG 240
 CCACCTGCGC GGGGACGCA CGGCCCGCTG GTGCAGTGA AGAGCCCGGC GGCAGCGGCC 300
 GCAGCCTTCT CGGCCCGCGC CCCCAGCGCC TGACCCCA TCTGCTCTTC CCGCGGGGG 360
 CCGCGCGGCG CGGGCTGGGG GCCCGGGCAG CCGCGCTCGG GCAGCGGGGG CCGGGGCTG 420
 CCGCTGCGCG TCGCAGCTGG TCGCGGTGCG CGCGCTCGGC CTGGGCCACC GCTCCGACGA 480
 85 GCTGGTGGCT TTCCGCTTCT GCAGCGGCTC CTGCCGCGC CGCGCTCTC CACACGACCT 540
 CAGCCTGGCC AGCCTACTGG GCGCCGGGGC CTGCGACCG CCCCAGGCT CCGCGCCGCT 600
 CAGCCAGCCC TGCTGCCGAC CCACGCGCTA CGAAGCGGTC TCCTTCATGG ACGTCAACAG 660

CACCTGGAGA ACCGTGGACC GCCTCTCCGC CACCGCCTGC GGCTGCCTGG GCTGAGGGCT 720
 CGCTCCAGGG CTTTGCAGAC TGGACCCCTTA CCGGTGGCTC TTCTTGCTCG GGACCCCTCCC 780
 GCAGAGTCCC ACTAGCCAGC GGCCTCAGCC AGGACGAGAG GCCTCAAAGC TGAGAGGCCC 840
 CTACCGGTGG GTGATGGATA TCATCCCGA ACAGGTGAAG GGACAACTGA CTAGCAGCCC 900
 CAGAGCCCTC ACCCTGCCGA TCCAGCCTA AAAGACACCA GAGACCTCAG CTATGGAGCC 960
 CTTGCGACCC ACTTCTCACA GACTCTGGCA CTGGCCAGGC CTCGAACCTG GGACCCCTCC 1020
 TCTGATGAAC ACTACAGTGG CTGAGGCATC AGCCCCGCC CAGGCCCTGT AGGGACAGCA 1080
 TTTGAAGGAC ACATATTGCA GTTGCTTGGT TGAAAGTGCC TGTGCTGGAA CTGGCCTGTA 1140
 CTCCTCATG GGAGCTGGCC CC

Seq ID NO: 281 Protein sequence:
 Protein Accession #: NP_476431.1

1 11 21 31 41 51
 MELGLGLST LSHCPWPRRQ APLGLSAQPA LWPTLAALAL LSSVAEASLG SAPRSPAPRE 60
 GPPVPLASPA GHLPGGRFAR WSGRRARRPP PQPSRPAPPP PAPPSPALPRG GRAARAGGPG 120
 SRARAAGARG CRLRSQLVFV RALGLGHRSD ELVRFRCFSG SCRARSPPHD LSLASLLGAG 180
 ALRPPPGSRP VSQPCRPRTR YEAVSFMDVN STWRTVDRLS ATACGCLG

Seq ID NO: 282 DNA sequence
 Nucleic Acid Accession #: Eos sequence

1 11 21 31 41 51
 CTACTGCACC TGCCCTCTGT TTCCTTTGGA AATCTCTTAC CTTTCATTAG GGTTCCTTTC 60
 ATAGCAATTT CTTTGGTGT TTAAGACTTC TACATTGCTT TTTCTTTTAT TATCTGTGCT 120
 CCGTGAACCT TATGAATGCT GCTTAAAAAT AATGTCAAAA TATGTTTTAG CTGCCTACTC 180
 AGGTAACTGT TTCTTTTGGT CTCATCTTGG TTTCCATATA CTATTTTTGG TTTTGTGTA 240
 GATCTAATCA ATGATCTAGT CAGAAGCTAC TTCCTGGCT AACAGTGATC ATGTTTCATGT 300
 GCTAAAAATG AACTTGAAC ACAGGAAGTAG TGGTTGGTCC AGTTTGAAAG CTCTTATAG 360
 TATTCTTCAT CCTGGCTGTA ATAATAGCCA TTATTGTGTA TGCCTTTGTT ATGTAGCAGA 420
 CACTCTTAAG GATTTTATGT GTATTATTCA AATTGCTATT ACTGTTCTTT TTATAGTTGA 480
 GAATCTCAGG ATACCTACAT TTATCACTTT TTCAATATAT ATGTATTCTT TATT

Seq ID NO: 283 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 564-1481

1 11 21 31 41 51
 GAGACTTTTA ATCATCTATC CCTTGTGCTT TACGCAGACC CTACAATACA CTAGAGGCTT 60
 CAAAGAGGTC AAAAATTCAC ATGTGTAGAC AAATTAGGTC CCTTAAGATG CCAGGCAAAC 120
 GAAGTGCTAC CAAAACACGC AATGACTGTC CTAAAAGTGC GTTCTGGGAT ACACCTGTAA 180
 ACTTGGATCA AGTTCCCTCC CCTCTCCTCA AAAATATATCG ACTTGTGCTG AAAGAAATCA 240
 CGACCGATGC TCACAATTCT GACCTCGTAA TTATATAGGG GGTGGTTTGT GTTCTGCGT 300
 CTTTCCCTGA TTAGGTGGCA GGTAAACATAT TTCATGTACA AAATGAAGTCA CAACACCACG 360
 GCAACAAGG GACAGGCCCT CAAAGTTGTC GGTAGGGAGC CAGGACCCCG CCAGTGGCGT 420
 GGGGAGACAC CGTACTAAAC AAGCTTGCAA ACAGCAGGCA CCTTCCTGCC ACTGAGGAGG 480
 AAGGGCTGGC TAAGGGAGGC CGGGCGGAG GAAAGCAAGC TCTGCAGGCC CTGACAAAGT 540
 CCTCCCGGCC TCCAGCGCTC GCCATGGCAA CGCGGGTCT GTGCTGGCCG GGATTGGCCG 600
 GCCTGGCGCG CGCAGGGCCC GCTGGGAAAG CGCGTCCCG CCGCGGCTCC GCCAGTTTGA 660
 ACTTGGCGGG CCAGATGTGG GCGGCGGGGC GCTGGGGGCC TACTTTTCCC TCTTCTACG 720
 CCGGTTTCTC TGCTGACTGC AGACCCAGGT CTCGCCCCCT CTCGAGCTCC TGCTCAGTCC 780
 CTATGACGGG CGCAGCTGGC CAGGGCTGG AGGTGGTGG CTCGCCGTCG CCGCCGCTCG 840
 CGCTGAGCTG CAGCAATTCC ACCAGGTGCG TGTGTCTCC CCTTGGCCAC CAGAGCTTCC 900
 AGTTTGACGA GGACGACGGT GACGGGGAGG ATGAGGAAGA CGTGGATGAT GAGGAAGACG 960
 TGGATGAAGA TGCCCATGAT TCAGAGGCCA AAGTGGCGAG CCTGAGAGGA ATGGAGTTAC 1020
 AGGGGTGCGC CAGCACTCAG GTTGAATCAG AAAATAACCA AGAAGAACAG AAACAGGTGC 1080
 GCTTACCAGA AAGCCGCTG ACACCATGGG AGGTGTGGTT TATTGGCAAA GAAAAAGAAG 1140
 AACGTGACCG GCTGCAACTG AAAGCTCTAG AGGAATTAAA TCAACAACCTA GAAAAAGAA 1200
 AAGAAATGGA AGAAGCTGAA AAAAGAAAGA TAATTGCTGA AGAAAAGCAC AAGGAAATGG 1260
 TTCAGAAAAA GAATGAGCAA AAAAGAAAG AAAGAGAACA AAAAATTAAT AAAGAAATGG 1320
 AGGAAAAAGC AGCAAAAGAA CTGGAGAAAG AATACTTGCA AGAAAAAGCA AAAGAAAAAT 1380
 ATCAAGATG GTTAAAGAAA AAAATGCTG AAGAAATGTA GAGGAAGAAG AAAGAAAAAG 1440
 AAAACAACAG CAAGCTGAAA TACAGGAGAA AAAGGAAATA GCAGAAAAAA AGTTTCAAGA 1500
 ATGGTTGGAA AATGCGAAAC ATAAACCTCG TCCAGCTGCA AAGAGCTATG GTTATGCCAA 1560
 TGGAAAACTT ACAGGTTTTT ACAGTGGAAA TTCCTATCCA GAACAGCCT TTTATAATCC 1620
 AATTCCGTGG AAACCAATTC ATATGCCACC TCCCAAAGAA GCTAAGGATC TATCAGGAAG 1680
 GAAGAGTAAA AGACCTGTGA TAAGTCAGCC ACACAAGTCA TCATCTCTGG TAATTCATAA 1740
 AGCCAGGAGC AATCTTTGCC TTGGAACTCT GTGCAGATA CAAAGATAGC GTATGTGGAA 1800
 AATAACATGC TTTTATCTGG AGCTATTTAA TTTAAAAATC AGAAATTGTT TTTTACTGCT 1860
 CAGTCAATAA CTCAACACTT AATGTGATTA TTGACAAATA GCAATTTTGT CATTTGTATA 1920
 TGGAGTCCTT AGAGTTGAGG AAGATATTTT CTGGATTTTG GTTTTATATA ACTTTTAAAG 1980
 GTTGATCTTG GCATGTTGTT TTGCAGATA AGTGGCTGAA TATGTAAGAA TTGTGTTTGT 2040
 ATTTAGCTTG TATTAAAAAGT AACTGTAAAT ACCAATAAAA CTAACAAATT TTCCTG

Seq ID NO: 284 Protein sequence:
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MATRGLCWPG LAGLARAGPA GKARPRRGS SLNLAQMWVA AGRWGPTFPS SYAGFSADCR 60
 PRSRPSSDSC SVPMTGARGQ GLEVVRSPSP PLPLSCSNST RSLSPGLHQ SFQFDEDDGD 120
 GEDEEDVDDE EDVDEDAHDS EAKVASLRGM ELQGCASQV ESENNOEBEQK QVRLPESRLT 180
 PWEVWFIKKE KEERDRLQK ALEELNQLE KRKEMEEREK RKI IAEKHK EWVQKKEQK 240
 RKERBQKINK EMEEKAAKEL EKEYLQEKAK EKYQEWLKKK NAECEKRRK EKKNSNKLKY 300

RRKRR

Seq ID NO: 285 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1-1746

	1	11	21	31	41	51	
5	ATGCCACTGA	AGCATTATCT	CCTTTTGCTG	GTGGGCTGCC	AAGCCTGGGG	TGCAGGGTTG	60
10	GCCTACCATG	GCTGCCCTAG	CGAGTGTACC	TGCTCCAGGG	CCTCCCAGGT	GGAGTGCACC	120
	GGGGCACGCA	TTGTGGCCGT	GCCCACCCCT	CTGCCCTGGA	ACGCCATGAG	CCTGCAGATC	180
	CTCAACACGC	ACATCACTGA	ACTCAATGAG	TCCCCGTTCC	TCAATATCTC	AGCCCTCATC	240
	GCCCTGAGGA	TTGAGAAAG	TGAGCTGTCT	CGCATCACGC	CTGGGGCCTT	CCGAAACCTG	300
15	GGCTCGCTGC	GCTATCTCAG	CCTCGCCAAC	AACAAGCTGC	AGGTTCTGCC	CATCGGCCTC	360
	TTCCAGGGCC	TGGACAGCCT	TGAGTCTCTC	CTTCTGTCCA	GTAACCAAGCT	GTTGCAGATC	420
	CAGCCGGCCC	ACTTCTCCCA	GTGCAGCAAC	CTCAAGGAGC	TGCAGTTGCA	CGGCAACCAC	480
	CTGGAATACA	TCCCTGACGG	AGCCTTCGAC	CACCTGGTAG	GACTCACGAA	GCTCAATCTG	540
	GGCAAGAATA	GCCTCACCCA	CATCTCACCC	AGGGTCTTCC	AGCACCTGGG	CAATCTCCAG	600
20	GTCTCTCCGG	TGTATGAGAA	CAGGCTCACG	GATATCCCCA	TGGGCACCTT	TGATGGGCTT	660
	GTTAACTTGC	AGGAACTGGC	TCTACAGCAG	AACCAGATTG	GACTGCTCTC	CCCTGGTCTC	720
	TTCCACAACA	ACCACAACCT	CCAGAGACTC	TACCTGTCCA	ACAACCACAT	CTCCAGCTG	780
	CCACCCAGCA	TCTTCATGCA	GCTGCCCCAG	CTCAACCCGTC	TTACTCTCTT	TGGGAATTCC	840
	CTGAAGGAGC	TCTCTCTGGG	GATCTTCGGG	CCCATGCCCA	ACCTGCGGGA	GCTTTGGCTC	900
25	TATGACAACC	ACATCTCTTC	TCTACCCGAC	AATGTCTTCA	GCAACCTCCG	CCAGTTGCAG	960
	GTCTGTGATT	TTAGCCGCAA	TCAGATCAGC	TTCTCTCTCC	CGGGTGCCTT	CAACGGGCTA	1020
	ACGGAGCTTC	GGGAGCTGTC	CCTCCACACC	AACGCACTGC	AGGACCTGGA	CGGGAATGTC	1080
	TTCCGATGT	TGGCCAACT	GCAGAACATC	TCCCTGCAGA	ACAATCGCCT	CAGACAGCTC	1140
	CCAGGGAATA	TCTTCGCCAA	CGTCAATGGC	CTCATGGCCA	TCCAGCTGCA	GAACAACCCG	1200
	CTGGAGAACT	TGCCCTCGG	CATCTTCGAT	CACCTGGGGA	AACTGTGTGA	GCTGCGGCTG	1260
30	TATGACAATC	CCTGGAGGTG	TGACTCAGAC	ATCCTTCCGC	TCCGCAACTG	GCTCCTGCTC	1320
	AACCAAGCTA	GGTTAGGGAC	GGACACTGTA	CCTGTGTGTT	TCAGCCAGC	CAATGTCCGA	1380
	GGCCAGTCCC	TCAATATCAT	CAATGTCAAC	GTGTGTGTTT	CAAGCGTCCA	TGTCCCTGAG	1440
	GTGCTAGATT	ACCCAGAAAC	ACCATGGTAC	CCAGACACAC	CCAGTTACCC	TGACACCACA	1500
35	TCCGTCTCTT	CTACCACTGA	GCTAACCAAG	CCTGTGGAAG	ACTACACTGA	TCTGACTACC	1560
	ATTCAAGTCA	CTGATGACCG	CAGCGTTTGG	GGCATGACCC	AGGCCACAGG	CGGGCTGGCC	1620
	ATTGCGGCCA	TTGTAATTTG	CATTGTGCGC	CTGGCCTGCT	CCCTGGCTGC	CTGCGTCGGC	1680
	TGTTGCTGCT	GCAAGAGAG	GAGCCAAGCT	GTCTGTATGC	AGATGAAGGC	ACCCAATGAG	1740
	TGTTAAAGAG	GCAGGCTGGA	GCAGGGCTGG	GGAATGATGG	GACTGGAGGA	CCTGGGAATT	1800
40	TCATCTTTCT	GCCTCCACCC	CTGGGTCCAT	GGAGCTTTCC	CGTGATTGCT	CTTTCTGGCC	1860
	CTAGATAAAG	GTGTGCTTAC	CTCTTCTCTG	CTTGCTGTAT	TCTCCCGTAG	AGAAGCAGGT	1920
	CGTGCCGGAC	CTTCTTACAA	TCAGGAAGAT	AGATCCAAC	GGCCATGGCA	AAAGCCCTGG	1980
	GGATTTCGGA	TTCATAACCC	TGGGCTTCTT	TCGAGAGGGC	TCTTCTCTCA	AATCCTCCCC	2040
	ACCTGTCTCT	CAAGAACAGC	CTTCCCTGCG	CCCAGGCCCC	CTCCGGGCTT	CTGTAGACTC	2100
45	AGTTAGTCCA	CAGCCTGCTC	ACTTCGTGGG	AATAGTTCTC	CGCTGAGATA	GCCCCCTCTG	2160
	CCTAAGTATT	ATGTAAGTTG	ATTTCCCTTC	TTTTGTTTCT	CTTGTTTGTG	CTATGGCTTG	2220
	ACCCAGCATG	TCCCCCTCAA	TGAAAGTTCT	CCCCTTGATT	TTCTGCTCCT	GAAGGCAGGG	2280
	TGAGTTCTCT	CCTCAAAGAA	GACTTCAAAC	CATTTAACTG	GTTTCTTAAG	AGCCGTCAAT	2340
	CAGCTCTGTT	TTGGGGATGC	TATGAAAGAG	AGAAGGAAAA	TCAATCCGCT	CAGTTCTCTG	2400
50	AGACAGAAGA	GCCGTCATCA	GTGTCTCACT	TGTGATTTTT	ATCTGGAAAA	GGAAGAAACA	2460
	CCCCAGCACA	GCAAGCTCAG	CCTTTTAGAG	AAGGATATTT	CCAAACTGCA	AACTTTGCTT	2520
	TGAAAAGTTT	AGCCCTTTAA	GGAATGAAAT	CATGTAGAAT	TTTGGAATTC	TAAAAACATT	2580
	AAAATCAGCT	TATTATATCG	GGATAGAGAA	AGAAATCTGG	TGCTGGGGGG	TCCCTGTGTT	2640
	CACCCCTAGA	GTTTGTTTTA	AAATTTTAA	TTGAAGCATG	TGAAGTGTAC	STGCAGAAAA	2700
55	GTGGGAACAT	GATAGTGTAT	GGCTTGGTGG	ATTTTTCACAA	ACTGAACATA	CCTGTGTAAT	2760
	CAGCATCTAG	ACCCAGACCC	AGAGCATCAC	AAATATCCCC	CATCTGGGCG	TTTTCCCAAG	2820
	GGAGATGGGG	GCTTCTGAAG	ATGGACTTAC	CTGGGACCTG	CCCCCATGTA	GCCAGGACGG	2880
	TCCCCCCACA	GTCAGCCTGT	GCAAAGGCC	CGTGGCCAGG	GGTGGAGGAG	AATATGTGGG	2940
	TGTGGACAGG	ATGGGAGACT	GTGGCCTGAA	CAGGAGATTT	TATTATATCT	GGAGACCCCTG	3000
60	AGAGACCCCTG	AGACCTGGGG	CACCATGGCT	GGCCAGGTCA	GAAGCATCCT	GACTGCAGAG	3060
	GTCCGTGACG	CCACACCTTC	TCCCTGCCCA	GCAAGTTGTC	TGCGGCTCAT	CGGAGGCCCC	3120
	TCCGCTTGGA	GCCTTCTATG	GACGTGATAT	GCCTGTATCT	GTTTTTAATT	TTCAATCTTC	3180
	ACCTTAGGGGA	AGTGAATTCG	CTCAGAGATG	AGATCCTTTA	ATTGAAAACG	AAGTGTAAAG	3240
	GAATCTAGTG	TCTTTCTAAT	GTGGTAAAT	TCTCCATCAA	CATCACAGTC	AGCTGGCAGC	3300
65	TGAACCTCAG	AATCTCACTT	ACAGCAGGCG	ACACGGGGGT	ACACCGATGG	GTCACTACTG	3360
	GTCTGGGGGC	TCCCTGGAGC	TCTCTCTCGG	TGTGCTCTGG	TTAGGAGTTG	AGTTGTTTGC	3420
	TCCAGGGTTA	TTCTCTCTCT	CGAGTCACAG	TCACACGAAT	ACCTGCCTTC	TCTGGCTTTC	3480
	CTGCTATACA	CATATTACAA	TGGCGCTCAA	GAAGTTAGGC	TCATGGCAAC	GTGTGTCTTT	3540
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	TCTTATTAGC	TCCCCGCTCC	ACAAGACACC	TGTGCTTTGG	AAATCCACCA	CCAATCCCGA	3720
	TCGGCTCTTA	TTAGCTCCCC	GCTCCACAAG	ACACCTGTGA	TCTGGAAATC	TACCACCAAT	3780
	CCCGATCGGC	TCTTATTAGC	TCCCGCTCC	ACAAGACACC	TGTGACATCC	TCCAGGGCCA	3840
	CAGGAGCAGC	TGCTGACCA	TTTTCCCTTC	CAGTTCTCTG	ACAAAAGATG	TCCAGAGGGC	3900
	TGTTTGGCAA	CACATAGTGA	CTTTGTAGCT	TTTCAACCTC	TGTCCCAGGG	AATCTAGGAG	3960
75	AGATGAGGCC	CGTCAGATGC	AAGAGATGTC	ATCCCCCAG	GGTCTCCAAG	GCATTTCCAC	4020
	ACTATTTGGT	GCACCTGGAG	GACATGCACC	AAGGCTTGCC	AGAGCCAACA	GGAAAGTGGC	4080
	CCAGACATGC	GACATGAGC	ATCACCCGCT	GATGGTGGCC	TGCTGTGCTC	GGTGCCAACA	4140
	GGGGCATCCC	GGCCCGTACC	CCTCCAGACA	GGAAGCATGG	GTTTGCCAC	AGACCTGTGC	4200
	GGTGCTCCTG	TGAGTGGCCT	CCAGATGTCT	TTGTGATAG	GCACAAGTGG	GCCAGGGCTG	4260
80	GAGGAGGGTG	GGAAACCTCA	TCATCCGGTG	GGCCCTGCCA	ATCTTAACCC	AGAACCTTTA	4320
	GGTATTCCTG	GCAGTAGCCA	TGACATTGGA	GCACCTTCTT	CTCCAGCCAG	AGGCTGACCT	4380
	GAGGGCCACT	GTCCTCAGAT	GACACCAACC	AGGAGCACCC	TAGGTGAGGG	GTGAGGGCCC	4440
	CCTTATGTGA	ACCTCTTGCC	TCTTCTTTTC	TCCCATCAGA	GTGGTTGGAT	GGAGCCATTG	4500
	GCCTCTCTTT	CTTCAGCGGG	CCCTTCAACC	TCTCTGCACC	ATGTTGTCTG	GCTGAGGAGC	4560
85	TACTAGAAAA	GCTGAGTGGG	GTCTCTTTTC	CAACAGGATG	ATGCATTTGC	TCAATTCTCA	4620
	GGGCTGGAAT	GAGCCGGCTG	GTCCCCCAGA	AAGCTGGAGT	GGGGTACAGA	GTTCAAGTTT	4680
	CCTCTCTGTT	TACAGCTCCT	TGACAGTCCC	ACGCCCATCT	GGAGTGGGAG	CTGGGAGTTA	4740

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 GGTGTTCAAT AGGCTGGGAG TTTTATTTAT CTCTTCAAAC TTTGTACAAG AGCTCATGGC 4980
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 GGAAAAAATA AACTCTTCCA TCCCTTAAAG AATAGAAATAG TTTGTCCCTC TCATGGGGAAT 5160
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 AACTTTTCAT GGACACAATT TCCACAACCT TTCAGATGCT GATGTAGAGC TATTGGGAAA 5280
 GAACCTCCAA ACTCAGGAAG TTTGCAGAGA GCAGACAGCT AGAGATAACT CCGGACCCAG 5340
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 CTCCTTCCGC CCCAGGTTTC TTCTTCTCTT AAGGAGAGAT TGTCTCTACC AACCCGCTGC 5580
 CTTTATGCTG CTTTCAAAGC TAGATCATGT TTGCCTTGCT TAGAGAAATA CTGCAAAATCA 5640
 GCCCCAGTGC TTGGCGATGC ATTTACAGAT TTCTAGGCCC TCAGGGTTT GTAGAGTGTG 5700
 AGCCCTGGTG GGCAGGGTTG GGGGGTCTGT CTTCTGCTGG ATGCTGCTTG TAATCCATTT 5760
 GGTGTACAGA ATCAACAATA AATAATATAC ATGTAT

Seq ID NO: 286 Protein sequence:
 Protein Accession #: NP_570843.1

1 11 21 31 41 51
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 MPLKHYLLLL VGCQAWGAGL AYHGCPSECT CSRASQVECT GARIVAVPTP LPWNAMSLQI 60
 LNTHITELNE SPFLNISALI ALRIEKNELS RITPGAFLNL GSLRYLSLAN NKLQVLPIGL 120
 PQGLDSLESL LLSSNQLLQI QPAHFSQCSN LKELQLHGNH LEYIPDGAFF HLVGLTKLNL 180
 GKNSLTHISP RVFOHLGNLQ VLRLYENRLT DIPMGTDFDL VNLQELALQQ NQIGLLSPGL 240
 FHNHNLRQL YLSNNHISQL PPSIFMQLPQ LNRLTLFGNS LKELSLGIFG PMPNLRBLWL 300
 YDNHISLPLD NVFSNLRQLQ VLILSRNQIS FISPGAFNGL TELRELSLHT NALQDLQDNV 360
 FRMLANLQNI SLQNNRLRQL PGNIFANVNG LMAIQLQNNQ LENLPLGIFD HLGKLCBLRL 420
 YDNWRCDSL ILPLRNWLLN NQPRLGTDIV PVCFSFANVR GQSLII INVN VAVPSVHVPE 480
 VPSYPETPMY PDTPSYPTIT SVSSTTELT S PVEDYDILT IQVTDDRSVW GMTQAQSLA 540
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Seq ID NO: 287 DNA sequence
 Nucleic Acid Accession #: NM_002362
 Coding sequence: 1..954

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 GGTCTCTCCC AGAGTCCTCA GGGAGCCTCT GCCTTACCCA CTACCATCAG CTTCACTTGC 240
 TGGAGGCAAC CCAATGAGGG TTCCAGCAGC CAAGAAGAGG AGGGGCCAAG CACCTCGCCT 300
 GACGCAGAGT CCTTGTTCGG AGAAGCACTC AGTAACAAGG TGGATGAGTT GGCTCATTTT 360
 CTGCTCCGCA AGTATCGAGC CAAGGAGCTG GTCACAAAGG CAGAAATGCT GGAGAGAGTC 420
 ATCAAAATT ACAAGCGCTG CTTTCTCTGT ATCTTCGGCA AAGCCTCCGA GTCCCTGAAG 480
 ATGATCTTTG GCATTGACGT GAAGGAAGTG GACCCCGCCA GCAACACCTA CACCCTTGTC 540
 ACCTGCCTGG GCCTTTCCTA TGATGGCCTG CTGGGTAATA ATCAGATCTT TCCCAAGACA 600
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 GAAATCTGGG AGGAGCTGGG TGTGATGGGG GTGATGATG GGAGGGAGCA CACTGTCTAT 720
 GGGGAGCCCA GGAACTGCT CACCCAAGAT TGGGTGCAGG AAAACTACCT GGAGTACCGG 780
 CAGGTACCCG GCAGTAATCC TGCGCGCTAT GAGTTCCTGT GGGGTCCAAG GGCTCTGGCT 840
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 GCCTACCCAT CCCTGCGTGA AGCAGCTTTG TTAGAGGAGG AAGAGGGAGT CTGA

Seq ID NO: 288 Protein sequence:
 Protein Accession #: NP_002353.1

1 11 21 31 41 51
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 GPPQSPQAS ALPTTISFTC WRQPNBSSS QEEEGPSTSP DAESLFREAL SNKVDELAHF 120
 LLRKYRAKEL VTKAEMLERV IKNYKRCFPV IFGKASESLK MIFGIDVKEV DPASNTYTLV 180
 TCLGLSYDGL LGNNQIFPKT GLLIIVLGTI AMEGDSASEE EIWEELGVMG VYDGREHTVY 240
 GEPRKLLTDQ WVQENYLEYR QVPGSNPARY EFLWGPRALA ETSYVKVLEH VVRVNRVRI 300
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Seq ID NO: 289 DNA sequence
 Nucleic Acid Accession #: NM_002362
 Coding sequence: 46..1344

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 CATCAGCGCG GCAGCAGCAC TGCAAGAAA GAAGACATAA ACCTGAGTGT TAGAAAGCTA 180
 CTCAACAGAC ATAATATTGT GTTGGTGAT TACACATGGA CTGAGTTTGA TGAACCTTTT 240
 TTGACAGAAA ATGTGAGTGT TGTGTCTATT ATTGACACAG AATTAAAGGT TAAAGACTCA 300
 CAGCCCATCG ATTTGAGTGC ATGCACTGTT GCACTTCACA TTTTCCAGCT GAATGAAGAT 360
 GGCCCCAGCA GTGAAAATCT GGAGGAAGAG ACAGAAAAA TAATTGCAGC AAATCACTGG 420
 GTTCTACCTG CAGCTGAATT CCATGGGCTT TGGGACAGCT TGGTATACGA TGTGGAAGTC 480
 AAATCCCATC TCCTCGATTA TGTGATGACA ACTTTACTGT TTTACAGCAA GAACGTCAAC 540

	AGCAACCTCA	TCACCTGGAA	CGGGGTGGTG	CTGCTCCACG	GTCCTCCTGG	CACTGGAAAA	600
	ACATCCCTGT	GTAAGCGGTT	AGCCCAGAAA	TTGACAATTA	GACTTTCAAG	CAGGTACCGA	660
	TATGGCCAAT	TAATTGAAAT	AAACAGCCAC	AGCCTCTTTT	CTAAGTGGTT	TTCGGAAGT	720
	GGCAAGCTGG	TAACCAAGAT	GTTTCAGAAG	ATTACAGGAT	TGATTGATGA	TAAAGACGCC	780
5	CTGGTGTTCG	TGCTGATTGA	TGAGGTGGAG	AGTCTCACAG	CCGCCCCGAA	TGCCTGCAGG	840
	GCGGGCACCG	AGCCATCAGA	TGCCATCCGC	GTGGTCAATG	CTGTCTTGAC	CCAAATTGAT	900
	CAGATTAAAA	GGCATTCCAA	TGTTGTGATT	CTGACCACTT	CTAACATCAC	CGAGAAGATC	960
	GACGTGGCCT	TGCTGGACAG	GGCTGACATC	AAGCAGTACA	TGGGCCACCC	CTCTGCAGCA	1020
10	GCCATCTTCA	AAATCTACCT	CTCTTGTTTG	GAAGAAGTGA	TGAAGTGTCA	GATCATATAC	1080
	CCTCGCCAGC	AGCTGCTGAC	CCTCCGAGAG	CTAGAGATGA	TTGGCTTCAT	TGAAAACAAC	1140
	GTGTCAAAAT	TGAGCCTTCT	TTTGAATGAC	ATTTCAAGGA	AGAGCGAGGG	CCTCAGCGGC	1200
	CGGGTCTTGA	GAAAACTCCC	CTTTCTGGCT	CATGCGCTGT	ATGTCAGGCG	CCCCACCGTC	1260
	ACCATAGAGG	GGTTCTCTCA	GGCCCTGTCT	CTGGCAGTGG	ACAAGCAGTT	TGAAGAGAGA	1320
15	AAGAAGCTTG	CAGCTTACAT	CTGATCCTGG	GCTTCCCCAT	CTGGTGTCTT	TCCCATGGAG	1380
	AACACACAA	CAGTAAGTGA	GGTTGCCCCA	CACAGCCGTC	TCCCAGGGAA	TCCCTTCTGC	1440
	AAACCAACCG	TTACTTAGAC	TGCAAGCTAG	AAAGCCACCA	AGGCCAGGCT	TTGTTAAAG	1500
	AAGTGATTTC	TATTTATGTT	GTTTTAAAA	GCATACTGAG	AGACAAACAT	CTTGTCATTT	1560
	TCACTGTTTG	TAAAAGATAA	TTCAGATTGT	TTGTCTCTTT	GTGAAGAACC	ATCGAAACCT	1620
	GTTTGTTCCT	AGCCCAACCC	CAGTGGATGG	GATGCATAAT	GCCAGCAAGT	TTTGTTTAAC	1680
20	AGCAAAAAAG	GAAAGATAAT	GCAGGTGTTA	TAGAAGCCAG	AAGAGAAACT	GTGTCAACCT	1740
	AAAGAAGCAT	ATAATCATAG	CATTAAAAAT	GCACACATTA	CTCCAGGTGG	AAGGTGGCAA	1800
	TTGCTTTCTG	ATATCAGCTC	GTTTGATTTA	GTGCAAAAA	GTTTTCAAGA	CTATTTAATG	1860
	GATGTAAAAA	AGCCTATTTC	TACATTATAC	CAACTGAGAA	AAAAATGGTC	GGTAAAGTGT	1920
	TCTTTTCATA	TAAATAATCA	AGACATGGTC	CCATTGTCAG	GAAAAGTGCA	GACTCTGAGT	1980
25	GTTCCAGGGA	AACACATGCT	GGACATCCCT	TGTAACCCGG	TATGGGCGCC	CCTGCATTGC	2040
	TGGGATGTTT	CTGCCACCGG	TTTTGTTTGT	GCAATAACGT	TATCACATTT	CTAATGAGGA	2100
	TTACATTAA	TATAATATAA	AATAAATAGG	TCAGTTACTG	GTCTCTTTCT	GCCGAATGTT	2160
	ATGTTTTGCT	TTTATCTCAC	AGTAAAAATA	ATATAATTAA	AAA		

Seq ID NO: 290 Protein sequence:
Protein Accession #: NP_004228

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	FDEPFLTRNV	QSVSIIDTEL	KVKDSQPIDL	SACTVALHIF	QLNEDGPSSE	NLEETENII	120
	ANHWVLPAA	EFHGLWDSL	YDVEVKSHLL	DYVMTLLFS	DKNVNSNLIT	WNRVLLHGP	180
	PGTGKTSLCK	ALAQLTIRL	SSRYRYGQLI	EINSHSLFSK	WFSESGKLV	KMFQKIQDLI	240
	DDKDALVFL	IDEVESLTAA	RNACRAGTEP	SDAIRVNVAV	LTQIDQIKRH	SNVVLITTSN	300
40	ITEKIDVAFV	DRADIKQYIG	PPSAAAIKFI	YLSCLBELMK	CQIIYPRQQL	LTLRELEMIG	360
	FIENNVSKLS	LLLNDISRKS	EGLSGRVLRK	LPFLAHLAYV	QAPTVTIEGF	LQALSILAVDK	420
	QFEERKKLAA	YI					

Seq ID NO: 291 DNA sequence
Nucleic Acid Accession #: NM_002658.1
Coding sequence: 77-1372

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	GAGCGACTCC	AAAGGCAGCA	ATGAAGTTCA	TCAAGTTCCA	TCGAAGTGTG	ACTGTCTAAA	180
	TGAGGAAACA	TGTGTGTCCA	ACAAGTACTT	CTCCAACATT	CAGTGGTGCA	ACTGCCCAAA	240
	GAAATTCGGA	GGGCAGCACT	GTGAAATAGA	TAAGTCAAAA	ACCTGCTATG	AGGGGAATGG	300
55	TCACTTTTAC	CGAGGAAAGG	CCAGCACTGA	CACCATGGGC	CGGCCCTGCC	TGCCCTGGAA	360
	CTCTGCCACT	GTCCCTTACG	AAACGTAACA	TGCCCCACAG	TCTGATGCTC	TTCACTGGGG	420
	CCTGGGGAAA	CATAATTACT	GCAGGAACCC	AGACAACCGG	AGGCGACCC	GGTGCTATGT	480
	GCAGGTGGGC	CTAAAGCCGC	TTGTCCAAGA	GTGCATGGTG	CATGACTGCG	CAGATGGAAA	540
	AAAGCCCTCC	TCTCTCCAG	AAGAATTAAA	ATTTCAAGTG	GGCCAAAAGA	CTCTGAGGCC	600
60	CCGCTTTAAG	ATTATTGGGG	GAGAATTAC	CACCATCGAG	AACGAGCCCT	GGTTTGGCGC	660
	CATCTACAGG	AGGCACCGGG	GGGGCTCTGT	CACCTACGTG	TGTGGAGGCA	GCCTCATCAG	720
	CCCTTGCTGG	GTGATCAGCG	CCACACACTG	CTTCATTGAT	TACCCAAAAG	AGGAGGACTA	780
	CATCGCTTAC	CTGGGTCGCT	CAAGGCTTAA	CTCCAACACG	CAAGGGGAGA	TGAAGTTTGA	840
	GGTGGAAAAA	CTCATCTTAC	ACAAGGACTA	CAGCGCTGAC	ACGCTTGCTC	ACCACAACGA	900
65	CATTGCCTTG	CTGAAGATCC	GTTCCAAGGA	GGGCAGGTGT	GCGCAGCCAT	CCCGGACTAT	960
	ACAGACCATC	TGCCTGCCCT	CGATGTATAA	CGATCCCCAG	TTTGGCACAA	GCTGTGAGAT	1020
	CACCTGGCTT	GGAAAAAGAG	ATTCTACCGA	CTATCTCTAT	CCGGAGCAGC	TGAAAATGAC	1080
	TGTTGTGAAG	CTGATTTCCT	ACCGGGAGTG	TCAGCAGCCC	CACCTACTAG	GCTCTGAAGT	1140
	CACCACCAAA	ATGCTATGTG	CTGCTGACCC	CCAATGGAAA	ACAGATTCTT	GCCAGGGAGA	1200
70	CTCAGGGGGA	CCCCCTCGT	GTTCCCTCCA	AGGCCGCGATG	ACTTTGACTG	GAATTGTGAG	1260
	CTGGGGCCGT	GGATGTGCCC	TGAAGGACAA	GCCAGGCGTC	TACACGAGAG	TCTCACACTT	1320
	CTTACCTCTG	ATCCGCAGTC	ACACCAAGGA	AGAGAATGGC	CTGGCCCTCT	GAGGGTCCCC	1380
	AGGGAGGAAA	CGGGCACCAC	CGCTTTCTTT	GCTGGTTGTC	ATTTTTCAG	TAGAGTCATC	1440
	TCCATCAGCT	GTAAGAAGAG	ACTGGGAAGA	TAGGCTCTGC	ACAGATGGAT	TTGCCTGTGG	1500
75	CACCACCAAG	GTGAAGGACA	ATAGCTTTAC	CCTCACGGAT	AGGCCTGGGT	GCTGGCTGCC	1560
	CAGACCTCTT	GGCCAGGATG	GAGGGGTGGT	CCTGACTCAA	CATGTTACTG	ACCAGCAACT	1620
	TGCTCTTTTC	TGGACTGAAG	CCTGCAGGAG	TAAAAAAGGG	CAGGGCATCT	CCTGTGCATG	1680
	GGCTCGAAGG	GAGAGCCAGC	TCCCCCGACC	GGTGGGCATT	TGTGAGGCCC	ATGGTTGAGA	1740
	AATGAATAAT	TTCCCAATTA	GGAAGTGTA	GCAGCTGAGG	TCTCTTGAGG	GAGCTTAGCC	1800
80	AATGTGGGAG	CAGCGGTTTG	GGGAGCAGAG	ACACTAACGA	CTTCAGGGCA	GGGCTCTGAT	1860
	ATTCCATGAA	TGTATCAGGA	AATATATATG	TGTGTGTATG	TTTGCACACT	TGTTGTGTGG	1920
	GCTGTGAGTG	TAAGTGTGAG	TAAGAGCTGG	TGTCTGATTG	TTAAGTCTAA	ATATTTCCTT	1980
	AAACTGTGTG	GACTGTGATG	CCACACAGAG	TGGTCTTTCT	GGAGAGGTTA	TAGGTCACTC	2040
	CTGGGGCCCT	TTGGGTCCCC	CACGTGACAG	TGCCTGGGAA	TGTACTTATT	CTGCAGCATG	2100
85	ACCTGTGACC	AGCACTGTCT	CAGTTTCACT	TTCAATAGAG	TGTCCTTTTC	TTGGCCAGTT	2160
	ATCCCTTCCT	TTTAGCCTAG	TTCATCCAA	CCTCACTGGG	TGGGGTGAGG	ACCACTCCTT	2220
	ACACTGAATA	TTTATATTTT	ACTATTTTAA	TTTATATTTT	TGTAATTTTA	AATAAAAGTG	2280

ATCAATAAAA TGTGATTTTT CTGA

Seq ID NO: 292 Protein sequence:
Protein Accession #: NP_002649.1

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YCRNPDNRRR PWCYVQVGLK PLVQECMVHD CADGKKPSSP PEELKFQCGQ KTLRPRFKII 180
GGEFTTIENQ PWFAAIYRRH RGGSVTYVCG GSLISPCWVI SATHCFIDYP KKEDYIVYLG 240
RSRLNSNTQG EMKFEBENLI LHKDYSADTL AHNDIALLK IRSKEGRCAQ PSRTIQITICL 300
PSMYNDPQFG TSCBITGFGK ENSTDYLYPE QLKMTVVKLI SHRECQPHY YGSEVTTKML 360
CAADPQWKTD SCQGDSSGGL VCSLQGRMTL TGIVSWGRGC ALKDKPGVYT RVSHFLPWIR 420
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Seq ID NO: 293 DNA sequence
Nucleic Acid Accession #: NM_001498
Coding sequence: 93..2006

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TGAGCTGGGA GGAACCAAG CGCCATGCCG ACCACGTGCG GCGGCACGGG ATCCTCCAGT 180
TCCTGCACAT CTACACGCG GTCAAGGACC GGCACAAGGA CGTTCTCAAG TGGGGCGATG 240
AGGTGGAATA CATGTTGGTA TCTTTTGATC ATGAAAAATA AAAAGTCCGG TTGGTCTCTG 300
CTGGGGAGAA AGTTCTTGA ACTCTGCAAG AGAAGGGGGA AAGGACAAAC CCAACCATC 360
CTACCCCTTG GAGACCAGAG TATGGGAGTT ACATGATTGA AGGGACACCA GGACAGCCCT 420
ACGGAGGAAC AATGTCCGAG TTCAATACAG TTGAGGCCAA CATGCGAAAA CGCCGGAAGG 480
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TAGGCTGTCC TGGGTTCACA CTGCCGAGG TCAAACCCAA CCCAGTGGAA GGAGGAGCTT 600
CCAAGTCCCT CTCTTTTCCA GATGAAGCAA TAAACAAGCA CCCTCGCTTC AGTACCTTAA 660
CAAGAAATAT CCGACATAGG AGAGGAGAAA AGGTTGTGAT CAATGTACCA ATATTAAAG 720
ACAAGAAATC ACCATCTCCA TTTATAGAAA CATTTACTGA GGATGATGAA GCTTCAAGGG 780
CTTCTAAGCC GGATCATATT TACATGGATG CCATGGGATT TGGAAATGGC AATTGCTGTC 840
TCCAGGTGAC ATTCCAAGCC TGCAGTATAT CTGAGGCCAG ATACCTTTAT GATCAGTTGG 900
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ACTCAATAGA CAGCTATTTA TCTAAGTGTG GTGAGAAATA TAATGACATC GACTTGACGA 1140
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ATGTTGTCTCA TCTCTTTAT AGAGACCCAC TGACACTGTT TGAAGAGAAA ATACACCTGG 1260
ATGATGCTAA TGAGTCTGAC CATTTTGAGA ATATTCAATC CACAAATTGG CAGACAATGA 1320
GATTTAAGCC CCTCTCTCCA AACTCAGACA TTGGATGGAG AGTAGAATTT CGACCATAGG 1380
AGGTGCAATT AACAGACTTT GAGAACTCTG CCTATGTGGT GTTTGTGGTA CTGCTACCA 1440
GAGTGATCCT TTCTTACAAA TTGGATTTTC TCATTCCACT GTCAAAGGTT GATGAGAA 1500
TGAAGGTAGC ACAGAAAAGA GATGCTGTCT TGCAGGGAAT GTTTTATTTC AGGAAAGATA 1560
TTTGCAAAGG TGGCAATGCA GTGGTGGATG GTTGTGGCAA GGCCGAGAAC AGCAGGAGC 1620
TCGCTGCAGA GGAGTACACC CTCATGAGCA TAGACACCAT CATCAATGGG AAGGAAGGTG 1680
TGTTTCTCTG ACTGATCCCA ATTCTGAACT CTTACCTTGA AAACATGGAA GTGGATGTGG 1740
ACACCAGATG TAGTATTCTG AACTACCTAA AGCTAATTAA GAAGAGAGCA TCTGGAGAAC 1800
TAATGACAGT TGCCAGATGG ATGAGGGAGT TTATCGCAAA CCATCCTGAC TACAAGCAAG 1860
ACAGTGTGAT AACTGATGAA ATGAATTATA GCCTTATTTT GAAGTGTAAC CAAATTGCAA 1920
ATGAATTATG TGAATGCCCA GAGTTACTTG GATCAGCATT TAGGAAAGTA AAATATAGTG 1980
GAAGTAAAC TGACTCATCC AACTAGACAT TCTACAGAAA GAAAAATGCA TTATTGACGA 2040
ACTGGCTACA GTACCATGCC TCTCAGCCCG TGTGTATAAT ATGAAGACCA AATGATAGAA 2100
CTGTACTGTT TTCTGGCCCA GTGAGCCAGA AATTGATTAA GGCTTTCTTT GGTAGGTAAA 2160
TCTAGAGTTT ATACAGTGTA CATGTACATA GTAAAGTATT TTTGATTAA AATGTATTTT 2220
AATAACATAT CTAAAGTCAK CATGAACTGG CTGTACATT TTTAAATTCT TACTCTGGAG 2280
CAACCTACTG TCTAAGCAGT TTTGTAAATG TACTGGTAAT TGTACAATAC TTGCAATCCA 2340
GAGTTAAAT GTTTACTGTA AATTTTGTGT CTTTAAAGA CTACCTGGGA CCTGATTTAT 2400
TGAAATTTT CTCTTAAAA ACATTTTCTC TCGTTAATTT TCCTTTGTCA TTCTTTTGT 2460
TGTCTACATT AAATCACTTG AATCCATTGA AAGTGCTTCA AGGGTAATCT TGGGTTTCTA 2520
GCACCTTATC TATGATGTTT CTTTGTCAAT TGAATAATC ACTTGGTCAC CTTGCCCAA 2580
GCTTTCCCTT CTGAATAAAT ACCCATTGAA CTCTGAAAAA AAAAAAAA AAAAA

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Seq ID NO: 294 Protein sequence:
Protein Accession #: NP_001489

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1      11      21      31      41      51
|      |      |      |      |      |
MGLLSQGSPL SWEETKRHAD HVRRHGILQF LHIYHAVKDR HKDVLKWGDE VEYMLVSFDH 60
ENKKVRLVLS GEKVLETLQE KGERTNPNHP TLWRPEYGSY MIEGTFPGQPY GGTMSFNTV 120
EANMRKRKE ATSILEENQA LCTITSFPRL GCPGFTLPEV KPNPVEGGAS KSLFFPDEAI 180
NKHPRFSTIL RNIRHRRGEK VVINVPFKD KNTSPPIET FTEDEASRA SKPDHIYMDA 240
MGFGMGNCCL QVTFQACSTIS EARYLYDQLA TICPIVMALS AASPFYRGYV SDIDCRWGI 300
SASVDDRTRE ERGLEPLKNN NYRISKSRVD SIDSYSKCG EKYNIDILTI DKEIYBQLLQ 360
EGIDHLLAQH VAHLFIRDPL TLFEKIHLD DANESDHFEN IQSTNQWQTM FKPPPNNSDI 420
GWRVEFRPME VQLTDFENSA YVVFVLLTR VILSYKLDFL IPLSKVDENM KVAQKRDAVL 480
QGMFYFRKDI CKGNAVVDG CGKAQNSTEL AAEYTLMSI DTIINGKEGV FPGLIPILNS 540
YLENMEVDVD TRCSILNLYK LIKKRASGEL MTVARWMREF IANHPDYKQD SVITDEMNSY 600
LILKNCQIAN ELCECEPELLG SAFRKVKYSG SKTSSN

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Seq ID NO: 295 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 247-816

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5      1      11      21      31      41      51
      |      |      |      |      |      |
      AGTGTTCGGC TGGGGCAGGC ACGCTGTGGC TGGCTACTTC CCTTCCTCCC ATCCCCCTTG 60
      GGCCAAACGG GATCGGTGCT TCTGGTGAGA CGCCTCCCCA TGCACATCAC TCCCAGGTGC 120
      CCTAGGGGGC ACATTTCCCA CACTCCCAG AGGGCAGGTT TCTAGAAAGT GCCACCAAGT 180
10     GGGAGGCGCC ACAACTTCAC TGCCATTTTG TGAGGTGCCG CCGTCTCTCC TCCAGCAAGG 240
      GAAACAATGA CCGATAAAAC AGAGAAGGTG GCTGTAGATC CTGAAACTGT GTTTAAACGT 300
      CCCAGGGAAT GTGACAGTCC TTCGTATCAG AAAAGGCAGA GGATGGCCCT GTTGGCAAGG 360
      AAACAAGGAG CAGGAGACAG CCTTATTGCA GGCTCTGCCA TGTCCAAAGA AAAGAAGCTT 420
      ATGACAGGAC ATGCTATTCC ACCCAGCCAA TTGGATTCTC AGATTGATGA CTTCACTGGT 480
15     TTCAGCAAAG ATAGGATGAT GCAGAAACCT GGTAGCAATG CACCTGTGGG AGGAAACGTT 540
      ACCAGCAGTT TCTCTGGAGA TGACCTAGAA TGCAGAGAAA CAGCCTCCTC TCCCAAAGC 600
      CAACGAGAAA TTAATGCTGA TATAAAACGT AAATTAGTGA AGGAACTCCG ATGCGTTGGA 660
      CAAAAATATG AAAAAATCTT CGAAATGCTT GAAGGAGTGC AAGGACCTAC TGCAGTCAGG 720
      AAGCGATTTT TTGAATCCAT CATCAAGGAA GCAGCAAGAT GTATGAGACG AGACTTTGTT 780
20     AAGCACCTTA AGAAGAAACT GAAACGTATG ATTTGAGAAT ACTTGTCCCT GGAGGATTAT 840
      CACACCCCAA ATGCTAATGA TCGTTAATGA TTGAGGAGAG AAAAGGATCA GATTGCTGTT 900
      TTCTACAATG GAGCAGGATA TTGCTGAAGT CTCCTGGCAT ATGTTACCGA ATCAAAATAGC 960
      CTTCCAGAGG CTAAGAAATT TCTGTTAGTA AAAAGATGTT TTTTCCCAA AGCATTTTAT 1020
      TTGAAAGGAT AACTTGTGTT TTGTTATT TTGATTCCCA CCTGTGCTGG TAGATATTAT 1080
25     TAACCCATTA GGTAAATACT ATTACAGTCG TGGTTTCTGC A

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Seq ID NO: 296 Protein sequence:
Protein Accession #: Eos sequence

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30     1      11      21      31      41      51
      |      |      |      |      |      |
      MTDKTEKVAV DPETVFKRPR ECDSPSYQKR QRMALLARKQ GAGDSLIAGS AMSKEKKLMT 60
      GHAIPPSQLD SQIDDFTFGS KDRMMQKPGS NAPVGGNVTS SFGDDLECR ETASSPKSQR 120
      EINADIKRKL VKELRCVGQK YEKIFEMLEG VQGPTAVRKR FFESIIEKAA RCMRRDFVKH 180
35     LKKLKRMI

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Seq ID NO: 297 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 247-815

```

40     1      11      21      31      41      51
      |      |      |      |      |      |
      AGTGTTCGGC TGGGGCAGGC ACGCTGTGGC TGGCTACTTC CCTTCCTCCC ATCCCCCTTG 60
      GGCCAAACGG GATCGGTGCT TCTGGTGAGA CGCCTCCCCA TGCACATCAC TCCCAGGTGC 120
      CCTAGGGGGC ACATTTCCCA CACTCCCAG AGGGCAGGTT TCTAGAAAGT GCCACCAAGT 180
45     GGGAGGCGCC ACAACTTCAC TGCCATTTTG TGAGGTGCCG CCGTCTCTCC TCCAGCAAGG 240
      GAAACAATGA CCGATAAAAC AGAGAAGGTG GCTGTAGATC CTGAAACTGT GTTTAAACGT 300
      CCCAGGGAAT GTGACAGTCC TTCGTATCAG AAAAGGCAGA GGATGGCCCT GTTGGCAAGG 360
      AAACAAGGAG CAGGAGACAG CCTTATTGCA GGCTCTGCCA TGTCCAAAGA AAAGAAGCTT 420
      ATGACAGGAC ATGCTATTCC ACCCAGCCAA TTGGATTCTC AGATTGATGA CTTCACTGGT 480
50     TTCAGCAAAG ATAGGATGAT GCAGAAACCT GGTAGCAATG CACCTGTGGG AGGAAACGTT 540
      ACCAGCAGTT TCTCTGGAGA TGACCTAGAA TGCAGAGAAA CAGCCTCCTC TCCCAAAGC 600
      CAACAAGAAA TTAATGCTGA TATAAAACGT AAATTAGTGA AGGAACTCCG ATGCGTTGGA 660
      CAAAAATATG AAAAAATCTT CGAAATGCTT GAAGGAGTGC AAGGACCTAC TGCAGTCAGG 720
55     AAAAGGATTT TTGAATCCAT CATCAAGGAA GCAGCAAGAT GTATGAGACG AGACTTTGTT 780
      AAGCACCTTA AGAAGAAACT GAAACGTATG ATTTGAGAAT ACTTGTCCCT GGAGGATTAT 840
      CACACCCCAA ATGCTAATC TCATTAATGA TTGAGGAGAG AAAAGGATCA GATTGCTGTT 900
      TTCTACAATG GAGCAGGATA TTGCTGAAGT CTCCTGGCAT ATGTTACCGA ATCAACTGGC 960
      CTTCCAGAGG CTAAGAAATT TCTGTTAGTA AAAAGATGTT TTTTCCCAA AGCAGTTTAT 1020
      TTGAAAGGAT AACTTGTGTT TTGTTATT TTGATTCCCA CCTGTGCTGG TAGATATTAT 1080
60     TAACCCATTA GGTAAATACT ATTACAGTCG TGGTTTCTGC A

```

Seq ID NO: 298 Protein sequence:
Protein Accession #: Eos sequence

```

65     1      11      21      31      41      51
      |      |      |      |      |      |
      MTDKTEKVAV DPETVFKRPR ECDSPSYQKR QRMALLARKQ GAGDSLIAGS AMSKEKKLMT 60
      GHAIPPSQLD SQIDDFTFGS KDRMMQKPGS NAPVGGNVTS SFGDDLECR ETASSPKSQQ 120
      EINADIKRKL VKELRCVGQK YEKIFEMLEG VQGPTAVRKR FFESIIEKAA RCMRRDFVKH 180
70     LKKLKRMI

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Seq ID NO: 299 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 247-815

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75     1      11      21      31      41      51
      |      |      |      |      |      |
      AGTGTTCGGC TGGGGCAGGC ACGCTGTGGC TGGCTACTTC CCTTCCTCCC ATCCCCCTTG 60
      GGCCAAACGG GATCGGTGCT TCTGGTGAGA CGCCTCCCCA TGCACATCAC TCCCAGGTGC 120
      CCTAGGGGGC ACATTTCCCA CACTCCCAG AGGGCAGGTT TCTAGAAAGT GCCACCAAGT 180
80     GGGAGGCGCC ACAACTTCAC TGCCATTTTG TGAGGTGCCG CCGTCTCTCC TCCAGCAAGG 240
      GAAACAATGA CCGATAAAAC AGAGAAGGTG GCTGTAGATC CTGAAACTGT GTTTAAACGT 300
      CCCAGGGAAT GTGACAGTCC TTCGTATCAG AAAAGGCAGA GGATGGCCCT GTTGGCAAGG 360
      AAACAAGGAG CAGGAGACAG CCTTATTGCA GGCTCTGCCA TGTCCAAAGC AAAGAGCTTA 420
      TGACAGGACA TGCTATTCCA CCCAGCCAA TGGATTCTCA GATTGATGAC TTTCACTGGT 480
85

```


TCAGCAAGA TAGGATGATG CAGAAACCTG GTAGCAATGC ACCTGTGGGA GGAAACGTTA 540
 CCAGCAGTTT CTCTGGAGAT GACCTAGAAT GCAGAGAAAC AGCCTCCTCT CCCAAAAGCC 600
 AACAAAGAAAT TAATGCTGAT ATAAAACGTA AATTAGTGAA GGAACCTCCG TCGTGTGGAC 660
 AAAAAATATGA AAAAACTTTC GAAATGCTTG AAGGAGTGCA AGGACCTACT GCAGTCAGGA 720
 AACGATTTTT TGAATCCATC ATCAAGGAAG CAGCAAGATG TATGAGACGA GACTTTGTTA 780
 AGCACCTTAA GAAGAAACTG AAACGTATGA TTTGAGAATA CTGTGCCCTG GAGGATTATC 840
 ACACCCCAA TGCATAATCT CATTATGAT TGAGGAGAGA AAAGGATCAG ATTGCTGTTT 900
 TCTACAATGG AGCAGGATAT TGCTGAAGTC TCCTGGCATA TGTTACCGAA TCAACTGGCC 960
 TTCCAGAGGC TAAGAAATTT CTGTTAGTAA AAGATGTTCT TTTTCCCAA GCGTTTTATT 1020
 TGAAAGGATA ACTTGTGTTT TGGTTATTTT GTATTCCAC CTGTGCTGGT AGATATTATT 1080
 AACCATTAG GTAAATACTA TTACAGTCGT GGTTCCTGCA

Seq ID NO: 300 Protein sequence:
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MTDKTEKVAV DPETVFKRPR ECDSPSYQKR QRMALLARKQ GAGDSLIIAGS AMSKAKKLMT 60
 GHAIPPSQLD SQIDDTGFGS KDRMMQKPGS NAPVGGNVTS SFGSDLECR ETASSPKSQQ 120
 EINADIKRKL VKELRCVGQK YEKIFEMLEG VQGP TAVRKR FFESIIEKAA RCMRRDFVKH 180
 LKKLKRMI

Seq ID NO: 301 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 247-812

1 11 21 31 41 51
 AGTGTTCGGC TGGGCGAGGC ACGCTGTGGC TGGCTACTTC CCTTCCTCCC ATCCCCCTTG 60
 GGCCAAACAG GATCGGTGCT TCTGGTGAGA CGCCTCCCA TGACATCAC TCCCAGGTGC 120
 CCTAGGGGCG ACATTTCCTCA CAACTCCAG AGGGCAGGTT TCTAGAAAGT GCCACCAGTG 180
 GGGAGGCGCC ACAACTTCAC TGCCATTTTG TGAGGTGCCG CCGTCTCTCC TCCAGCAAGG 240
 GAAACAATGA CCGATAAAAC AGAGAAGGTG GCTGTAGATC CTGAAACTGT GTTTAAACGT 300
 CCCAGGGAAT GTGACAGTCC TTCGTATCAG AAAAGGCAGA GGATGGCCCT GTTGGCAAGG 360
 AAACAAGGAG CAGGAGACAG CTTATTGCA GGCTCTGCCA TGTCCAAAGA AAAGAGCTTA 420
 TGACAGGACA TGCTATTCCA CCCAGCCAAT TGGATTCTCA GATTGATGAC TTCCTGGTT 480
 TCAGCAAGA TGCGATGATG CAGAAACCTG GTAGCAATGC ACCTGTGGGA GGAAATGTTA 540
 CCAGCAATTT CTCTGGAGAT GACCTAGAAT GCAGAGGAAT AGCCTCCTCT CCCAAAAGCC 600
 AACAGAAAT TAATGCTGAT ATAAAATGTC AAGTAGTGAA GGAAATCCGA TGCCTTGGAC 660
 AATATGAAAA AATCTTCGAA ATGCTTGAAG GAGTGCAAGG ACCTACTGCA GTCAGGAAAC 720
 GATTTTTTGA ATCCATCATC AAGGAAGCAG CAAGATGTAT GAGACGAGAC TTTGTTAAGC 780
 ACCTTAAGAA GAAACTGAAA CGTATGATT GAGAATACTT GTCCCTGGAG GATTATCACA 840
 CCCCAATATG ATAATCTCAT TAATGATTGA GGAGAGAAAA GGATCAGATT GCTGTTTTCT 900
 ACAATGGAGC AGGATATTGC TGAAGTCTCC TGGCATATGT TACCGAATCA ACTGGCCTTC 960
 CAGAGGCTAA GAAATTTCTG TTAGTAAAAG ATGTTCTTTT TCCCAAAGCG TTTTATTTGA 1020
 AAGGATAACT TGTGTTTGGG TTATTTTGTG TTCCACCTG TGCTGCTAGA TATTATTAAC 1080
 CATTAGGTA AATACTATTA CAGTCGTGGT TTCTGCA

Seq ID NO: 302 Protein sequence:
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MTDKTEKVAV DPETVFKRPR ECDSPSYQKR QRMALLARKQ GAGDSLIIAGS AMSKEKKLMT 60
 GHAIPPSQLD SQIDDTGFGS KDRMMQKPGS NAPVGGNVTS NFGSDLECR GIASSPKSQQ 120
 EINADIKCQV VKEIRCLGQY EKIFEMLEGV QGP TAVRKR FFESIIEAAR CMRRDFVKHL 180
 KKKLKRMI

Seq ID NO: 303 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 247-815

1 11 21 31 41 51
 AGTGTTCGGC TGGGCGAGGC ACGCTGTGGC TGGCTACTTC CCTTCCTTCC ATCCCCCTTG 60
 GGCCAAACAG GATCGGTGCT TCTGGTGAGA CGTCTCCCA TGACATCAC TCCCAGATGC 120
 CCTAGGGGCG ACATTTCCTCA CAACTCCAG AGGGCAGGTT TCTAGAAAGT GCCACCAGTG 180
 GGGAGGCGCC ACAACTTCAC TGCCATTTTG TGAGGTGCCG CCGTCTCTCC TCCAGCAAGG 240
 GAAACAATGA CCGATAAAAC AGAGAAGGTG GCTGTAGATC CTGAAACTGT GTTTAAACGT 300
 CCCAGGGAAT GTGACAGTCC TTCGTATCAG AAAAGGCAGA GGATGGCCCT GTTGGCAAGG 360
 AAACAAGGAG CAGGAGACAG CTTATTGCA GGCTCTGCCA TGTCCAAAGC AAAGAGCTTA 420
 TGACAGGACA TGCTATTCCA CCCAGCCAAT TGGATTCTCA GATTGATGAC TTCCTGGTT 480
 TCAGCAAGA TAGGATGATG CAGAAACCTG GTAGCAATGC ACCTGTGGGA GGAAACGTTA 540
 CCAGCAGTTT CTCTGGAGAT GACCTAGAAT GCAGAGAAAC AGCCTCCTCT CCCAAAAGCC 600
 AACAGAAAT TAATGCTGAT ATAAAACGTA AATTAGTGAA GGAACCTCCG TCGTGTGGAC 660
 AAAAAATATGA AAAAACTTTC GAAATGCTTG AAGGAGTGCA AGGACCTACT GCAGTCAGGA 720
 AACGATTTTT TGAATCCATC ATCAAGGAAG CAGCAAGATG TATGAGACGA GACTTTGTTA 780
 AGCACCTTAA GAAGAAACTG AAACGTATGA TTTGAGAATA CTGTGCCCTG GAGGATTATC 840
 ACACCCCAA TGCATAATCT CGTTAATGAT TGAGGAGAGA AAAGGATCAG ATTGCTGTTT 900
 TCTACAATGG AGCAGGATAT TGCTGAAGTC TCCTGGCATA TGTTACCGAA TCAACTGGCC 960
 TTCCAGAGGC TAAGAAATTT CTGTTAGTAA AAGATGTTCT TTTTCCCAA GCGTTTTATT 1020
 TGAAAGGATA ACTTGTGTTT TGGTTATTTT GTATTCCAC CTGTGCTGGT AGATATTATT 1080
 AACCATTAG GTAAATACTA TTACAGTCGT GGTTCCTGCA

Seq ID NO: 304 Protein sequence:
 Protein Accession #: Eos sequence

1	11	21	31	41	51	
MTDKTEKQVAV	DPETVFKRPR	ECDSPSYQKR	QRMALLARKQ	GAGDSLIAGS	AMSKAKKLMT	60
GHAIPPSQLD	SQIDDFTFGS	KDRMMQKPGS	NAPVGGNVTS	SFSGDDLECR	ETASSPKSQQ	120
EINADIKRKL	VKELRCVQKQ	YEKIFEMLEB	VQGPFAVRKR	FFESIIKEAA	RCMRRDFVKH	180
LKKKLKRLMI						

Seq ID NO: 305 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 87-689

1	11	21	31	41	51	
CGTGGAGGCA	GCTAGCGCGA	GGCTGGGGAG	CGCTGAGCCG	CGCGTCGTGC	CCTGCGCTGC	60
CCAGACTAGC	GAACAATACA	GTCAGGATGG	CTAAGAGTGA	CCCCAAGAAA	CCAAAGGGCA	120
AGATGTCCGC	TTATGCCCTC	TTTGTGCAGA	CATGCAGAGA	AGAACATAAG	AAGAAAAACC	180
CAGAGGTCCC	TGTCAATTTT	GCGGAATTTT	CCAAGAAGTG	CTCTGAGAGG	TGGAAGACGA	240
TGTCCGGGAA	AGAGAAATCT	AAATTTGATG	AAATGGCAAA	GGCAGATAAA	GTGCGCTATG	300
ATCGGGAAAT	GAAGGATTAT	GGACCAGCTA	AGGGAGGCCA	GAAAGAAGAG	GATCCTAATG	360
CTCCCAAAAG	GCCACCGTCT	GGATTCTTCC	TGTTCTGTTC	AGAATTCGCG	CCCAAGATCA	420
AATCCACAAA	CCCCGGCATC	TCTATTGGAG	ACGTGGCAAA	AAAGCTGGGT	GAGATGTGGA	480
ATAATTTAAA	TGACAGTGAA	AAGCAGCCTT	ACATCACTAA	GGCGGCAAG	CTGAAGGAGA	540
AGTATGAGAA	GGATGTTGCT	GACTATAAGT	CGAAAGGAAA	GTTTGATGGT	GCAAAGGGTC	600
CTGCTAAAGT	TGCCCGGAA	AAGGTGGAA	AGGAAGATGA	AGAAGAGGAG	GAGGAAGAAG	660
AGGAGGAGGA	GGAGGAGGAG	GATGAATAAA	GAAACTGTTT	ATCTGTCTCC	TTGTGAATAC	720
TTAGAGTAGG	GGAGCGCCGT	AATTGACACA	TCTCTTATTT	GAGAAGTGTC	TGTTGCCCTC	780
ATTAGGTTTA	ATTACAAAAT	TTGATCACGA	TCATATTGTA	GTCTCTCAAA	GTGCTCTAGA	840
AATTGTCACT	GGTTTACATG	AAGTGGCCAT	GGGTGTCTGG	AGCACCCCTG	AACCTGTATCA	900
AAGTTGTACA	TTCTTCCAAA	CATTTTAAAA	ATGAAAAGGC	ACTCTCGTGT	TCTCCTCACT	960
CTGTGCACCT	TGCTGTTGGT	GTGACAAGGC	ATTTAAAGAT	GTTTCTGGCA	TTTTCTTTTT	1020
ATTTGTAAAG	TGGTGGTAAC	TATGGTTATT	GGCTAGAAAT	CCTGAGTTT	CAACTGTATA	1080
TATCTATAGT	TGTATAAAG	AACAAAACAA	CCGAGACAAA	CCCTTGATGC	TCCTTGCTCG	1140
GCCTTGAGGC	TGTGGGGAAG	ATGCCTTTTG	GGAGAGGCTG	TAGCTCAGGG	CGTGCACTGT	1200
GAGGCTGGAC	CTGTTGACTC	TGCAGGGGGC	ATCCATTTAG	CTTCAGGTTG	TCTTGTTTCT	1260
GTATATAGTG	ACATAGCAAT	CTGCTGCCAT	CTTAGCTGTG	GACAAAGGGG	GGTCAGCTGG	1320
CATGAGAATA	TTTTTTTTTT	TAAGTGCGGT	AGTTTTTAAA	CTGTTTGTTC	TTAAACAAAC	1380
TATAGAATCT	TTCAATGTCA	GCAAAGCAAA	GAGTCACTGC	ATCAATGAAA	GTTCAAGAAC	1440
CTCCTGTACT	TAAACACGAT	TCGCAACGTT	CTGTTATTTT	TTTTGTATGT	TTAGAATGCT	1500
GAAATGTTTT	TGAAGTTAAA	TAAACAGTAT	TACATTTTAA	AAACTCTTCT	CTATTATAAC	1560
AGTCAATTTT	TGACTCACAG	CAGTGAACAA	ACCCCCACTC	CATTGTATTT	GGAGACTGGC	1620
CTCCCTATAA	ATGTGGTAGC	TTCTTTTATT	ACTCAGTGGC	CAGCTCACTT	AGGGCTGAGA	1680
TGAAGGAGAG	GGCTACTTGA	AGCTACTGTG	TGATTTTGT	TGTGTCTGAG	TGGCATTGAG	1740
ATGAAGTCTG	GAGGAGTTAG	GAGAACGACA	TAGGCAAGGT	TCAGCAGCCT	TCCAAGGTAT	1800
AGGAAGGTGG	GTGATTAGGA	CTGAGGCTAT	CTAGGTTTAA	CTTTTGTCCC	ACCTCCACCC	1860
CCTATTTTGT	GGGGCCAAAT	GCATTGCTAA	ACAGCAATTT	CAGAGTGTAT	GGTGTGTCAA	1920
AAATTAAGGC	CTTATTGTTT	TTCTCTTTCA	CCCCTACCCC	CCGTGCTCCT	GGCACATATC	1980
ACATTATTTG	TGGTGCCCAA	CATTTGGGGT	CTTGAGCCTG	CTGCTGGTCT	CCTGGATGCC	2040
AGTGAGGGTA	TGTGGGATGG	GGTGGTGGGG	TAGGGGACGG	TATCCTTTTT	TTGCTCCTAC	2100
TTGGAAACAC	CAAAACCCCC	AAGGAAGATG	ATAGGCTCCA	TCTTGGGCCA	CCTGAGCTAT	2160
AGGGCAGGCT	AATGGAATCA	ACCATTCTCG	AGCACTAAAT	GTATCATGAA	AAGTTGAATG	2220
GCCTGCTCAT	AAGTTTAGCT	CATTCACTGG	AAATGTAGAT	TGATGTTCAA	TGTTAAACTG	2280
GAAGGAGCTT	GGTTTGTGTG	TCAGTGGTTA	TATTAGTGGG	TAGTGTAAAC	TTTTATCCAG	2340
GTGGGGGTGA	GGGGGTGAG	CCACAGTAGC	AAGTGGTGAC	ACTAAATACC	ATTTTGAAGG	2400
CTGATGTGTA	TATACATCAT	TACTGTCCGT	AGCAATGAAG	GATACAGTAC	TGTGTGTGGG	2460
GTGAGTGTTG	CTATTGCCCA	GCATTAAATAT	TTGGGTGTGT	ATGTTTGAGG	CTATGAAACA	2520
CGCAGGAGTG	TTTTTGTGCT	ATTAATTTTA	AGAGAAAGCA	GCTTTTCTTT	AAAAATCACT	2580
GTTGAGAAAC	TTGCATGTCT	GGAGGCGGTG	TCCTCTCCGC	CCTGTCCGGT	CCTGGATGAG	2640
TACGAGTTAT	GGTCACGGTC	ACAGCCTGAT	CTCTTATGTG	TTCATAGCCA	TTGCTCTTCC	2700
CATCAGAACT	GTTTGTCTCG	AATGTGTTCC	TCTAGTTCTA	GAAAAAGACC	ACTAATTTAA	2760
AAAACCTCGT	TGTGAGGTTT	GCCCAGAGGC	ACTTGTTCCT	GAAATTCCTC	TCCTGCTTCA	2820
GCCATGTCCT	TGTCACTTGG	CATTCTAAGC	TAAAGCTTTA	GCTTCCCAAT	TCGTGATGTG	2880
CTAGGCCAAG	ATTCCGGGAGC	TGTTGCCAGC	CTCGTCAAAT	ATGGAAGAGA	AACAACCTGC	2940
GGTCAAAAGG	GAGTGATTGG	TTAAGTGGTG	CGCGTCTATC	TCATAACTAG	ATGTACCAAC	3000
CAGGGAAGGG	CCAAGGATGG	AAAGGGGTAA	CTTTTGTGCT	TCCAAAGTAG	CTAAGCAGAA	3060
GTGGGGGAGC	AGTTTAGCCA	GATGATCTTT	GATTAGGCCA	ACATTGAGTT	TTAAGAGGCG	3120
TGTCAAGTTG	AGGCCACTTG	GTCCATTAGC	TGGGGCAGCA	AGATCACTAC	TCAACGTTT	3180
CACACTGTGG	CAAGATTGCT	CTTCTAGTGG	AATAATGCCC	TAGTTTCTCT	GAGATGATGT	3240
AAGTGGCATG	ATGTTACCTA	AGGCTTAGGC	TAGCTTGAT	TTCTGGGCCC	ACTGTCTGTG	3300
TTCTTAAGAT	GCCCACTCTG	TGCTTTTTTT	TTTTTTTTTCC	CCCATTTAAA	AGGATAGTAC	3360
CTACTCCCTC	TAACCACCTC	ACCCCATCTC	TGAATGACAT	TTTATCCTTC	GGAAAGAAC	3420
AGGCTGTGAT	GTAGTGACTA	TTGTCGTGTG	CTCCTGTGTG	TGCTGTCTCT	TGTCACAAAT	3480
GTATTTGGGG	ACGTTGGATG	CATTCAATTT	CTGTAATAAA	G		

Seq ID NO: 306 Protein sequence:
Protein Accession #: NP_005333.1

1	11	21	31	41	51	
MAKGDPKPKK	GKMSAYAFFV	QTCREEHKKK	NPEVPVNFAB	FSKKCSERWK	TMSGKEKSKF	60
DEMAKADKVR	YDREMKDYGP	AKGGKKKKDP	NAPKRPPSGF	FLFCSEFRPK	IKSTNPGISI	120
GDVAKKLGM	WNNLNDSEKQ	PYITKAALKK	EKYEKDVADY	KSKGKFDGAK	GPAKVARKKV	180
EEEEEEEEEE	EEEEEEEEEE					

Seq ID NO: 307 DNA sequence
Nucleic Acid Accession #: NM_022342
Coding sequence: 1..2178

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1      11      21      31      41      51
|      |      |      |      |      |
5  ATGGGTACTA GGAAAAAGT TCATGCATT GTCCGTGTCA AACCCACCGA TGACTTTGCT 60
   CATGAAATGA TCAGATACGG AGATGACAAA AGAAGCATTG ATATTCACTT AAAAAAAGAC 120
   ATTCGGAGAG GAGTTGTCAA TAACCAACAG ACAGACTGGT CGTTTAAGTT GGATGGAGTT 180
   TTCACGATG CCTCCACAGG CTGGGTTTAT GAGACAGTTG CAAAGGATGT GGTTCCTCAG 240
   CCTCGATG GCTATAATGG CACCATCATG TGTATGGGCG AGACGGGAGC TGGCAAGACA 300
10  ACACCATGA TGGGGGCAAC TGAGAATTAC AAGCACCAGG GGATCTCTCC TCGTGCCCTG 360
   AGCAGGTTT TTAGGATGAT CGAAGAACGC CCCACACATG CCATCACTGT GCGTGTTTCC 420
   ACTTGGAAA TCTATAATGA GAGCCTGTTT GATCTCCTGT CCACCTCGCC CTATGTTGGA 480
   CCTCAGTCA CACCAATGAC CATCGTGGAA AACCCCTCAAG GAGTCTTCAT TAAGGGCTTG 540
   CAGTTTACC TCACAAGTCA GGAGGAGGAT GCATTGAGCC TCCTTTTGA GGGTGAGACC 600
15  ACAGGATTA TAGCCTCCCA CACTATGAAC AAAAATCTTT CCAGATCACA CTGCATTTTC 660
   CCATCTACT TAGAGGCCCA TTCCCGGACC TTATCAGAGG AAAAGTACAT CACTTCCAAA 720
   TTAACCTGG TGGATCTGGC AGGCTCAGAG AGGCTGGGGA AGTCTGGGTC TGAGGGCCAA 780
   TCCTGAAGG AAGCCACCTA CATCAACAAA TCGCTCTCAT TCCTGGAGCA GGCCATCATT 840
   CCCTTGGGG ACCAGAAGCG GGACCACATC CCCTTTCGGC AGTGCAAGCT CACCCACGCT 900
20  TGAAGGACT CGTTAGGGGG AAATGCAAT ATGGTCTCTG TGACAAACAT CTATGGAGAA 960
   CTGCCCATG TAGAAGAAAC GCTATCTTCA CTGAGATTG CCAGCAGGAT GAAGCTAGTC 1020
   CCACGTAGC TGGCCATCAA TGAAAAGTAT GATGCTGAGA GAATGGTCAA GAACCTGGAG 1080
   AGGAACTAG CACTACTCAA GCAGGAGCTG GCTATCCATG ACAGCCTGAC CAACCGCACC 1140
   TTGTGACCT ATGACCCCAT GGATGAAATC CAGATTGCTG AGATCAACTC CCAGGTGCGG 1200
25  GGTACCTGG AGGGGACACT GGACGAGATC GACATAATCA GCCTTAGACA GATCAAGGAG 1260
   TGTTCAACC AGTTCCGGGT GGTCTGAGC CAACAGGAAC AGGAAGTGGA GTCCACTTTG 1320
   GCAGGAAGT ACACCTCAT TGACAGGAAT GACTTTGCGC CCATTTCTGC TATCCAGAAG 1380
   CGGGGCTTG TGGATGTTGA TGGCCACCTA GTGGGTGAGC CTGAAGGACA AAACCTTGGA 1440
   TCGGAGTCG CCCTTTCTCT TACCAAACTT GGAAGAAAG CCAAGTCCAA GAAGACATTC 1500
30  AAGAGCCAC TCAGGCCCGA CACCCACCC TCCAAACAG TGGCCTTTGA GGAGTTAAG 1560
   ATGAGCAAG GTAGTGAGAT CAACCGAATT TTCAAAGAAA ACAATCCAT CTGGAATGAA 1620
   GGAGGAAAA GGGCCACGCA GACCACACAG CACATCAATG CCATCAAGCG GGAGATTGAT 1680
   TGACCAAGG AGGCCCTGAA TTTCAGAA GTCACACGGG AGAAGCAAGG CAAGTACGAA 1740
   ACAAGGGGC TGATGATCAT CGATGAGGAA GAATTCCTGC TGATCTCTCA GCTCAAAGAC 1800
35  TCAAGAAGC AGTACCGCAG CGAGTACCAG GACCTGCGTG ACCTCAGGGC TGAGATCCAG 1860
   ATTGCCAGC ACCTAGTGGG TCAGTGTGCG CACCGCTCGC TCATGGAATT TGACATCTGG 1920
   ACAATGAGT CCTTTGTGAT CCCTGAGGAC ATGCAGATGG CACTGAAGCC AGGCGGCAGC 1980
   TCCGGCCAG GCATGTGCTC TGTGAACAGG ATTGTGCTC TGGGAGAAGA TGACCAGGAC 2040
   AATTCAGCC AGCTGCAGCA GAGGGTGCTT CTGAGGGGCC CTGATTCCAT CTCCTTCTAC 2100
40  ATGCCAAG TCAGATAGA GCAGAAGCAT AATTACTTGA AAACCATGAT GGGCCTCCAG 2160
   AGGCACATA GAAAAATAG

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Seq ID NO: 308 Protein sequence:

Protein Accession #: NP_071737

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   LHDASQDLVY ETVAKDVVSQ ALDGYNGTIM CYGQTGAGKT YTMGATENY KHRGILPRAL 120
   QQVFRMIEER PTHATTVRVV YLEIYNESLF DLLSTLPYVG PSVTPMTIVE NPQGVFIKGL 180
50  SVHLTSQEED AFSLLFEGET NRIIASHTMN KNSSRSHCIF TIYLEAHSRT LSEEKYITSK 240
   INLVDLAGEE RLKSGSGSEQ VLKEATYINK SLSFLEQAI ALGDQKRDHI PFRQCKLTHA 300
   LKDSLGGNCN MVLVNIYIGE AAQLEETLSS LRFASRMKLV TPEPAINEKY DAERMVKNLE 360
   KELALLKQEL AIHDSLTNRT FVTYDPMDEI QIAEINSQVR RYLEGTLDEI DIISLRQIKE 420
55  VFNQFRVVLV QQEQEVESL RRKYTLIDRN DFAAISAIQK AGLVDVDGHL VGEPEGQNF 480
   LGVAPFSTKP GKAKSKKTF KEPLRPDTPP SKPVAFEEFK NEQGSEINRI FKENKSILNE 540
   RKRRASETTQ HINAIKREID VTKEALNFQK SLREKQGYE NKGLMIDEE EFLILKLDK 600
   LKQYRSEYQ DLRDRAEIQ YCQHLVDQCR HRLLEFEDIW YNESFVIED MQMALKPGGS 660
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   QAHRK

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Seq ID NO: 309 DNA sequence

Nucleic Acid Accession #: CAT cluster

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   CACATTGAAG ACCAAAGGAA AGAGTGAAAG AGTGTAGTTG GGTCAATTGT AATGGATGTT 180
   TAGATTGTCA AGAAAAGTGG GCCAGAGGCC CCACCTCACA CTAGGACGGC AATTGCCTCT 240
70  CATTAGTATC TCAGGCACCA TGGGTCTTAT TTGGTGTCAT AAGAAACACC CTCACAAAG 300
   TAATGAACCC TCAGCCTCCA GCTTCTCTTC TTCGGGATTC TTCTTAGGGC CTCCTTTTTC 360
   CTTTTATGTT TCCAGTACCC TGAATTTCTT ATTCCCATCC CCATTAAAAA TCTGCTTCAA 420
   AGAAAAACA AGAAGGACAC ATTCACCTTA AGATCCAAAT GAATGATAAG AGCTTAAAC 480
75  ATTATACTTA TCAGTATTAT TTGCATTTT ATAGAAACCA AAACCATATT TCAACAAC

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Seq ID NO: 310 DNA sequence

Nucleic Acid Accession #: NM_018622.2

Coding sequence: 1-1140

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   GTGGGCGGCC GCAGCTGCGA GGAGCTCACT GCGGTCTCTA CCCC GCCGCA GCTCCTCGGA 120
   CGCAGGTTTA ACTTCTTTAT TCAACAAAAA TGCGGATTCA GAAAAGCACC CAGGAAGGTT 180
85  GAACCTCGAA GATCAGACCC AGGGACAAGT GGTGAAGCAT ACAAGAGAAG TGCTTTGATT 240
   CCTCCTGTGG AAGAAACAGT CTTTATCCT TCTCCCTATC CTATAAGGAG TCTCATAAAA 300
   CTTTATTTT TACTGTGG GTTTACAGGC TGTGCATTG GATCAGCTGC TATTTGGCAA 360

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TATGAATCAC TGAATCCAG GGTCCAGAGT TATTTTGATG GTATAAAAGC TGATTGGTGTG 420
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 TGTATTATGA GAGTACCTTC TCTGCAGCGG ACAATGATCA GATATTTTAC ATCGAATCCA 600
 GCCTCAAAAG TCCCTTGTTC TCCAATGTTG CTGTCAACAT TCAGTCACTT CTCCTTATTT 660
 CACATGGCAG CAAATATGTA TGTTTTGTGG AGCTTCTCTT CCAGCATAGT GAACATTCTG 720
 GGTCAAGAGC AGTTTCATGC AGTGTACCTA TCTGCAGGTG TTATTTCCTA TTTTGTCTAGT 780
 TACCTGGGTA AAGTTGCCAC AGGAAGATAT GGACCATCAC TTGGTGCATC TGGTGGCCATC 840
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 CTTCCGATGT TCACGTTCAG AGCAGGGAAT GCCCTGAAAG CCATTATCGC CATGGATACA 960
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 TTTGGAATAT GGTATGTTAC TTACGGTCAT GAACTGATT GGAAGAACAG GGAGCCGCTA 1080
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Seq ID NO: 311 Protein sequence:
 Protein Accession #: NP_061092.2

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 EPRRSDPGTS GEAYKRSALI PPVEETVFYP SPYPIRSLIK PLFFTVGFTG CAFGSAAIWQ 120
 YESLKSRLVQS YFDGKADWL DSIRPQKEGD FRKEINKWNN NLSDGQRTVT GIIAANVLVF 180
 CLWRVPRLQR TMIRYFTSNP ASKVLCSPLM LSTFHSFSLF HMAANMYVLW SFSSSIVNIL 240
 GGEQFMAVYL SAGVISNFFVS YLGKVTATGRY GPSLGASGAI MTVLAAVCTK IPEGRLAIF 300
 LPMFTFTAGN ALKAIAMDT AGMILGWKFF DHAHLGGAL FGIWYVTYGH ELIWNREPL 360
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Seq ID NO: 312 DNA sequence
 Nucleic Acid Accession #: NM_000625
 Coding sequence: 195..3656

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 GCCCCACAGT GAAGAACATC TGAGCTCAA TCCAGATAAG TGACATAAGT GACCTGCTTT 180
 GTAAAGCCAT AGAGATGGCC TGTCTTGGGA AATTTCTGTT CAAGACCAAA TTCCACCAGT 240
 ATGCAATGAA TGGGGAAAAA GGCATCAACA ACAATGTGGA GAAAGCCCCC TGTGCCACCT 300
 CCAGTCCAGT GACACAGGAT GACCTTCAGT ATCACAACCT CAGCAAGCAG CAGAATGAGT 360
 CCCCAGCAGC CCTCGTGGAG ACGGGAAAGA AGTCTCCAGA ATCTCTGTGC AAGCTGGATG 420
 CAACCCCATTT GTCCTCCCCA CGGCATGTGA GGATCAAAAA CTGGGGCAGC GGGATGACTT 480
 TCCAAGACAC ACTTCACCAT AAGGCCAAAG GGATTTTAAC TTGCAGGTCC AAATCTTGCC 540
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 CAGATGAGCT TCTACCTCAA GCTATCGAAT TTGTCAACCA ATATTACGGC TCCCTCAAAG 660
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 CAGTAACCTA CCAATGACG GGAGATGAGC TCATCTTCC CACCAAGCAG GCCTGGCGCA 780
 ATGCCCCAGC CTGCATTGGG AGGATCCAGT GGTCCAACCT GCAGGTCTTC GATGCCCGCA 840
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 CTGAGGTCAC AGGGCTGGG GAGATGGAGG AAAGTGATAT CCCCAGCCT CAAGTCTTAT 3780
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 ATTGATCGGA GCCTC

Seq ID NO: 313 Protein sequence:
 Protein Accession #: NP_000616

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 LTGDELIFAT KQAWRNAPRC IGRIQWSNLQ VFDARSCSTA REMFEHICRH VRYSTNNGNI 240
 RSAITVFPQR SDGKHDFRVW NAQLIRYAGY QMPDGSIRGD PANVEFTQLC IDLGWKPKYG 300
 RFDVVLVLQ ANGRDPELFE IPPDLVLEVA MEHPKYEWFR ELELKWYALP AVANMLLEV 360
 GLEFPCCPFN GWYMGTEIGV RDFCDVQRYN LLEEVGRRMG LETHKLASLW KDQAVVEINI 420
 LNLHSEFQKQN VTIMDHHSAA ESFMKYMONE YSRGCGCPAD WIWLVPPMSG SITPVFHEM 480
 LVYVLSFFYY YQVEAWKTHV WQDEKRRPKR REIPLKVLVK AVLFACMLMR KTMASRVVVT 540
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 ELSGGEDAFR SWAVQTFKAA CETFDVRGKQ HIQIPKLYTS NVTWDPHHR LVQDSQPLDL 720
 SKALSSMHAK NVFTMLRKLKR QNLQSPSSR ATILVELSCE DGQGLNLYLP EHLGVCPGNQ 780
 PALVQIGILER VVDGPTPHQA VRLEALDESG SYWVSDKRLP PCSLSQALTY FLDITTPPTQ 840
 LLLQKLAQVA TEPPERQRIE ALCQPSEYSK WKFTNSPTFL EVLEEFPSLR VSAGFLLSQL 900
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 VRNAGSFHLP EDPSPHCILI GPGGTGIAPFR SFWQORLHDS QHKGVRGGRM TLVFGCRRPD 1020
 EDHIYQEML EMAQKGVLHA VHTAYSRLPG KPKVYVQDIL RQQLASEVLR VLHKEPGHL 1080
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Seq ID NO: 315 Protein sequence:
 Protein Accession #: XP_087254

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Protein Accession #: NP_004464

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 70 LAAPFPVYYP AASPGRVYF GLVPERPLSP ELGPAPSGPG GSCAFASAGA PATTTGYQPA 300
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 85 GAGAACTCG ACCGTGGGAA TGCCAAAGATG CCTTGGAAC AGCAGCCCGA GCCGAGGGCC 300
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	AAGTTGGGCC	AGACGGCTGCT	TCCTTGGGAA	GGTTTGTGTG	GATCTTCTGC	CGCACCCAGC	660
5	TCATCTGTGC	CATCGTGTGC	CTGATGATCA	CGCAGCTGGC	TGGCTTCAGT	GGACCCAGCT	720
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5

Seq ID NO: 319 Protein sequence:
 Protein Accession #: NP_005679

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 15 LSIVCLMITQ LAGFSGPAPM VKHLLLEYTQA TESNLQYSLL LVLGLLLTEI VRSWSLALTW 240
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 CCLRPDLAIL PSSDLTEIGE RGANLSSGQR QRISLARALY SDRSIYILDD PLSALDAHVG 720
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 FNNLLLGEPF PVEINSKKET SGSQKKSQDK GPKTGSVKKE KAVKPEEGQL VQLEEKQGS 840
 25 VPWSVYGVYI QAAGGPLAFL VIMALFMLNV GSTAFSTWWL SYWIKQSGSN TTVTRGNETS 900
 VSDSMKDNPH MQYASIAYL SMAMVILKA IRGVVFVKGT LRASSRLHDE LFRRLRSPM 960
 KFFDTPTTGR ILNRFSPKMD EVDVRLPPQA EMFIQNVILV FFCVGMIAVG PFWFLVAVGP 1020
 LVILFSLVLI VSRVILRELK RLDNITQSPF LSHITSSIQG LATIHAYNKG QEFHLRYQEL 1080
 30 LDDNQAPFPL FTCAMRWLAV RLDLSIALI TTTGLMIVLM HGQIPPAYAG LAISYAVQLT 1140
 GLFQFTVRLA SETEARFTSV ERINHYIKTL SLEAPARIKN KAPSPDPWQE GEVTFENAEM 1200
 RYRENLPVLV KKVSPTIKPK EKIGIVGRGT SGKSSLGML FRLVELSGGC IKIDGVRI SD 1260
 IGLADLRSLK SLIPQEPVLF SGTVRSNLDL FNQYTEDQIW DALERTHMKC CIAQLPLKLE 1320
 SEVMENGDNF SVGERQLLCI ARALLRHCKI LILDEATAAM DTETDLLEQE TIREAFADCT 1380
 35 MLTIAHRLHT VLGSDRIMVL AQGQVVEFDT PSVLNSNDSS RFYAMFAAAE NKVAVKKG

35

Seq ID NO: 320 DNA sequence
 Nucleic Acid Accession #: AK022089.1
 Coding sequence: 181-1488

40

1 11 21 31 41 51
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 45 ACATCCGAGG AGAAGAGAAA GCTTCCAGCC CTCCTCCCTT CACCTCGGAA ATCCAGACAC 120
 CCCCACCCCC ACCCTCAGAT CACTTAAAGA TAATTCTTTT ATTCGTTTGC CCGACAGACC 180
 ATGGCTCCCT TTGGAAGAAA CTGCTAAAG ACTCGGCATA AAAACAGATC TCCAACTAAA 240
 GACATGGATT CAGAAGAGAA GGAAATTGTG GTTTGGGTTT GCCAAGAAGA GAAGCTTGTC 300
 TGTGGGCTGA CTAAACGCAC CACCTCTGCT GATGTCATCC AGGCTTTGCT TGAGGAACAT 360
 50 GAGGCTACGT TTGGAAGAAA ACGATTCTCT CTGGGGAAGC CCAGTGATTA CTGCATCATA 420
 GAGAAAGTGA GAGGCTCCGA AAGGGTCTCT CCTCCACTAA CTAGAATCCT GAAGCTTTGG 480
 AAAGCGTGGG GAGATGAGCA GCCCAATATG CAATTGTGTT TGGTTAAAGC AGATGCTTTT 540
 CTTCCAGTTC CTTTGTGGCG GACAGCTGAA GCCAAATTAG TGCAAAACAC AGAAAAATTG 600
 TGGGAGCTCA GCCCAGCAAA CTACATGAAG ACTTTACCAC CAGATAAACA AAAAAGAATA 660
 55 TGCAGGAAAA CTTTCCGAAA ACTGGCTAAA ATTAAGCAGG ACACAGTTTC TCATGATCGA 720
 GATAATATGG AGACATTAGT TCATCTGATC ATTTCCAGG ACCATACTAT TCATCAGCAA 780
 GTCAAAGAGAA TGAAAGAGCT GGATCTGGAA ATTGAAAGT GTGAAGCTAA GTTCCATCTT 840
 GATCGAGTAG AAAATGATGG AGAAAATAT GTTCAGGATG CATATTTAAT GCCCAGTTTC 900
 AGTGAAAGTT AGCAAAATCT AGACTTGCAG TATGAGGAAA ACCAGACTCT GGAGGACCTG 960
 60 AGCGAAAGTG ATGGAATTGA ACAGCTGGAA GAACGACTGA AATATTACCG AATACTCATT 1020
 GATAAGCTCT CTGCTGAAAT AGAAAAAGAG GTAAAAAGTG TTTGCATTGA TATAAATGAA 1080
 GATGCGGAAG GCGAAGCTGC AAGTGAAC TGAAAGCTCTA ATTTAGAGAG TGTTAAGTGT 1140
 GATTTGAGAA AAAGCATGAA AGCTGGTTTG AAAATTCAT CTCAATTGAG TGGCATCCAG 1200
 AAAGAGATTA AATACAGTGA CTCATTGCTT CAGATGAAAG CAAAAGAATA TGAATCCTG 1260
 65 GCCAAGGAAT TCAATTCACT TCACATTAGC AACAAAGATG GGTGCCAGTT AAAGGAAAAC 1320
 AGAGCGAAGG AATCTGAGGT TCCAGTAGC AATGGGAGG TTCCTCCCTT TACTCAAAGA 1380
 GTATTAGCA ATTACACAAA TGACACAGAC TCGGACACTG GTATCAGTTC TAACACAGT 1440
 CAGGACTCCG AAACAACAGT AGGAGATGTG GTGCTGTTGT CAACATAGTT CCAATGGCTC 1500
 CTTTCTGACC TGCTTTCATG TTTTAATGTT TGTTTAATTT AATAGGAAAC CTCATTTTAA 1560
 70 ATATAACACT CAAAAAATG TAAATCATAT TGTAGTATTC AATAGTTAAT AAAAAGCTCGA 1620
 GAAATGTGTT GTTTCTG

70

Seq ID NO: 321 Protein sequence:
 Protein Accession #: NP_005438.1

75

1 11 21 31 41 51
 MAPFGRNLLK TRHKNRSPK DMDSEKEIV VWVCQEEKLV CGLTKRTTSA DVIQALLLEH 60
 EATFGEKRF LKGPSYDCII EKWRGSEVL PPLTRILKLW KAWGDEQPM QFVLVKADAF 120
 80 LPVPLWRTAE AKLVQNTKEL WELSPANYMK TLPPDKQKRI VRKTRFKLAK IKQDTVSHDR 180
 DNMTLVHLLI ISQDHTIHQQ VKRMKELDLE IEKCEAKFHL DRVENDGENY VQDAYLMPF 240
 SEVEQNLDLQ YBENQTLDEL SESDGIQLE ERLKYRILI DKLSAEIEKE VKSVCIDINE 300
 DAEGEAASEL ESSNLESVKC DLEKSMKAGL KIHSHLSGIQ KEIKYSDSL QMKAKEYELL 360
 AKEFNSLHIS NKDGCQLKEN RAKESEVPSS NGEIIPPFTQR VFSNYTNDTD SDTGISSNHS 420
 85 QDSEITVGDV VLLST

Seq ID NO: 322 DNA sequence
 Nucleic Acid Accession #: NM_030920.1

Coding sequence: 317-1123

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	GGCGCGTGGG	TGCGTGTGTG	TGCGCGCGCT	AGTGTGTGGA	CAAGGAGGTG	GGGGCAGCTG	120
	AGTTAGAGTC	CCAACTCTTG	GACTCCATTT	GCTATTCTCT	TCTTTCTCCC	CCACACCTAT	180
	CTGGTGGTGG	TAGTGGGCGT	TTATATTTGC	GTTCCTTTTC	ATTCAATTTCT	AAATCTCTTA	240
10	AAAAATTTTG	GTTGGGGGTA	TTGGGGAAGG	CAGGAAAGGG	AAAAGGAGAG	TAGTAGCTGA	300
	AGAGCAAGAG	GAGGACATGG	AGATGAAGAA	GAAGATTAA	CTGGAGTTAA	GGAACAGATC	360
	CCCCGAGGAG	GTGACAGAGT	TAGTCTTTGA	TAATTGCGCTG	TGTGTCAATG	GGGAAATTGA	420
	AGGCCCTGAAT	GATACCTTTCA	AAGAACTAGA	ATTTCTGAGT	ATGGCTAATG	TGGAACCTAAG	480
	TTCTGCTGGCC	CGGCTTCCCA	GCTTAAATAA	ACTTCGAAAA	TGGAGCTTA	GTGATAATAT	540
15	AATTTCTGGA	GGCTTGGGAG	TCCTGGCAGA	GAAATGTCCA	AATCTTACCT	ACCTCAATCT	600
	GAGTGGAAAC	AAAAATAAAG	ATCTCAGTAC	AGTAGAAGCT	CTGCAAAATC	TTAAAAATTT	660
	GAAAAGTCTT	GACCTGTTTA	ACTGTGAGAT	CACAAACCTG	GAAAGATTATA	GAGAAAGTAT	720
	TTTTGAACCTA	CTGCAGCAAA	TCACATACCT	AGATGGATTT	GATCAGGAGG	ATAATGAAGC	780
	GCCGGAATCT	GAAGAGGAGG	ATGATGAGGA	TGGAGATGAA	GATGATGAAG	AGGAAGAGGA	840
20	AAATGAAGCT	GCTCCACCGG	AAGGATATGA	GGAAGAGGAG	GAGGAAGAGG	AAGAGGAGGA	900
	TGAGGATGAG	GATGAAGATG	AAGATGAAGC	AGGTTTCAGAG	TGGGAGAGAG	GAGAAGAGGA	960
	AGTGGGCCCTC	TCATACCTTAA	TGAAAGAAGA	AATTCAGGAT	GAAGAAGATG	ATGATGACTA	1020
	TGTTGAAGAA	GGGGAAGAAG	AGGAAGAAGA	GGAAGAAGGA	GGTCTTCGAG	GGGAGAAGAG	1080
	GAAACGAGAT	GCTGAAGACG	ATGGAGAGGA	AGAAGATGAC	TAGATCATTG	TAAGACCAGA	1140
25	TTCTCTAATG	TTTCTGGGTG	TGCAATAGAG	TGATCACATC	TTTGTCTTCT	CATGTACGAT	1200
	AGCTATCCCT	ACAGAAGATA	ATGTGTAAC	TTTTATAGGA	AAAGTGTGGT	TTTACTATTT	1260
	TTGCCTTATC	ATTCCAAATA	AGAACTAGTC	TGTTAATGAT	CATATTGTAT	GTAGAGAAAA	1320
	ATTTTCATTTG	ACTCCCATTTG	TGGAATTCCT	TAGCAATTTA	TTTAGACTTA	ATTTTTTAAA	1380
	TTCAAGCTTA	CTGTATTAGT	CATTTTATAGC	CCATAATTAA	AACATGATCA	CTTTTAAACA	1440
	GGTGTAGTAT	GGTGCATTTG	ATTCCTTATT	TATAGATTAA	CTGAAATTAC	AGTTTGCTAT	1500
30	AATATAAAAT	GACAATAGTC	TCTTGAGTGG	TAAGTTGGTT	ATTTTTTTAG	AGGTGATCCA	1560
	GGAATCTTTA	GTTTGAAGGC	AGTTACCTTT	TTTTTTTTTT	TTTTTTTTTG	ACTAAGAGTG	1620
	TTTGGTTGCT	TTTTGTCTAC	AAGTAACCTG	GAAAATAGAA	GCAGAATAGT	AAAGGTTCTA	1680
	TTCAGCAACA	TAGTTCATGG	ATTTGTGGA	GGTCTTATTC	AGTAATATGG	TTCATGGATT	1740
35	TAGTGGTGAC	TGATAAGATT	TTATTTTGA	AGGAAAAATT	GCTTATACTA	AGTCCAGAGA	1800
	CATGCAGGTG	AGCCCTTTTG	TCAGGCTGCA	AATCATGACA	TGCCGATGGT	TGTTTATTTT	1860
	GTTTTTAGGT	GTGCATCTCT	TTCTTCTTA	GCAATTCCTT	TATGATCACC	TTCCCTTCTT	1920
	GTTTCACTCC	CTCCCGCTCT	CTCAAAAGGA	ACTTGGGAAA	CTTGTGAAAC	CCAGGAAAAAC	1980
	CTTTAGTCTT	ATACCTCAAC	TACGTTTCAG	TCCTGTCTGG	GTTTTAAATA	AGTGAAGTAG	2040
40	AAGAATATGA	GTATTTTCTG	ACATAAGAA	ATATTATCAA	TACAGTTTAA	TGCAGTAAGC	2100
	TTCTCTTACC	ATAAATGTTT	CTTGGTTGAC	AACATCTAAG	ACAATATTAG	TGGGATGAAG	2160
	AAAGAAAAGC	AGGGGTGCTT	TTGGAAGCAG	TGTTAGTGT	CCTCAAAAGT	CGGAACAATT	2220
	GCCTGTTGAT	ATATTAATAA	GACATTAAAG	TCAAAATTTA	ATGTTGGCCT	CTCAAATGAT	2280
	TTGGATACCA	CTCTGCAAG	TATTTCTAAC	CTTTAATTCC	CAGTTTAAAT	ACAGATATAA	2340
45	TAATAGCAT	TAATTTGAA	ATACTAGGCA	GCTGGAAAAG	TATTTGAAAC	TAAATTGACA	2400
	TTAAATATAA	GATTTGTTTT	CAAGTGGATG	TCCATTAAAA	GTAGAAAAAT	ATTTGGGATA	2460
	AGTGAGTGTG	TGTTTCCTTA	CATGGCTACT	AAATAAAATA	TAATGAGTAT	ACAAGTATAT	2520
	CTCCCTCTTT	GCTATGGAGG	CTCCATGTTT	AAGGCAATGG	CTTTTAAAT	CTTGGCTATC	2580
50	TAAAAATTTT	TCCCTTTGTT	TGAAATATT	GTAAGTTTTT	AAGAAGTTAG	TGTCAGCAAA	2640
	TTAATGAAG	TTATGCTTCT	ATACTGGGAC	ATATTAAAT	ACTGAGTATA	GTACTGCTGC	2700
	TACTGCTTCT	ACAATGTAAA	ATGTATGACT	TGGTGTTTTA	AAGTAAAAAT	TATGATGTTA	2760
	CTTGTGGAGA	AACTAAAAAT	GTTGTACAAC	TGACCGAAAG	AAAAACCTTG	GGGATAAGTT	2820
	TAGTAGGGGG	ATTGGAATCC	CCAAAAAGAT	AACATTTTTC	TTCTGCTTTT	AAAAACTGAA	2880
	ATTCCGCTGT	TAGTTCCTTA	ACAATCTCA	TTACATACTA	TGCCAGATTA	CAAAATACCT	2940
55	ATTTTAAAAA	TGAAATCTAT	ATATTGACTT	TCATTATCAAT	CATCTTACTG	TGCAATCAAA	3000
	ATTAGAGTAC	TTTGGTTTGA	AAACAACACT	TAGAGCCTCC	AGATAACTTT	TAAGACTTAT	3060
	TTAGCTTTGT	GGGTGGTATT	TTCAATGCAA	TAAGTAAGGG	TGGGTTTAT	ATTTTGTAGA	3120
	AGTTTTCGGT	CCTATTTTAA	TGCTCTTTGT	ATGGCAGTAT	GTATATATTG	TGTTAAGTTC	3180
60	CTCAAGAAATC	TCCTTAAAAA	CTTTGAAGTT	AATACTTTTG	TGCAACTGTG	TTTTGAATAA	3240
	AGCCATGACA	GTGTTAAAAA	CAAAAC				

Seq ID NO: 323 Protein sequence:
Protein Accession #: NP_112182.1

	1	11	21	31	41	51	
65	MEMKKKINLE	LRNRSPEEVT	ELVLDNCLCV	NGEIEGLNDT	FKELEPLSMA	NVELSSLARL	60
	PSLNKLRLKE	LSDNIISGGL	EVLAERKCPNL	TYLNLSGNKI	KDLSTVEALQ	NLKNLKSDDL	120
	FNCEITNLED	YRESIFELLQ	QITYLDGFDQ	EDNEAPDSEE	EDDEDGDEDD	EEEEENEAGP	180
70	PEGYEEEEEE	EEEEDEDEDE	DEDEAGSELG	EGEEVEGLSY	LMKEEIQDEE	DDDDVVEEGE	240
	EEEEEEEGGL	RGEKRKRDAE	DDGEEEDD				

Seq ID NO: 324 DNA sequence
Nucleic Acid Accession #: NM_003812
Coding sequence: 224..2722

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75	TCCTCTGCGT	CCCGCCCCGG	GAGTGGCTGC	GAGGCTAGGC	GAGCCGGGAA	AGGGGGCGCC	60
	GCCCAGCCCC	GAGCCCCGGG	CCCGGTGCCC	CGAGCCCGGA	GCCCCCTGCC	CGCGGGCGCA	120
80	CCATGCGCGC	CGAGCCGGCG	TGACCGGCTC	CGCCCCGGCG	CGCCCCCGAG	CTAGCCCCGC	180
	GCTCTCGCCG	GCCACACGGA	GCGGCGCCCG	GGAGCTATGA	GCCATGAAGC	CGCCCCGCGC	240
	CAGCTCGCGG	CAGCCGCCCC	TGGCGGGCTG	CAGCCTTGCC	GCGGCTTCTT	GCGGCCCCCA	300
	ACGCGGCCCC	GCCGGCTCGG	TGCCTGCCAG	CGCCCCGGCC	CAGCAGCCGC	CCTGCCGCCT	360
	GCTTCTCGTC	CTTCTCTGTC	TGCCTCCGCT	CGCCGCTCG	TCCCGGCCCC	GCGCCTGGGG	420
85	GGCTGCTGCG	CCGAGCGCTC	CGCATTGGAA	TGAAACTGCA	GAAAAAAT	TGGGAGTCTT	480
	GGCAGATGAA	GACAATACAT	TGCAACAGAA	TAGCAGCAGT	AATATCAGTT	ACAGCAATGC	540
	AATGCAGAAA	GAAATCACAC	TGCCTTCAAG	ACTCATATAT	TACATCAACC	AAGACTCGGA	600

	AAGCCCTTAT	CACGTCTTGT	ACACAAAGGC	AAGACACCAG	CAAAAACATA	ATAAGGCTGT	660
	CCATCTGGCC	CAGGCAAGCT	TCCAGATTGA	AGCCTTCGGC	TCCAAATTCA	TTCTTGACCT	720
	CATACTGAAC	AATGGTTTGT	TGTCTTCTGA	TTATGTGGAG	ATTCACCTAC	AAAATGGGAA	780
5	ACCACAGTAC	TCTAAGGGTG	GAGAGCACTG	TTACTACCAT	GGAAGCATCA	GAGGCGTCAA	840
	AGACTCCAAAG	GTGGCTCTGT	CAACCTGCAA	TGGACTTCAT	GGCATGTTTG	AAGATGATAC	900
	CTTCGTGTAT	ATGATAGAGC	CACTAGAGCT	GGTTCATGAT	GAGAAAAGCA	CAGGTCGACC	960
	ACATATAATC	CAGAAAACCT	TGGCAGGACA	GTATTCTAAG	CAAAATGAAGA	ATCTCACTAT	1020
	GGAAAGAGGT	GACCACTGGC	CCTTTCTCTC	TGAATTACAG	TGGTTGAAAA	GAAGGAAGAG	1080
	AGCAGTGAAT	CCATCACGTG	GTATATTTGA	AGAAATGAAA	TATTTGGAAC	TTATGATTGT	1140
10	TAATGATCAC	AAAAGCTATA	AGAAGCATCG	CTCTTCTCAT	GCACATACCA	ACAACCTTTCG	1200
	AAAGTCCGTG	GTCAACCTTG	TGGATTCTAT	TTACAAGGAG	CAGCTCAACA	CCAGGGTTGT	1260
	CCTGGTGGCT	GTAGAGACCT	GGACTGAGAA	GGATCAGATT	GACATCACC	CCAACCTCTG	1320
	GCAGATGCTC	CATGAGTTCT	CAAAATACCG	GCAGCGCATT	AAGCAGCATG	CTGATGCTGT	1380
	GCACCTCATC	TCGCGGGTGA	CATTTCACTA	TAAGAGAAGC	AGTCTGAGTT	ACTTTGGAGG	1440
15	TGTCTGTTCT	CGCACAAAG	GAGTTGGTGT	GAATGATAT	GGTCTTCCAA	TGGCAGTGGC	1500
	ACAAGTATTA	TCGCAGAGCC	TGGCTCAAAA	CCTTGGAATC	CAATGGGAAC	CTTCTAGCAG	1560
	AAAGCCAAAA	TGTGACTGCA	CAGAAATCCTG	GGGTGGCTGC	ATCATGGAGG	AAACAGGGGT	1620
	GTCCCATTTCT	CGAAAATTTT	CAAAAGTGCAG	CATTTTGGAG	TATAGAGACT	TTTACAGAG	1680
20	AGGAGGTGGA	GCCTGCCTTT	TCAACAGGCC	AACAAAGCTA	TTTGAGCCCA	CGGAATGTGG	1740
	AAATGGATAC	GTGGAAGCTG	GGGAGGAGTG	TGATTGTGGT	TTTCATGTGG	AATGCTATGG	1800
	ATTATGCTGT	AAGAAATGTT	CCCTCTCCAA	CGGGGCTCAC	TGCAGCGACG	AGGCCTGCTG	1860
	TAACAATACC	TCATGCTTTT	TTCAGCCACG	AGGGTATGAA	TGCCGGGATG	CTGTGAACGA	1920
	GTGTGATATT	ACTGAATATT	GTACTGGAGA	CTCTGGTCAG	TGCCCAACCA	ATCTTCATAA	1980
25	GCAAGACGGA	TATGCATGCA	ATCAAAATCA	GGGCCGCTGC	TACAAATGGC	AGTGAAGAC	2040
	CAGAGACAAC	CAGTGTCACT	ACATCTGGGG	AACAAAGGCT	GCAGGGTCTG	ACAAGTTCTG	2100
	CTATGAATAAG	CTGAATACAG	AAGGCATGA	GAAGGGAAC	TGCGGGAAGG	ATGGAGACCG	2160
	GTGGATTGAG	TGCAGCAAC	ATGATGTGTT	CTGTGGATTC	TTACTCTGTA	CCAATCTTAC	2220
	TCGAGCTCCA	CGTATTGGTC	AACTTCAGGG	TGAGATCATT	CCAACCTCCT	TCTACCATCA	2280
30	AGGCCGGGTG	ATTGACTGCA	GTGGTGCCCA	TGTAGTTTGA	GATGATGATA	CGGATGTGGG	2340
	CTATGTAGAA	GATGGAACGC	CATGTGGCCC	GTCTATGATG	TGTTTAGATC	GGAAGTGCCT	2400
	ACAAATTCAA	GCCCTAAATA	TGAGCAGCTG	TCCACTCGAT	TCCAAGGGTA	AAGTCTGTTC	2460
	GGGCCATGGG	GTGTGTAGTA	ATGAAGCCAC	CTGCATTTGT	GATTTTCACT	GGGCAAGGAC	2520
	AGATTGCACT	ATCCGGGATC	CAGTTAGGAA	CCTTCACCCC	CCCAAGGATG	AAGGACCCAA	2580
35	GGGTCCCTAGT	GCCCACTAAT	TCATAATAGG	CTCCATCGCT	GGTGCCATCC	TGGTAGCAGC	2640
	TATTGTCTTT	GGGGGCACAG	GCTGGGGATT	TAAAAATGTC	AAGAAGAGAA	GGTTCGATCC	2700
	TACTCAGCAA	GGCCCCATCT	GAATCAGCTG	CGCTGGATGG	ACACCGCCTT	GCAGTGTGGG	2760
40	ATTCTGGGTA	TGACATACTC	GCAGCAGTGT	TACTGGAACT	ATTAAGTTTG	TAAACAAAAC	2820
	CTTTGGGTGG	TAATGACTAC	GGAGCTAAAG	TTGGGGTGAC	AAGGATGGGG	TAAAGAAAAA	2880
	CTGTCTCTTT	TGGAATAAT	GTCAAAGAAC	ACCTTTCACC	ACCTGTGAGT	AAACGGGGGA	2940
	GGGGGCAAAA	GACCATGCTA	TAAAAAGAAC	TGTTCCAGAA	TCTTTTTTTT	TCCCTAATGG	3000
	ACGAAGGAAC	AACACACACA	CAAAAATTAA	ATGCAATAAA	GGAAATCATT	AAAA	

Seq ID NO: 325 Protein sequence:
Protein Accession #: NP_003803

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	RPRAGAAAP	SAPHNNETAE	KNLGLVADED	NTLQONSSSN	ISYSNAMQKE	ITLPSRLIYY	120
50	INQDESPPYH	VLDTKARHQA	KHNKAVHLAQ	ASFQIEAFGS	KFILDILINN	GLLSSDYVEI	180
	HYENGKFPQYS	KGGEHCYYHG	SIRGVKDSKV	ALSTCNGLHG	MFEDDTFVYM	IEPLELVHDE	240
	KSTGRPHIIQ	KTLAQYYSKQ	MKNLTMERGD	QWPFLLSELQW	LKRRKRANVP	SRGIFEEMKY	300
	LELMIVNDHK	TYKKHRSSHA	HTNNFAKSVV	NLVDSTYKEQ	LNTRVVLVAV	ETWTEKDQID	360
55	ITTNVQMLH	EFISKYRQRIK	QHADAHVHLIS	RVTFFHYKRSS	LSYFGGVCSR	TRGVGVNEYG	420
	LPMVAQVLS	QSLAQNQLHQ	WEPSSRKPKC	DCTESWGGCI	MEETGVSHSR	KFSKCSILEY	480
	RDFLQRGGGA	CLFNRPRTKLF	EPTECGNGYV	EAGEECDGCF	HVECYGLCK	KCSLSNGAHC	540
	SDGPCCNNNTS	CLFQPRGYEC	RDVNECDIT	EYCTGDSGQC	PPNLHKQDGY	ACNQNGRCY	600
	NGECKTRDNQ	CQYIINGTKA	GSDKFCYEKL	NTEGTEKGN	GKDGDRWICQ	SKHDVFCGFL	660
60	LCTNLTRAPR	IGQLQGEIIP	TSFYHQGRVI	DCSGAHVVL	DDTDVGYVED	GTPCGPSMMC	720
	LDRKCLQIQA	LNMSSCPPLDS	KGKVCSGHGV	CSNEATCICD	FTWAGTDCSI	RDPVRNLHPP	780
	KDEGPKGPSA	LNLIIGSIAG	AILVAIIVLG	GTGWGFKNVK	KRRFDEPTQQ	PI	

Seq ID NO: 326 DNA sequence
Nucleic Acid Accession #: AK074418.1
Coding sequence: 244-1515

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	ACCTGAGAGC	CTGTGGAACC	TGCCCGTCTC	CCCTCTCTCA	TCAGACACAC	CTGCCCTAGGA	120
70	AACAGATGGA	AAAAGTGAGG	GACCGGTGAG	TGACTTGCTG	CTAAAGTTTA	TACCAGATGC	180
	AAATGACAGA	GCTGGAGTTC	TGCTGTGCCT	GGAAAGGACC	TCGGAAGTCT	TCTAAGGAGA	240
	GTCATGGCGT	ATTACAGAGA	GCCTTCAGTG	GAGACCTCCA	TCATCAAGTT	CAAAGACCAG	300
75	GACTTTACCA	CCTTGCGGGA	TCACTGCCTG	AGCATGGGCC	GGACGTTTAA	GGATGAGACA	360
	TTCCCGCAG	CAGATTCTTC	CATAGGCCAG	AAGCTGCTCC	AGGAAAAACG	CCTCTCCAAT	420
	GTGATATGGA	AGCGGCCACA	GGATCTACCA	GGGGGTCCTC	CTCACTTCAT	CCTGGATGAT	480
	ATAAGCAGAT	TGACATATCA	ACAAGGAGGC	GCAGCTGACT	GCTGGTTCTC	GGCAGCACTG	540
	GGATCCCTGA	CTCAGAACCC	ACAGTACAGG	CAGAAGATCC	TGATGGTCCA	AAGCTTTTCA	600
80	CACCAATATG	CTGGCATTTT	CCGTTTCCGG	TTCTGGCAAT	GTGGCCAGTG	GGTGGAAAGT	660
	GTGATTGATG	ACCGCCTACC	TGTCCAGGGA	GATAAATGCC	TCTTTGTGCG	TCCTCGCCAC	720
	CAAAACCAAG	AGTTCTGGCC	CTGCCTGCTG	GAGAAGGCCT	ATGCCAAGCT	GCTCGGATCC	780
	TATTCGATC	TGCATATGG	CTTCTCGAG	GATGCCCTGG	TGGACCTCAC	AGGAGGCGTG	840
	ATCACCACAA	TCCATCTGCA	CTCTTCCCCT	GTGGACCTGG	TGAAGGCAGT	GAAGACACAG	900
85	ACCAAGGCAG	GCTCCCTGAT	AACCTGTGCC	ACTCCAAGTG	GGCCAACAGA	TACAGCACAG	960
	CGCATGGAGA	ATGGGCTGGT	GAGTCTCCAT	GCCTACACTG	TGACTGGGGG	TGAGCAGATT	1020
	CAATACCGAA	GGGGCTGGGA	AGAAATTATC	TCCTGTGGGA	ACCCCTGGGG	CTGGGGCGAG	1080
	ACCGAATGGA	GAGGGCGCTG	GAGTGATGGG	TCTCAGGAGT	GGGAGGAAC	CTGTGATCCG	1140

	CGGAAAAGCC	AGCTACATAA	GAAACGGGAA	GATGGCGAGT	TTTGGATGTC	GTGTCAAGAT	1200
	TTCCAAACAGA	AATTCATCGC	CATGTTTATA	TGTAGCGAAA	TTCCAATTAC	CCTGGACCAT	1260
	GGAAACACAC	TCCACGAAAG	ATGGTCCCAA	ATAATGTTTA	GGAAGCAAGT	GATTCTAGGA	1320
5	AACACTGCAG	GAGGACCTCG	GAATGATGCT	CAATTCAACT	TCTCTGTGCA	AGAGCCAATG	1380
	GAAGGCACCA	ATGTTGTCTG	GTGCGTCACA	GTGCTGTGCA	CACCATCAAA	TTTGAAAGCA	1440
	GAAGATGCAA	AATTTCCACT	CGATTTCCAA	GTGATTCTGG	CTGGCTCACA	GAAACACTGT	1500
	CCAAAGCTCA	AATAATAAAT	TCCGCCGCAA	CTTCACCATG	ACTTACCATC	TGAGCCCTGG	1560
	GAACTATGTT	GTGGTTGTCAC	AGACACGGAG	AAAATCAGCG	GAGTTCCTGC	TCCGAATCTT	1620
10	CCTGAAAATG	CCAGACAGTG	ACAGGCACCT	GAGCAGCCAT	TTCAACCTCA	GAATGAAGGG	1680
	AAGCCCTTCA	GAACATGGCT	CCCAACAAAG	CATTTTCAAC	AGATATGCTC	AGCAGGTATG	1740
	GTACCTAGCA	CCCAGGGGCC	TTACGTGGGA	TTGGAGAAAG	GGGACCTGAG	GGAGGGACAG	1800
	CCCTCACAGG	CCCTTACTGG	GATGCAGAGA	GGAGAAGTGA	CTTGATGGAC	TATTTTACCT	1860
	GCCTCTCTTC	CTGGATCGTG	TCCAGAACTG	CTGTGGCTGC	CAAGCTCGGT	AGAGACGTGG	1920
	CGCCCCACCC	AGTCTCATCC	GGGGGACTTC	AAGCTGGAAT	GCAGAGCTTA	GAAAGGGAGG	1980
15	GGATAATTAT	GGGGTGTGAG	GTGCATTGCC	CTCTAAATCT	TTAAACAAGC	AATTGGCAGT	2040
	ACCCCGTGAA	ACCTTTCCTT	CTCCTACTCG	GCCACCTCCC	ACCAACCTGG	CATCGTTCCT	2100
	CCCGGGAGCT	AGCCAGCTTC	AGAAAGCACA	TACAGCATCC	TTGCTGCCAA	ACCACCTATG	2160
	TGCACACAGG	ATTTCCTTAA	TGGCTTAAAT	AACTGTTATA	AAGAACTCCT	TGACTTGTCA	2220
20	GAATAAAATA	GCTGCCAGGG	GCTCTGCACA	ATGAGCCTCT	TACCGTTAAA	AAAAAAAAAA	2280
	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA				

Seq ID NO: 327 Protein sequence:
Protein Accession #: BAB85075.1

25	1	11	21	31	41	51	
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	IWKRPQDLPG	GPPHILDDI	SRFDIQQGGA	ADCWFLAALG	SLTQNPQYRQ	KILMVQSFSSH	120
	QYAGIFRFRF	WQCGQWVEVV	IDDLPLVQGD	KCLFVRPRHQ	NQEFWPCLE	KAYAKLLGSY	180
30	SDLHYGFLED	ALVDLTGGVI	TNIHLHSSPV	DLVKAVKTAT	KAGSLITCAT	PSGPTDTAQA	240
	MENGLVSLHA	YTVTGAEIQI	YRRGWEEIIS	LWNPWGNET	ENRGRWSDGS	QEWEETCDPR	300
	KSQLEHKKRED	GEFWMSCQDF	QQKFIAMFIC	SEIPITLDHG	NTLHEGWSQI	MFRKQVILGN	360
	TAGGPRNDAQ	FNFSVQPEME	GTNVVVCVTV	AVTPSNLKA	DAKFPLDFQV	ILAGSQKHCP	420
35	KLK						

Seq ID NO: 328 DNA sequence
Nucleic Acid Accession #: BC017490.1
Coding sequence: 74-2788

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45	GGTCGCGCGA	GCAATGATC	CTCTCACTTC	CAGCCCTGGC	GGAAGCTCCC	GGCGTACTGA	180
	TGCCCTCAC	TCCAGCCCTG	GCCGTGACCT	TCCACCATT	GAGGATGAGT	CCGAGGGGCT	240
	CTTAGGCACA	GAGGGGCCCT	TGGAGGAAGA	AGAGGATGGA	GAGGAGCTCA	TTGAGATGG	300
	CATGGAAAGG	GACTACCGCG	CCATCCCAGA	GCTGGACGCC	TATGAGGCCG	AGGGACTGGC	360
	TCTGGATGAT	GAGGACGTAG	AGGAGCTGAC	GGCCAGTCAG	AGGGAGGCAG	CAGAGCGGGC	420
50	CATGCGGCAG	CGTGACCGGG	AGGCTGGCCG	GGGCTGGGCC	CAGATGCCGC	GTGGGCTCCT	480
	GTATGACAGC	GATGAGGAGG	ACGAGGAGCG	CCCTGCCCGC	AAGCGCCGCC	AGGTGGAGCG	540
	GGCCACGGAG	GACGCGCAGG	AGGACGAGGA	GATGATCGAG	AGCATCGAGA	ACCTGGAGGA	600
	TCTCAAAGGC	CACCTGTGTC	GCGAGTGGGT	GAGCATGGCG	GGCCCCCGGC	TGGAGATCCA	660
55	CCACGCGCTC	AAGAACTTCC	TGCGCACTCA	CGTCGACAGC	CACGGCCACA	ACGTCTTCAA	720
	GGAGCGCATC	AGCGCATGTG	GCAAAGAGAA	CCGTGAGAGC	CTGGTGGTGA	ACTATGAGGA	780
	CTTGGCAGCC	AGGGAGCAGC	TGCTGGCCTA	CTTCTGCCT	GAGGCACCGG	CGGAGCTGCT	840
	GCAGATCTTT	GATGAGGCTG	CCCTGGAGGT	GGTACTGGCC	ATGTACCCCA	AGTACGACCG	900
	CATCACCAAC	CACATCCATG	TCCGCATCTC	CCACCTGCCT	CTGGTGGAGG	AGCTCGCTC	960
60	GCTGAGGCAG	CTGCATCTGA	ACCAGCTGAT	CCGCACCACT	GGGGTGGTGA	CCAGCTGCAC	1020
	TGGGCTCCTG	CCCCAGCTCA	GCATGGTCAA	GTACAACCTG	AACAAGTGCA	ATTTCTGTCT	1080
	GGGTCCCTTC	TGCCAGTCCC	AGAACCAAGG	GGTGAAACCA	GGCTCTCTGC	CTGAGTGCCA	1140
	GTCCGCGCGC	CCCTTTGAGG	TCAACATGGA	GGAGACCACT	TATCAGAAGT	ACCAGCGTAT	1200
	CCGAATCCAG	GAGAGTCCAG	GCAAAGTGGC	GGCTGGCCGG	CTGCCCGGCT	CCAAGGACGC	1260
65	CATTCTCCTC	GCAGATCTGG	TGGACAGCTG	CAAGCCAGGA	GACGAGATAG	AGCTGACTGG	1320
	CATCTATCAC	AACAACATAG	ATGGCTCCCT	CAACACTGCC	AATGGCTTCC	CTGTCTTTGC	1380
	CACCTGTATC	CTAGCCAAAC	ACGTGGCCAA	GAAGGACAAC	AAGGTTGCTG	TAGGGGAACT	1440
	GACCGATGAA	GATGTGAAGA	TGATCACTAG	CCTCTCCAAG	GATCAGCAGA	TCGGAGAGAA	1500
	GATCTTTGCC	AGCATTGCTC	CTTCCATCTA	TGGTCATGAA	GACATCAAGA	GAGGCCTGGC	1560
70	TCTGGCCCTG	TTCCGAGGGG	AGCCCCAAAA	CCCAGGTGGC	AAGCACAAGG	TACGTGGTGA	1620
	TATCAACGTG	CTCTTGTGCG	GAGACCTTGG	CACAGCGAAG	TCGCAGTTTC	TCAAGTATAT	1680
	TGAGAAAGTG	TCCAGCCGAG	CCATCTTCAC	CACCTGGCCG	GGGGCGTCCG	CTGTGGGCTC	1740
	CACGGCGTAT	GTCCAGCGGC	ACCCTGTGAG	CAGGGAGTGG	ACCTTGGAGG	CTGGGGCCCT	1800
	GGTTCCTGGT	GACCGAGGAG	TGTGTCTCAT	TGATGAATTT	GACAAGATGA	ATGACCAGGA	1860
75	CAGAAACGAG	ATCCATGAGG	CCATGGAGCA	ACAGAGCATC	TCCATCTCGA	AGGCTGGCAT	1920
	CGTCACCTCC	CTGCAGGCTC	GCTGCACGGT	CATTGCTGCC	GCCAACCCCA	TAGGAGGGCG	1980
	CTACGACCCC	TCGCTGACTT	TCTCTGAGAA	CGTGGACCTC	ACAGAGCCCA	TCATCTCACG	2040
	CTTTGACATC	CTGTGTGTGG	TGAGGGACAC	CGTGGACCCA	GTCCAGGACG	AGATGCTGGC	2100
	CGCCTTCGTG	GTGGGCAGCC	ACGTGAGACA	CCACCCGAGC	AACAAGGAGG	AGGAGGGGCT	2160
	GGCCAATGGC	AGCGCTGCTG	AGCCCGCCAT	GCCCAACACG	TATGGCGTGG	AGCCCTTGCC	2220
80	CCAGGAGGTC	CTGAAGAAGT	ACATCATCTA	CGCCAAGGAG	AGGGTCCACC	CGAAGCTCAA	2280
	CCAGATGGAC	CAGGACAAGG	TGGCCAAAGT	GTACAGTGAC	CTGAGGAAAG	AATCTATGGC	2340
	GACAGGCAGC	ATCCCATTA	CGGTGGCGCA	CATCGAGTCC	ATGATCCGCA	TGGCGGAGGC	2400
	CCACGCGCGC	ATCCATCTGC	GGGACTATGT	GATCGAAGAC	GACGTCAACA	TGGCCATCCG	2460
	CGTGATGCTG	GAGAGCTTCA	TAGACACACA	GAAGTTCAGC	GTCATGCGCA	GCATGCGCAA	2520
85	GACTTTTGCC	CGCTACCTTT	CATTCCGGCG	TGACAACAAT	GAGCTGTTGC	TCTTCATACT	2580
	GAAGCAGTTA	GTGGCAGAGC	AGGTGACATA	TCAGCGCAAC	CGCTTTGGGG	CCCAGCAGGA	2640
	CACATATTGAG	GTCCCTGAGA	AGGACTTGGT	GGATAAGGCT	CGTCAGATCA	ACATCCACAA	2700

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 TGTCTTACTT GGTGTCTGAA CATCTTGCCA CCTCCGAGTG CTTTGTCTCC ACTCAGTACC 3060
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 TTGCTCCCTG TCTGTTTCCC CACTCTCTTA TTTGTGCATT CGGTTTGGTT TCTGTAGTTT 3420
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Seq ID NO: 329 Protein sequence:
 Protein Accession #: AAH17490.1

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 DREAGRGLGR MRRGLLYDS D EDEEREPARK RROVERATED GDEDEEMIES IENLEDLKGH 180
 SVREWVSMAG PRLEIHHRFK NPLRTHVDHSH GHNVFKERIS DMCKENRESL VVNYEDLAAR 240
 EHVLAFLPE APAELLQIFD EAALEVLAM YPKYDRITNH IHVRISHLPL VEELRSLRQL 300
 HLNQLIRTSV VVTSTCTGVLP QLSMVKYNCN KCFNVLGPPC QSQNQEVKFG SCPECQSAGP 360
 FVNNMEETIY QNYQRIQOE SPGKVAAGRL PRSKDAILLA DLVDSCKPGD EIELTGIYHN 420
 NYDGSINTAN GFPVFATVIL ANHVAKKDNK VAVGELTDED VKMITSLSKD QQIGEKIFAS 480
 IAPSIYGHED IKRGLALALF GGEPEKNPGBK HKVRGDINVL LCGDPGTAKS QFLKYIEKVS 540
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 HEAMEQQSIS ISKAGIVTSL QARCTVIAAA NPIGGRYDPS LTFSENVDLT EPIISRFDIL 660
 CVVRDITVDPV QDEMLARFVV GSHVRHHPN KEEEGLANGS AAEPAMPNTY GVEPLPQEV 720
 KKYIYAKER VHPKLNQMDV DKVAKMYS DL RKESMATGSI PITVRHIESM IRMAEAHARI 780
 HLRDVIYIED VNMALRVMLE SFIDTQKFSV MRSMRKTFAR YLSFRRDNNE LLLFILKQLV 840
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 Nucleic Acid Accession #: M17254
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 GGAGGAGAAG CACATGCCAC CCCCACCAAT GACCACGAAC GAGCGCAGAG TTATCGTGCC 660
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Seq ID NO: 331 Protein sequence
 Protein Accession #: AAA52398

1 11 21 31 41 51
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 PPNMTTNER RVIVPADPTL WSTDHVRQWL EWAVKEYGLP DVNILLFQNI DGKELCKMTK 180
 DDFQRLTPSY NADILLSHLH YLRETPHPLH TSDDVDKALQ NSPRLMHARN TDLPEYPPRR 240
 SAWTGHGHTP PQSKAAQPSF STVPKTEDQR PQLDPYQILG PTSRLANPG SQQIQLWQFL 300
 LELLSDSNS SCITWEGTNG EFKMTDPDEV ARRWGERKSK PNMNYDKLSR ALRYYYDKNI 360
 MTKVHGKRYA YKFFDHGIAQ ALQHPPESS LYKYPDLPLY MGSYHAHPQK MNFVAPHPPA 420
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Seq ID NO: 332 DNA sequence
 Nucleic Acid Accession #: NM_000020
 Coding sequence: 283-1794

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Seq ID NO: 333 Protein sequence
 Protein Accession #: NP_000011

1 11 21 31 41 51
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 LILGVLALL ALVALGVLLG WHVRRRQEKQ RGLHSELGES SLILKASEQG DTMLGDLDS 180
 DCTTSGSGL PFLVQRTVAR QVALVECVGK GRYGEVWRGL WHGESVAVKI FSSRDEQSWF 240
 RETEYNTVL LRHDNILGFI ASDMTSRNSS TQLWLITHYH EHGSYLDLQ RQTLPHLAL 300
 RLAVSAACGL AHLHVEIFGT QGKPAIAHRD FKSRNVLVKS NLQCCIADLG LAVMHSQGS 360
 YLDIGNNPRV GTRKRYMAPEV LDEQIRTDCE ESKWTDIWA FGLVLWEIAR RTIVNGIVED 420
 YRPPFYDVVP NDPSFEDMKK VVCVDQQTPT IPNRLADPV LSLAQMRE CWYPNPSARL 480
 TALRIKKTLQ KISNSPEKPK VIQ

Seq ID NO: 334 DNA sequence
 Nucleic Acid Accession #: NM_004126.1
 Coding sequence: 108-329

1 11 21 31 41 51
 GGCACGAGCT CGTGCCGGCC TTCAGTTGTT TCGGGACGCG CCGAGCTTCG CCGCTCTTCC 60
 AGCGGCTCCG CTGCCAGAGC TAGCCCGAGC CCGGTCTCG GCGGAAAATG CCTGCCCCTC 120
 ACATCGAAGA TTGTCAGAGC AAGGAAAAAC TGAAAATGGA AGTTGAGCAG CTTGCAAAAG 180
 AAGTGAAGTT GCAGAGACAA CAAGTGTCTA AATGTCTGA AGAAATAAAG AACTATATTG 240
 AAGAACGTTT TGGAGAGGAT CCTCTAGTAA AGGGAATTCC AGAAGACAAG AACCCCTTTA 300
 AAGAAAAAGG CAGCTGTGTT ATTTCAATAA TAACCTGGGA GAAACTGCAT CTAAGTGGGA 360
 AGAAGTAGTT TGTCTTAGTT TTCCAGATA AAACCAACAT GCTTTTAAAG GAAGGAAGAA 420
 TGAAATTAAG AGGAGACTTT CTTAAGCACC ATATAGATAG GGTATGTAT AAAAGCATAT 480
 GTGCTACTCA TCTTTGCTCA CTATGCAGTC TTTTAAAG GAGCAGAGAG TATCAGATGT 540
 ACAATATATG AAATAAGAAC ATTACTTGAG CATGACACTT CTTTCAGTAT ATTGCTTGAT 600
 GCTTCAATAA AAGTTTGTCT TT

Seq ID NO: 335 Protein sequence
 Protein Accession #: NP_004117.1

1 11 21 31 41 51
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 KNPFKEKSGC VIS

Seq ID NO: 336 DNA sequence
 Nucleic Acid Accession #: NM_005795
 Coding sequence: 555-1940

1 11 21 31 41 51
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 TTCCACCTT GCTTGTGGGT AAATCTCTTC TGCAGGATCT CAGAAAGTAA AGTTCCATCC 180
 TGAGAAATAT TCACAAGAA TTTCCTTAAG AGCTGGAGCT GGTCTTGACC CCTGGAATTT 240
 AAGAAATCT TAAAGACAAT GTCAAAATATG ATCCAAGAGA AAATGTGATT TGAGTCTGGA 300
 GACAATTGTG CATATCGTCT AATAATAAAA ACCCATACTA GCCTATAGAA AACATATTT 360
 GAATAATAAA AACCCATACT AGCCTATAGA AAACAATATT TGAAAGATTG CTACCACTAA 420
 AAGAAAAACT ACTACAACCT GACAAGACTG CTGCAAACTT CAATTGGTCA CCACAACCTG 480
 ACAAGGTTGC TATAAACAAC GATTGTCTACA ACTTCTAGTT TATGTTATAC AGCATATTTT 540
 ATTTGGGCTT AATGATGGAG AAAAAGTGTA CCCTGTATTT TCTGGTCTCT TTGCTTTTTT 600
 TTATGATTCT TGTTCAGACA GAATTAGAAG AGAGTCTCTG GGACTCAATT CAGTTGGGAG 660
 TTAAGTAAAG TAAATCATG ACAGCTCAAT ATGAATGTGA CCAAAAGATT ATGCAAGACC 720
 CCATTCAACA AGCAGAAGGC GTTACTGCA ACAGAACCTG GGATGGATGG CTCTGCTGGA 780
 ACGATGTTGC AGCAGGAAGT GAATCAATGC AGCTCTGCCC TGATTACTTT CAGGACTTTG 840
 ATCCATCAGA AAAAGTTACA AAGATCTGTG ACCAAGATGG AAACCTGGTT AGACATCCAG 900
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 AGACTGCACT AAATTTGTTT TACCTGACCA TAATTGGACA CGGATTGTCT ATTGCATCAC 1020
 TGCTTATCTC GCTTGGCATA TTCTTTTATT TCAAGAGCCT AAGTTGCCAA AGGATTACCT 1080
 TACACAAAAA TCTGTTCTTC TCATTTGTTT GTAACCTCTG TGTAAACATC ATTCACCTCA 1140
 CTGCAGTGGC CACAAACAGC GCCTTAGTAG CCACAATCC TGTAGTTGTC AAAGTGTCCC 1200
 AGTTCATTCA TCTTATCTG ATGGGCTGTA ATTACTTTTG GATGCTCTGT GAAGGCATT 1260
 ACCTACACAC ACTCATTTGT GTGGCCGTGT TTGCAGAGAA GCAACATTTA ATGTGTTATT 1320
 ATTTCTTGG CTGGGGATT CCCTGATTC CTGCTGTAT ACATGCCATT GCTAGAAGCT 1380

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 GCCCAATTTG TGCTGCTTTA CTGGTGAATC TTTTTCCTT GTTAAATATT GTACGCGTTC 1500
 TCATCACCAA GTTAAAGTT ACACACCAAG CGGAATCCAA TCTGTACATG AAAGCTGTGA 1560
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 CTGAAGGAAA GATTGCAGAG GAGGTATATG ACTACATCAT GCACATCCTT ATGCACTTCC 1680
 AGGGTCTTTT GGTCTCTACC ATTTTCTGCT TCTTTAATGG AGAGGTTCAA GCAATCTCTGA 1740
 GAAGAAACTG GAATCAATAC AAAATCCAA TTTGGAACAG CTTTTCACAC TCAGAAGCTC 1800
 TTCTAGTAGC GTCTTACACA GTGTCAACAA TCAGTGTAGG TCCAGGTTAT AGTCATGACT 1860
 GTCTAGTGA ACACTTAAAT GGAAAAAGCA TCCATGATAT TGAATATGTT CTCTTAAAC 1920
 CAGAAAAATT ATATAATTGA AAATAGAAGG ATGGTTGTCT CACTGTTTGG TGCTTCTCCT 1980
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 ATCCAGCTCT ATGTGGGAAA AAAGAAATCC TGGTTGTAA TGTTTGTGAG TAAATACTCC 2160
 CACTATGCCT GATGTGACGC TACTAACCTG ACATCACCAA GTGTGGAATT GGAGAAAAGC 2220
 ACAATCAACT TTTCTGAGCT GGTGTAAGCC AGTTCACAGA CACCATTTGAT GAATTCAAAC 2280
 AAATGGCTGT AAAACTAAAC ATACATGTTG GGCATGATT TACCCTTAT CCCCCAAGA 2340
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 TTCTATATCA TTAGGAAAAC ATCTTAGTTG ATGCTACAAA ACACCTTGTC AACCTCTTCC 2700
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 ATTTTCTTGG AATTTGTAA AAAGAAATTG TGAATAATGA GCTTGTAAT ACTCCATTAT 2880
 TTTATTTTAT AGTCTCAAT CAATACATA CAACCTATGT AATTTTAAAC GCAATATAT 2940
 AATGCAACAA TGTGTGATG TTAATATCTG ATACTGTAT TGGGCTGATT TTTTAAATAA 3000
 AATAGAGTCT GGAATGCT

Seq ID NO: 337 protein sequence
 Protein Accession #: NP_005786.1

1 11 21 31 41 51
 MEKKCTLYFL VLLPFFMILV TAELEESPED SIQLGVTRNK IMTAQYECYQ KIMQDPIQQA 60
 EGVYCNRTWD GWLWCNDVAA GTESMQLCPD YFQDFDPSEK VTKICDQDGN WFRHPASNRT 120
 WNTYTQCNVN THEKVKATLN LFLYLTIIHG LSIASLLISL GIFFYFKSL SQRITLHKNL 180
 FFSFVNCNVV TIIHLTAVAN NQALVATNPV SCKVSQFIHL YLMGCNYFWM LCEGIYHLTL 240
 IVVAVFAEKQ HLMWYFPLGW GFPLIPACIH AIARSLYND NCWISSDTHL LYIIHGPICA 300
 ALLVNLFFLL NTVRVLITKL KVTHQAESNL YMKAVRATLI LVPLLGLIEFV LIPWRPEGKI 360
 ABEVYDIIMH ILMHFQGLLV STIFCFNNGE VQAILRRNWN QYKIQFNGSF SNSEALRSAS 420
 YTVSTISDGP GYSHDCPSEH LNGKSIHDIE NVLLKPENLY N

Seq ID NO: 338 DNA sequence
 Nucleic Acid Accession #: NM_001795
 Coding sequence: 25-2379

1 11 21 31 41 51
 GCACGATCTG TTCCTCTCGG GAAGATGCAG AGGCTCATGA TGCTCCTCGC CACATCGGGC 60
 GCCTGCCTGG GCCTGCTGGC AGTGGCAGCA GTGGCAGCAG CAGGTGCTAA CCCTGCCCAA 120
 CGGGACACCC ACAGCCTGCT GCCCACCCAC CGGCGCCAAA AGAGAGATTG GATTTGGAAC 180
 CAGATGCACA TGTATGAAGA GAAAAACACC TCACTTCCCC ATCATGTAGG CAAGATCAAG 240
 TCAAGCGTGA GTCGCAAGAA TGCCAAGTAC CTGCTCAAAG GAGAATATGT GGGCAAGGTC 300
 TTCGGGTCG ATGCAGAGAC AGGAGACGTG TTCGCCATTG AGAGGCTGGA CCGGGAGAAT 360
 ATCTCAGAGT ACCACCTCAC TGCTGTCTAT GTGGACAAGG ACACTGGTGA AAACCTGGAG 420
 ACTCCTTCCA GCTTCACCAT CAAAGTTTCT GACGTGAACG ACACTGGGCC TGTGTTCAAG 480
 CATCGGTTGT TCAATGCGTC CGTGCTGAG TCGTCGGCTG TGGGGACCTC AGTCATCTCT 540
 GTGACAGCAG TGGATGCAGA CGACCCCACT GTGGGAGACC ACGCCTCTGT CATGTACCAA 600
 ATCTTGAAGG GGAAGAGTGA TTTTGCCATC GATAATTCTG GACGTATTAT CACAATAACG 660
 AAAAGCTTGG ACCGAGAGAA GCAGGCCAGG TATGAGATCG TGGTGAAGC GCGAGATGCC 720
 CAGGGCCTCC GGGGGGACTC GGGCACGGCC ACCGTGCTGG TCACTCTGCA AGACATCAAT 780
 GACAACCTCC CCTTCTTCTC CCAGACCAAG TACACATTTG TCGTGCTGTA AGACACCCGT 840
 GTGGGCACCT CTGTGGGCTC TCTGTTTGTG GAGGACCCAG ATGAGCCCCA GAACCGGATG 900
 ACCAAGTACA GCATCTTGCG GGGCGACTAC CAGGACGCTT TCACCATTTG GACAAACCCC 960
 GCCCACAACG AGGGCATCAT CAAGCCCTG AAGCCTCTGG ATTTATGAATA CATCCAGCAA 1020
 TACAGCTTCA TCGTCGAGGC CACAGACCCC ACCATCGACC TCCGATACAT GAGCCCTCCC 1080
 GCGGGAAACA GAGCCCAAGT CATTATCAAC ATCAGAGATG TGGACGAGCC CCCCATTTC 1140
 CAGCAGCCTT TCTACCACTT CCAGCTGAAG GAAAACCAGA AGAAGCCTCT GATTGGCACA 1200
 GTGCTGGCCA TGGACCTTGA TGCGGCTAGG CATAGCATTG GATACTCCAT CCGCAGGACC 1260
 AGTGACAAGG GCCAGTCTCT CCGAGTCACA AAAAAGGGGG ACATTTCACA TGAGAAAGAA 1320
 CTGGACAGAG AAGTCTACCC CTGGTATAAC CTGACTGTGG AGGCCAAAGA ACTGGATTCC 1380
 ACTGGAACCC CCACAGGAAA AGAATCCATT GTGCAAGTCC ACATTGAAGT TTTGGATGAG 1440
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 CATGGCCAGC TGGTCTCGCA GATCTCGCA ATAGACAAGG ACATAACACC ACGAAACGTG 1560
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 ACGGCCAACA TCACAGTCAA GTATGGGCAG TTTGACCGGG AGCATAACAA GGTCCACTTC 1680
 CTACCCGTGG TCATCTCAGA CAATGGGATG CCAAGTCGCA CCGGCACCA GACGCTGACC 1740
 GTGGCCGTGT GCAAGTGCAC CGAGCAGGGC GAGTTTCACT TCTGCGAGGA TATGGCCGCC 1800
 CAGGTGGGCG TGAGCATGCA GGCAGTGGTA GCCATCTTAC TCTGCATCCT CACCATCACA 1860
 GTGATCACCC TGCTCATCTT CCGTGGCGGG CGGCTCCGGA AGCAGGCCCC CGCGCACGGC 1920
 AAGAGCGTGC CGGAGATCCA CGAGCAGCTG GTCACTACG ACGAGGAGGG CGGCGGGGAG 1980
 ATGGACACCA CCAAGTACGA TGTGTCGGTG CTCAACTCGG TCGCGCGGG CGGGGCCAAG 2040
 CCCCCTGGCG CCGCGCTGGA CGCCCGGCTT TCCCTCTATG CGCAGGTGCA GAAGCCACCG 2100
 AGGCACGCGC CTGGGGCACA CGGAGGGCCC GGGGAGATGG CAGCCATGAT CGAGGTGAAG 2160
 AAGGACGAGG CGGACCACGA CGGCGACGGC CCCCCTACG ACACGCTGCA CATCTACGGC 2220
 TACGAGGGCT CCGAGTCCAT AGCCGAGTCC CTGAGCTCCC TGGGCACCGA CTCATCCGAC 2280

	TCTGACGTGG	ATTAGACATT	CCTTAACGAC	TGGGGACCCA	GGTTTAAGAT	GCTGGCTGAG	2340
	CTGTACGGCT	CGGACCCCGG	GGAGGAGCTG	CTGTATTAGG	CGGCCGAGGT	CACTCTGGGC	2400
	CTGGGGACCC	AAACCCCTCG	CAGCCCAGGC	CAGTCAGACT	CCAGGCACCA	CAGCCTCCAA	2460
	AAATGGCAGT	GACTCCCCAG	CCCAGCACCC	CTTCTCTGTG	GGTCCCAGAG	ACCTCATCAG	2520
5	CCTTGGGATA	GCAAACTCCA	GGTTCTTGAA	ATATCCAGGA	ATATATGTCA	GTGATGACTA	2580
	TTCTCAAATG	CTGGCAAATC	CAGGCTGGTG	TTCTGTCTGG	GCTCAGACAT	CCACATAACC	2640
	CTGTACCCCA	CAGACCCGCG	TCTAACTCAA	AGACTTCCTC	TGGCTCCCCA	AGGCTGCAAA	2700
	GCAAAACAGA	CTGTGTTTAA	CTGCTGCAGG	GTCTTTTTCT	AGGGTCCCCTG	AACGCCCTGG	2760
10	TAAGGCTGGT	GAGGTCTCTG	TGCCTATCTG	CCTGGAGGCA	AAGGCCTGGA	CAGCTTGACT	2820
	TGTGGGGCAG	GATTCTCTGC	AGCCCATTTCC	CAAGGGAGAC	TGACCATCAT	GCCCTCTCTC	2880
	GGGAGCCCTA	GCCCTGCTCC	AACTCCATAC	TCCACTCCAA	GTGCCCCACC	ACTCCCCAAC	2940
	CCCTCTCCAG	GCCTGTCAAG	AGGGAGGAAG	GGGCCCCATG	GCAGCTCCTG	ACCTTGGGTC	3000
	CTGAAGTGAC	CTCACTGGCC	TGCCATGCCA	GTAACGTGTC	TGTACTGAGC	ACTGAACCAC	3060
15	ATTCAAGGAA	ATGCTTATTA	AACCTTGAAG	CAACTGTGAA	TTCATTCTGG	AGGGGCAGTG	3120
	GAGATCAGGA	GTGACAGATC	ACAGGGTGAG	GGCCACCTCC	ACACCCACCC	CCTCTGGAGA	3180
	AGGCCTGGAA	GAGCTGAGAC	CTTGCTTTGA	GACTCCTCAG	CACCCCTCCA	GTTTTCCTGG	3240
	AGAAGGGGCA	GATGTTCCCG	GAGATCAGAA	GACGTCTCCC	CTTCTCTGCC	TCACCTGGTC	3300
	GCCAAATCCAT	GCTCTCTTTC	TTTTCTCTGT	CTACTCCTTA	TCCCTTGGTT	TAGAGGAACC	3360
20	CAAGATGTGG	CCTTTAGCAA	AACTGACAAAT	GTCCAAAACCC	ACTCATGACT	GCATGACGGA	3420
	GCCGAGCATG	TGCTCTTACA	CCTCGCTGTT	GTCACATCTC	AGGGAACCTGA	CCCTCAGGCA	3480
	CACCTTGCGAG	AAGGAAGGCC	CTGCCCTGCC	CAACCTCTGT	GGTCACCCAT	GCATCATTTCC	3540
	ACTGGAACGT	TTCATGCGAA	ACACACCTTG	GAGAAGTGGC	ATCAGTCAAC	AGAGAGGGGC	3600
	AGGGAAGGAG	ACACCAAGCT	CACCCCTCGT	CATGGACCGA	GGTTCCTCACT	CTGGCAAAAGC	3660
	CCCTCACACT	GCAAGGGATT	GTAGATAACA	CTGACTTGTT	TGTTTTAAAC	AATAACTAGC	3720
25	TTCTTATAAT	GATTTTTTTA	CTAATGATAC	TTACAAGTTT	CTAGCTCTCA	CAGACATATA	3780
	GAATAAGGGT	TTTTGCATAA	TAAGCAGGTT	GTTATTTAGG	TTAACAATAT	TAATTCAGGT	3840
	TTTTTAGTTG	GAAAAACAAT	TCCTGTAACC	TTCTATTTTC	TATAATTGTA	GTAATTGCTC	3900
	TACAGATAAT	GTCTATATAT	TGGCCAAACT	GGTGCATGAC	AAGTACTGTA	TTTTTTTATA	3960
30	CCTAATAAAA	GAAAAATCTT	TAGCCTGGGC	AACAAAAAAA			

Seq ID NO: 339 Protein sequence
Protein Accession #: NP_001786

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	VIVDKDTGEN	LETSSSFTIK	VHDVNDNWPV	FTHRLFNASV	PESSAVGTSV	ISVTAVDADD	180
	PTVGHDHASM	YQILKGEYF	AIDNSGRIIT	ITKSLDREKQ	ARYEIVVEAR	DAQGLRGDSG	240
40	TATVLVTLQD	INDNPFPTQ	TKYTFVVPED	TRVGTSVGSL	FVEDPDEPQN	RMTKYSILRG	300
	DYQDAFTIET	NPAHNEGIK	PMKPLDYEYI	QQYSFIVEAT	DPTIDLRYMS	PPAGNRAQVI	360
	INITDVDEPP	IFQQPFYHFW	LKENQKKPLI	GTVLAMPDPA	ARHSIGYSIR	RTSDKQGFPR	420
	VTKKGDIYNE	KELDRVYFP	YNLTVEAKEL	DSTGTPTEKE	SIVQVHIEVL	DENDNAPEFA	480
	KPYQPKVCEN	AVHGLQLVLI	SAIDKIDITPR	NVKFKFTLNT	ENNFTLTDNH	DNTANITVKY	540
45	GQFDRHETKV	HFLPVPVISDN	GMPSRTGTST	LTVAVCKCNE	QGEFTFCEDM	AAQGVGSIOA	600
	VVAILLCILIT	ITVITLLIPL	RRRLRKQARA	HGKSVPEIHE	QLVTYDEEGG	GEMDITSYDV	660
	SVLNSVRRGG	AKPPRPALDA	RPSLYAQVQK	PPRHAPGAHG	GPGEMAAMIE	VKKDEADHDG	720
	DGPPYDTLHI	YGYEGSESIA	ESLSSSLGTD	SDSDVDYDFL	NDWGRPRFRL	AELYGSDPRE	780
50	ELLY						

Seq ID NO: 340 DNA sequence
Nucleic Acid Accession #: NM_003088
Coding sequence: 112-1593

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60	AACGGCACAG	CCGAGGGCGT	GCAGATCCAG	TTCGGCCTCA	TCAACTGCGG	CAACAAGTAC	180
	CTGACGGCCG	AGGCGTTCGG	GTTCAAGGTG	AACGCGTCCG	CCAGCAGCCT	GAAGAAGAAG	240
	CAGATCTGGA	CGCTGGAGCA	GCCCCCTGAC	GAGGCGGGCA	GCGCGGCCGT	GTGCTGCGC	300
	AGCCACCTGG	GCCGTACTCT	GGCGGCGGAC	AAGGACGGCA	ACGTGACCTG	CGAGCGCGAG	360
	GTGCCCCGTC	CCGACTGCGG	TTTCTCATC	GTGGCGCACG	ACGACGGTCG	CTGGTCGCTG	420
65	CAGTCCGAGG	CGACCGGCG	CTACTTCGGC	GGCACCGAGG	ACCGCCTGTC	CTGCTTCGCG	480
	CAGACGGTGT	CCCCGCCCGA	GAAGTGGAGC	GTGCACATCG	CCATGCACCC	TCAGGTCAAC	540
	ATCTACAGTG	TCACCGGTAA	GCGCTACGCG	CACCTGAGCG	CGCGGCGCGC	CGACGAGATC	600
	GCCGTGGACC	GCGACGTGCC	CTGGGCGGTC	GACTCGCTCA	TCACCTCGC	CTTCCAGGAC	660
	CAGCGCTACA	GCGTGCAGTC	CGCCGACCAC	CGCTTCCTGC	GCCACGACGG	GCGCCTGGTG	720
70	GCGCGCCCCG	AGCCGGCCAC	TGGCTACACG	CTGGAGTTCC	GCTCCGGCAA	GGTGGCCTTC	780
	CGCGACTCGG	AGGGCCGTTA	CCTGGCGCGG	TCGGGGCCCA	GCGGCACGCT	CAAGGCGGGC	840
	AAGGCCACCA	AGGTGGGCAA	GGACGAGCTC	TTTGCTCTGG	AGCAGAGCTG	CGCCAGGTC	900
	GTGCTGCAGG	CGGCCAACGA	GAGGAACGTG	TCCACGCGCC	AGGGTATGGA	CCTGTCTGCC	960
	AATCAGGACG	AGGAGACCCA	CCAGGAGACC	TTCCAGCTGG	AGATCGACCG	CGACACCAAA	1020
75	AAGTGTGCCT	TCCGTACCCA	CACGGGCAAG	TACTGGACGC	TGACGGCCAC	CGGGGCGGTG	1080
	CAGTCCACCG	CCTCCAGCAA	GAATGCCAGC	TGCTACTTTG	ACATCGAGTG	GCGTGACCGG	1140
	CGCATCACAC	TGAGGGCGTC	CAATGGCAAG	TTTGAGACCT	CCAAGAAGAA	TGGGCAGCTG	1200
	GCCGCTCGG	TGGAGACAGC	AGGGGACTCA	GAGCTCTTCC	TCATGAAGCT	CATCAACCGC	1260
	CCCATCATCG	TGTTCCCGGG	GGAGCATGGC	TTTCATCGGT	GCCGCAAGGT	CACGGGCACC	1320
80	CTGGACGCCA	ACCGCTCCAG	CTATGACGTC	TTCCAGCTGG	AGTTCAACGA	TGGCGCCTAC	1380
	AACATCAAAG	ACTCCACAGG	CAAATACTGG	ACGGTGGGCA	GTGACTCCGC	GGTCAACCAGC	1440
	AGCGGCGACA	CTCCTGTGGA	CTTCTCTTTC	GAGTCTGTGC	ACTATAACAA	GGTGGCCATC	1500
	AAGGTGGGCG	GCGCTACCT	GAAGGGCGAC	CACGCAGGCG	TCCTGAAGGC	CTCGGCGGAA	1560
	ACCGTGGACC	CGCCTCGCT	CTGGGAGTAC	TAGGGCCGGC	CCGTCTCTCC	CCGCCCTTGC	1620
85	CCACATGGCG	GCTCTGCGCA	ACCCTCCCTG	CTAACCCCTT	CTCCGCGCAGG	TGGGCTCCAG	1680
	GGCGGGAGGC	AAGCCCCCTT	GCCTTTCAAA	CTGGAACACC	CAGAGAAAAC	GGTGGCCCA	1740
	CCTGTGCGCC	CTATGGACTC	CCCCTCTCC	CCTCCGCGCG	GGTTCCTTAC	TCCCTCTGGG	1800

5
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15

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TACAGCGGCTG CGGCCTGGCC CTGGGAGGGA TTTCAGATGC CCCTGCCCTC TTGTCTGCCA 1860
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GAAGCGGCTA AGGGACGGTT GGGGGCTGGG AGCCCTGGGC GTGTAGTGTA ACTGGAATCT 1980
TTTGCTCTCT CCAGCCACCT CCTCCAGGCC CCCCAGGAGA GCTGGGCACA TGTCCCAAGC 2040
CTGTCACTGG CCTCCCTGG TGCACGTGCC CCGAAACCCC TGCTTGGGAA GGGAAAGCTGT 2100
CGGGAGGGCT AGGACTGACC CTTGTGGTGT TTTTTTGGGT GGTGGCTGGA AACAGCCCCT 2160
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ACAGGGTCTG CCGCTGCAC GTTCTGCCAA GGTGGTGGTG GCGGGCGGGT AGGGGTGTGG 2280
GGGCGCTCTT CCTCTGTCTT CTTCTCTTTC ACCCTAGCCT GACTGGAAGC AGAAAATGAC 2340
CAAATCAGTA TTTTTTTTAA TGAATATTA TTGCTGGAGG CGTCCCAGGC AAGCCTGGCT 2400
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CCCCCTCTTT CCGTCTCTCC CGTCCAGCCC CAGCCCTGGG CCTGGGCTGC CGACACCTGG 2520
GCCAGAGCCC CTGCTGTGAT TGGTGTCTCC TGGGCCTCCC GGGTGGATGA AGCCAGGCCGT 2580
CGCCCCCTCC GGGAGCCCTG GGGTGAGCCG CCGGGGCCCC CCTGTGCTCA GCCTCCCCCG 2640
TCCCCAACAT GCATCTCACT CTGGGTGTCT TGGTCTTTTA TTTTTTGTAA GTGTCAATTG 2700
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AGTCTGC

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20 Seq ID NO: 341 Protein sequence
Protein Accession #: NP_003079

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1 11 21 31 41 51
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CFAQTVSPA E KWSVHIAMHP QVNIYSVTRK RYAHLSARPA DEIAVDRDVP WGVDSLITLA 180
FQDQRYSVQT ADHRFLRHDG RLVARPEPAT GYTFEPRSGK VAFRDCEGRY LAPSGPSGTL 240
KAGKATKVGK DELFALEQSC AQVVLQAANE RNVSRTQGM D LSAHQDEETD QETFQLEIDR 300
DTKKCAFRTH TGYWTLTAT GGVQSTASSK NASCYFDIEW RDRRITLRAS NGKFVTSKKN 360
GQLAASVETA GDSLEFLMKL INRPIIVFRG EHGFIGCRKV TGTLDANRSS YDVFQLEFND 420
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SAETVDPASL WEY

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35 Seq ID NO: 342 DNA sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 660..1705

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1 11 21 31 41 51
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Seq ID NO: 343 Protein sequence
Protein Accession #: FGENESH predicted

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Seq ID NO: 344 DNA sequence
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	GCTGCTGCTC	CTGACCCAGC	CCGGGGCGGG	GACGGGAGCT	GACACGGAGG	CGGTGGTCTG	240
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Seq ID NO: 345 Protein sequence
Protein Accession #: NP_036204

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Seq ID NO: 348 DNA sequence
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Seq ID NO: 349 Protein sequence:
Protein Accession #: NP_002629

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AGGCCCGCAG CCTTCAGGCC GTGCCTAGGC TGGTGAAGCT CTTCAACCAC GCCAACCAAG 1200
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AGCTGGCCCT GGTGGAGGAG AACGGGATCT TCGAGCTGCT GCGGACACTG CGGGAGCAGG 1320
ATGATGAGCT TCGCAAAAAT GTCACAGGGA TCCTGTGGAA CCTTTCATCC AGCGACCACC 1380
TGAAGGACCG CCTGGCCAGA GACACGCTGG AGCAGCTCAC GGACCTGGTG TTGAGCCCCC 1440
TGTCGGGGGC TGGGGGTCCC CCCCTCATCC AGCAGAACGC CTCGGAGGCG GAGATCTTCT 1500
ACAACGCCAC CGGCTTCCTC AGGAAACCTC GCTCAGCCTC TCAGGCCACT CGCCAGAAGA 1560
TGCGGGAGTG CCACGGGCTG GTGACGCCC TGGTCACTC TATCAACCAC GCCCTGGACG 1620
CGGGCAAATG CGAGGACAAG AGCGTGGAGA ACGCGGTGTG CGTCTGCGG AACCTGTCTC 1680
ACCGCCTCTA CGACGAGATG CCGCCGTCCG CGCTGCAGCG GCTGGAGGGT CGCGGCCGCA 1740
GGGACCTGGC GGGGGCGCCG CCGGGAGAGG TCGTGGGCTG CTTACGCGC CAGAGCCGCG 1800
GGCTGCGCGA GCTGCCCCCT GCCGCGATG CGCTCACCTT CGCGGAGGTG TCCAAGGACC 1860
CCAAGGGCCT CGAGTGGCTG TGGAGCCCC AGATCGTGGG GCTGTACAAC CGGCTGCTGC 1920
AGCGCTGCCA GCTCAACCGG CACACGACGG AGGCGGCCG CCGGGCGCTG CAGAACATCA 1980
CGGCAGGCCA CCGCAGGTGG GCGGGGGTGC TGAGCCGCTT GGCCCTGGAG CAGGAGCGTA 2040
TTCTGAACCC CTGCTAGAC CGTGTACAG CCGCCGACCA CCACCACTG CGTCACTGA 2100
CTGGCCTCAT CCGAAACCTG TCTCGGAACG CTAGGAACAA GGACGAGATG TCCACGAAGG 2160
TGGTGAAGCA CCTGATCGAG AAGCTGCCAG GCAGCGTGGG TGAGAAGTCG CCCCAGCCG 2220
AGGTGCTGGT CAACATCATA GCTGTGCTCA ACAACCTGGT GGTGGCCAGC CCCATCGCTG 2280
CCCGAGACCT GCTGTATTTT GACGGACTCC GAAAGCTCAT CTTTCATCAG AAGAAGCGGG 2340
ACAGCCCCGA CAGTGAGAAG TCCTCCCGGG CAGCATCCAG CCTCTGGCC AACCTGTGGC 2400
AGTACAACAA GCTCCACCGT GACTTTCGGG CGAAGGGCTA TCGGAAGGAG GACTTCTTGG 2460
GCCATAGGTG GAAGCCTTCT GGAGGAGAAG GTGACGTGGC CCAGCGTCCA AGGGACAGAC 2520
TCAGTCCAG GCTGCTTGGC AGCCCAGCCT GGAGGAGAAG GCTAATGACG GAGGGGCCCC 2580
TCGCTGGGGC CCCTGTGTGC ATCTTTGAGG GTCTTGGGCC ACCAGGAGGG GCAGGGTCTT 2640
ATAGCTGGGG ACTTGGCTTC CGCAGGGCAG GGGGTGGGGC AGGGCTCAAG GCTGCTCTGG 2700
TGTATGGGGT GGTGACCCAG TCACATTGGC AGAGGTGGGG GTTGGCTGTG GCCTGGCAGT 2760
ATCTTGGGAT AGCCAGCACT GGAATAAAG ATGGCCATGA ACAGTCACAA AAAAAAAAAA 2820
AAAAGGAATT C
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Seq ID NO: 351 Protein sequence
Protein Accession #: NP_009114.1

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1      11      21      31      41      51
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	MQDGNFLLSA	LQPEAGVCSL	ALPSDLQLDR	RGAEGPEAER	LRAARVQEQV	RARLLQLGQQ 60
	PRHNGAAEPE	PEAETARGTS	RGQYHTLQAG	FSSRSQGLSG	DKTSGFRPIA	KPAYSPASWS 120
5	SRSVAVDLSCS	RRLSSAHNGG	SAFGAAGYGG	AQPTPPMPTR	PVSFHERGGV	GSRADYDTLS 180
	LRSLRLGPGG	LDRLYSLVSE	QLEPAATSTY	RAFAYERQAS	SSSSRAGGLD	WPEATEVSPS 240
	RTIRAPAVRT	LQRFQSSHRS	RGVGGAVPGA	VLEPVARAPS	VRSLSLSLAD	SGHLPDVHGF 300
	NSYGSHTLTQ	RLSSGPDID	LPSAVKYLMA	SDPNLQVLGA	AYIQHKCYSD	AAAKKQARSL 360
	QAVPRLVKLF	NHANQEVQRH	ATGAMRNLIY	DNADNKLALV	EENGIFELLR	TLREQDDELRL 420
10	KNVTGILWNL	SSSDHLKDRL	ARDTLEQLTD	LVLSPLSGAG	GPPLIQONAS	EAEIFYNATG 480
	FLRNLSSASQ	ATRQKMRECH	GLVDALVTSI	NHALDAGKCE	DKSVENAVCV	LRNLSYRLVD 540
	EMPPSALQRL	EGRGRRDLAG	APPGEVVGC	TPQSRRLREL	PLAADALTFA	EVSKDPKGLE 600
	WLWSPQIVGL	YNRLLRCEL	NRHTTEAAG	ALQNTAGDR	RWAGVLSRLA	LEQERILNPL 660
	LDRVRTADHH	QLRSLTGLIR	NLSRNARNKD	EMSTKVVS	IEKLPGSVGE	KSPPAEVLVN 720
15	IIAVLNNLVV	ASPIAARDLL	YFDGLRKLIF	IKKKRDSFDS	EKSSRAASSL	LANLWQYNKL 780
	HRDFRAGYR	KEDFLGP				

Seq ID NO: 352 DNA sequence
Nucleic Acid Accession #: M31469
Coding sequence: 1-651

	1	11	21	31	41	51	
25	ATGGCTGCGC	AGGGAGAGCC	CCAGGTCCAG	TTCAAACCTTG	TATTGGTTGG	TGATGGTGGT	60
	ACTGGAAAAA	CGACCTTCGT	GAAACGTCAT	TTGACTGGTG	AATTGTAGAA	GAAGTATGTA	120
	GCCACCTTGG	GTGTTGAGGT	TCATCCCCTA	GTGTTCCACA	CCAACAGAGG	ACCTATTAAG	180
	TTCAATGTAT	GGGACACAGC	CGGCCAGGAG	AAATTCGGTG	GACTGAGAGA	TGGCTATTAT	240
	ATCCAAGCCC	AGTGTGCCAT	CATAATGTTT	GATGTAACAT	CGAGAGTTAC	TTACAAGAAAT	300
30	GTGCTAACT	GGCATAGAGA	TCTGGTACGA	GTGTGTGAAA	ACATCCCAT	TGTGTTGTGT	360
	GGCAACAAAG	TGGATATTAA	GGACAGGAAA	GTGAAGCGCA	AATCCATTGT	CTTCCACCGA	420
	AAGAAGAAAT	TTCACTACTA	CGACATTCT	GCCAAAAGTA	ACTACAACCT	TGAAAAGCCC	480
	TTCTCTGGC	TTGCTAGGAA	GCTCATTTGA	GACCCCTAAT	TGGAATTGT	TGCCATGCC	540
	GCTCTCGCCC	CACCAGAGT	TGTCATGGAC	CCAGCTTTGG	CAGCACAGTA	TGAGCACGAC	600
35	TTAGAGGTTG	CTCAGACAAC	TGCTCTCCCG	GATGAGGATG	ATGACCTGTG	A	

Seq ID NO: 353 Protein sequence
Protein Accession #: AAA36546

	1	11	21	31	41	51	
40	MAAQGEPOVQ	FKLVLVGDGG	TGKTTFVKRH	LTGEFEKKYV	ATLGVEVHPL	VFHTNRGPIK	60
	FNVDWTDAGQ	KFGGLRDGY	IQAQCAIMF	DVTSRVTYKN	VPNWHRLDVR	VCEINIPVL	120
	GNKVDIKDRK	VKAQSIKVR	KNNLQYDIS	AKSNYNFEKP	FLWLARKLIG	DPNLEFVAMP	180
45	ALAPPEVVM	PALAAQYEH	LEVAQTALP	DEDDDL			

Seq ID NO: 354 DNA sequence
Nucleic Acid Accession #: NM_002820
Coding sequence: 304-831

	1	11	21	31	41	51	
55	CCGGTTGCA	AAGAAGCTGA	CTTCAGAGGG	GGAAACTTTC	TTCTTTTAGG	AGGCGGTTAG	60
	CCCTGTTCCA	CGAACCCAGG	AGAACTGCTG	GCCAGATTAA	TTAGACATTG	CTATGGGAGA	120
	CGTGTAACA	CACACTATAT	CATTGATGCA	TATATAAAAC	CATTTTATTT	TCGCTATTAT	180
	TTCCAGAGAA	GCGCCTCTGA	TTTGTTCCTT	TTTCCCTTTT	TTGCTCTTTC	TGGCTGTGTG	240
	GTTTGGAGAA	AGCACAGTTG	GAGTAGCCGG	TTGCTAAATA	AGTCCCGAGC	GCGAGCGGAG	300
	ACGATGCAGC	GGAGACTGGT	TCAGCAGTGG	AGCGTCGCGG	TGTTCTGCT	GAGCTACGCG	360
60	GTGCGCTCCT	GCGGCGGCTC	GGTGGAGGGT	CTCAGCCGCC	GCCTCAAAAG	AGCTGTGTCT	420
	GAACATCAGC	TCCTCCATGA	CAAGGGGAAG	TCCATCCAAG	ATTACCGCG	ACGATTCTTC	480
	CTTCACCATC	TGATCGCAGA	AATCCACACA	GCTGAAATCA	GAGCTACCTC	GGAGGTGTCC	540
	CCTAACTCCA	AGCCCTCTCC	CAACACAAAG	AACCACCCCG	TCCGATTG	GTCTGATGAT	600
	GAGGGCAGAT	ACCTAACTCA	GGAACTAATC	AAGGTGGAGA	CGTACAAAGA	GCAGCCGCTC	660
	AAGACACCTG	GGAGAAAAAA	GAAAGGCAAG	CCCGGGAAC	GCAAGGAGCA	GGAAAAAGAA	720
65	AAACGGCGAA	CTGCTCTG	CTGGTTAGAC	TCTGGAGTGA	CTGGGAGTGG	GCTAGAAGGG	780
	GACCACCTGT	CTGACACCTC	CACAACGTCG	CTGGAGCTCG	ATTACCGGTA	ACAGGCTTCT	840
	CTGGCCCGTA	GCCTCAGCGG	GGTGTCTCTA	GCTGGGTTTT	GGAGCCTCCC	TTCTGCCTTG	900
	GCTTGGACAA	ACCTAGAATT	TTCTCCCTTT	ATGTATCTCT	ATCGATTGTG	TAGCAATTGA	960
	CAGAGAATAA	CTCAGAATAT	TGCTGCCTTT	AAAGCAGTAC	CCCCCTACCA	CACACACCCC	1020
70	TGTCCTCCAG	CACCATAGAG	AGGCGCTAGA	GCCATTCTCT	CTTCTCCAC	CGTCACCCAA	1080
	CATCAATCCT	TTACCACTCT	ACCAATAAAT	TTCATATTCA	AGCTTCAGAA	GCTAGTGACC	1140
	ATCTTCATAA	TTTGTCTGGG	AAGTGATTTT	CTTCCCTTTA	CTCTCACACC	TGGGCAAACT	1200
	TTCTTCAGTG	TTTTTCATTT	CTTACGTTCT	TTCACTTCAA	GGGAGAATAT	AGAAGCATTT	1260
	GATATTATCT	ACAACACTG	CAGAACAGCA	TCATGTCATA	AACGATTCTG	AGCCATTCAC	1320
75	ACTTTTATTT	TAATTAATAT	TATTTAATTA	AATCTCAAAT	TTATTTTAAT	GTAAGAAGCT	1380
	TAAATTATGT	TTTAAACACA	TGCCTTAAAT	TTGTTTAATT	AAATTTAACT	CTGGTTTCTA	1440
	CCAGCTCATA	CAAAATAAAT	GGTTTCTGAA	AATGTTTAAG	TATTAACCTA	CAAGGATATA	1500
	GGTTTCTCTC	ATGTATCTTT	TTGTTTCTTT	GCAAGATGAA	ATAATTTTTC	TAGGGTAATG	1560
80	CCGTAGGAAA	AATAAACTT	CACATTTAAA	AAAAA			

Seq ID NO: 355 Protein sequence
Protein Accession #: NM_002820

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85	MQRRLVQQWS	VAVFLLSYAV	PSCGRSVEGL	SRRLKRAVSE	HQLLHDKGKS	IQDLRRRFFL	60
	HHLIAEIHITA	EIRATSEVSP	NSKPSPNTKN	HPVRFGSDDE	GRYLTQETNK	VETYKEQPLK	120

TPGKKKKGKP GKRKEQEKKK RRTRSAWLDS GVTGSGLEGD HLSDTSTTSL ELSDR

Seq ID NO: 356 DNA sequence
Nucleic Acid Accession #: NM_017522
Coding sequence: 1-2100

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1	11	21	31	41	51	
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CTGCTGCTGC	TGCGGCTCCA	GCATCTTGCG	GCGGCAGCGG	CTGATCCGCT	GCTCGGCGGC	120
CAAGGGCCGG	CCAAGGAGTG	CGAAAAGGAC	CAATTCCAGT	GCCGGAACGA	GCGCTGCATC	180
CCCTCTGTGT	GGAGATGCGA	CGAGGACGAT	GACTGCTTAG	ACCACAGCGA	CGAGGACGAC	240
TGCCCCAAGA	AGACCTGTGC	AGACAGTGAC	TTACCTGTG	ACAACGGCCA	CTGCATCCAC	300
GAACGGTGGA	AGTGTGACGG	CGAGGAGGAG	TGTCCTGATG	GCTCCGATGA	GTCCGAGGCC	360
ACTTGCACCA	AGCAGGTGTG	TCCTGCAGAG	AAGCTGAGCT	GTGGAGCCAC	CAGCCACAAG	420
TGTGTACCTG	CCTCGTGGCG	CTGCGACGGG	GAGAAGGACT	GCGAGGGTGG	AGCGGATGAG	480
GCCGGCTGTG	CTACCTCACT	GGGCACCTGC	CGTGGGGACG	AGTTCAGTG	TGGGGATGGG	540
ACATGTGTCC	TTGCAATCAA	GCACTGCAAC	CAGGAGCAGG	ACTGTCCAGA	TGGGAGTGAT	600
GAAGCTGGCT	GCCATACAGG	GCTGAACGAG	TGCTGCACAC	ACAATGGCGG	CTGCTCACAC	660
ATCTGCACTG	ACCTCAAGAT	TGGCTTTGAA	TGCACGTGCC	CAGCAGGCTT	CCAGCTCCTG	720
GACCAGAAGA	CTTGTGGCGA	CATTGATGAG	TGCAAGGACC	CAGATGCCTG	CAGCCAGATC	780
TGTGTCAATT	ACAAGGGCTA	TTTTAAGTGT	GAGTGTCTACC	CTGGCTGCGA	GATGGACCTA	840
CTGACCAAGA	ACTGCAAGGC	TGCTGCTGGC	AAGAGCCCAT	CCCTAATCTT	CACCAACCCG	900
ACGAGTGGG	AGGATCGACC	TGTGAAGCGG	AACATATTCAC	GCCCTCATCCC	CATGCTCAAG	960
AATGTCGTGG	CACATAGATGT	GGAAAGTTGCC	ACCAATCGCA	TCTACTGGTG	TGACCTCTCC	1020
TACCGTAAGA	TCTATAGCGC	CTACATGGAC	AAGGCCAGTG	ACCCGAAGA	GCGGGAGGTC	1080
CTCATTGACG	AGCAGTTGCA	CTCTCCAGAG	GGCCTGGCAG	TGGACTGGGT	CCACAAGCAC	1140
ATCTACTGGA	CTGACTCGGG	CAATAAGACC	ATCTCAGTGG	CCACAGTTGA	TGGTGGCCGC	1200
CGACGCACTC	TCTTCAAGCG	TAACTCAGT	GAACCCCGGG	CCATCGCTGT	TGACCCCTCG	1260
CGAGGGTTCA	TGTATTGGTC	TGACTGGGGG	GACCAGGCCA	AGATTGAGAA	ATCTGGGCTC	1320
AACGGTGTGG	ACCGGCAAAAC	ACTGGTGTCA	GACAATATTG	AATGGCCCAA	CGGAATCACC	1380
CTGGATCTGC	TGAGCCAGCG	CTTGTACTGG	GTAGACTCCA	AGCTACACCA	ACTGTCCAGC	1440
ATTGACTTCA	GTGGAGGCAA	CAGAAAGACG	CTGATCTCCT	CCACTGACTT	CCTGAGCCAC	1500
CCTTTTGGGA	TAGCTGTGTT	TGAGGACAAG	GTGTTCTGGA	CAGACCTGGA	GAACGAGGCC	1560
ATTTTCAGTG	CAATCCGGCT	CAATGGCCTG	GAAATCTCCA	TCCTGGCTGA	GAACCTCAAC	1620
AACCCACATG	ACATTGTGAT	CTTCCATGAG	CTGAAGCAGC	CAAGAGCTCC	AGATGCCTGT	1680
GAGCTGAGTG	TCCAGCCTAA	TGGAGGCTGT	GAATACCTGT	GCCTTCCTGC	TCCTCAGATC	1740
TCCAGCCACT	CTCCCAAGTA	CACATGTGCC	TGTCCTGACA	CAATGTGGCT	GGTCCAGAC	1800
ATGAAGAGGT	GCTACCCAGA	TGCAAAATGAA	GACAGTAAGA	TGGGCTCAAC	AGTCACCTGCC	1860
GCTGTATATC	GGATCATCGT	GCCCATAGTG	GTGATAGCCC	TCCTGTGCAT	GAGTGGATAC	1920
CTGATCTGGA	GAAACTGGAA	GCGGAAGAAC	ACCAAAAGCA	TGAATTTTGA	CAACCCAGTC	1980
TACAGGAAAA	CAACAGAAGA	AGAAGATGAA	GATGAGCTCC	ATATAGGGAG	AACTGCTCAG	2040
ATTGGCCATG	TCATATCTGC	ACGAGTGGCA	TTAAGCCTTG	AAGATGATGG	ACTACCTCGA	2100
GGATGGGATC	ACCCCTTTCG	TGCCTCATGG	AATTCAGTCC	CTGCACTAC	ACTCCGGATG	2160
GTGTATGACT	GGATGAATGG	GTTTCTATAT	ATGGGTCTGT	GTGAGTGTAT	GTGTGTGTGT	2220
GATTTTTTTT	TTTAAATTTA	TGTTGCGGAA	AGGTAACCA	AAAGTTATGA	TGAACTGCAA	2280
ACATCCAAAG	GATGTGAGAG	TTTTTCTATG	TATAATGTTT	TATACACTTT	TTAACTGGTT	2340
GCACTACCCA	TGAGGAATTC	GTGGAATGGC	TACTGCTGAC	TAAACATGATG	CACATAACCA	2400
AATGGGGGCC	AATGGCACAT	TACCTTACTC	ATCATTTAAA	AACTATATTT	ACAGAAGATG	2460
TTTGGTTGCT	GGGGGGCTTT	TTTAGGTTTT	GGGCATTTGT	TTTTTGTA	TAAGATGATT	2520
ATGCTTTGTG	GCTATCCATC	AACATAAGT				

Seq ID NO: 357 Protein sequence
Protein Accession #: NP_059992

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70

1	11	21	31	41	51	
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PSVWRDDEDD	DCLDHSDEDD	CPKKTCAUSD	FTCDNGHCIH	ERWKCDEGEE	CPDGSDESEA	120
TCTKQVCPAE	KLSCGPTSHK	CVPASWRCDG	EKDCGEGADE	AGCATSLGTC	RGDEFQCGDG	180
TCVLAIKHCN	QEQDCPDGSD	EAGCLQGLNE	CLHNNGGCSH	ICTDLKIGFE	CTCPAGFQLL	240
DQKTCGDIDE	CKDPDACSQI	CVNYKGYFKC	ECYPGCEMDL	LTKNCKAAAG	KSPSLIFTNR	300
TSABDRPVKR	NYSRLLPMLK	NVVALDVEVA	TNRIYWCDSL	YRKIYSAYMD	KASDPKEREV	360
LIDELHSPSE	GLAVDWHVHK	IYWTDSGNKT	ISVATVDGGR	RRTLFNRNLS	EPRAIAVDPL	420
RGFMYSWDWG	DQAKIEKSGL	NGVDRQTLVS	DNIEWPNGIT	LDLLSQRLYW	VDSKLHQLSS	480
IDFSGGNRKT	LISSTDFLSH	PFGIAVPEDK	VFWTDLENEA	IFSANRLNGL	EISILAENLN	540
NPHDIVIFHE	LKQPRAPDAC	ELSVQPNGGC	EYLCPLPAPQI	SSHSPKYTC	CPDTMWLGPD	600
MKRCYRDANE	DSKMGSTVTA	AVIGIIVPIV	VIALLCMSGY	LIWRNWKRN	TKSMNFDNPV	660
YRKTTEEDE	DELHIGRTAQ	IGHVYPARVA	LSLEDDGLP			

Seq ID NO: 358 DNA sequence
Nucleic Acid Accession #: M27826
Coding sequence: <1-503

75
80
85

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AGCCCAAGAA	ACATCTCACC	AATTTCAAAT	CTGATCTATT	CGGCTTAGCG	ACTGAAGATT	60
GACGCTGCCC	GATCGCCTCG	GAAGTCCCTT	GGACCATCAC	AGAAGCCGAG	CTTCGGGTAA	120
CTCTCAGAGT	GGAGGGTAAG	TCCATCCCTT	GTTTAATCGA	TACGGGGGCT	ACCCACTCCA	180
CGTTGCTTTC	TTTTCAAGGG	CCTTTTCCCT	TTGCCCCCAT	AACTGTTGTG	GGTATTGACG	240
GCCAAAGCTT	AAAACCCCTG	AAAACCTCCC	CACCTCTGGT	CCAACTTGGA	CAACACTCTT	300
TTATGCACTC	TTTTTTAGTT	ATCCCCACCT	GCCCACTTCC	CTTATTAGGC	CGAAATATTT	360
TAACCAAAAT	ATCTGCTTCC	CTGACTATTC	CTGGAGTACA	GCTACATCTC	ATTGCTGCCC	420
TTCTTCCCAA	TCCAAAGCCT	CCTTTGTGTC	CTCTAACATC	CCCACAATAT	CAGCCCTTAC	480
CACAAAGACT	CCCTTCAGCT	TAACTCTTCC	CACCTAGGTT	TCCCAACGCG	CCCCTAATCC	540
CACCTGAAGC	AGCCCTGAGA	AACATCGCCC	ATTCTCTCTC	CATACCAACC	CCCAAAATTT	600
TTCGCGCTC	CAACACTTCA	ACACTATTTT	GTTTTATTGT	TCTTATTAAT	ATCAGAAGGC	660

AGGAATGTCA GGCCTCTGAG CCCAGGCCAG GCCATCGCAT CCCCTGTGAC TTGCACGTAT 720
 ACATCCAGAT GGCCTGAAGT AACTGAAGAT CCACAAAAGA AGTAAAAACA GCCTTAAGTG 780
 ATGACATTCC ACCATTGTGA TTTGTTCTCG CCCACCCTA ACTGATCAAT GTACTTTGTA 840
 ATCTCCCCCA CCCTTAAGAA GGTTCCTTGT AATTCTCCCC ACCCTTGAGA ATGTAATTTG 900
 TGAGATCCAC CCTGCCCCAC CAGAGAACAA CCCCTTTGA TTGTAATTTT TTATTACCTT 960
 CCCAAATCCT ATAAACAGC CCCACCCTA TCTTCCTTCA CTGACTCTCT TTTCCGACTC 1020
 AGCCACCGGC ACCCAGGTGA AATAAACAGC TTTATTGCTC AC

Seq ID NO: 359 Protein sequence
 Protein Accession #: AAA65999

1 11 21 31 41 51
 PKKHLTNFKS DLFGLATEDW RCPPIASEVPW TITEAELRVT LTVEGKSIPC LIDTGATHST 60
 LPSPQGPVSL APITVVVGIDG QASKPLKTPP LWCQLGQHSF MHSFLVIPTC PLPLLRNRL 120
 TKLSASLTIP GVQLHLIAAL LPNPKPLCLP LTPQYQPLP QDLPSA

Seq ID NO: 360 DNA sequence
 Nucleic Acid Accession #: NM_001854
 Coding sequence: 162-5582

1 11 21 31 41 51
 AACCATCAAA TTTAGAAGAA AAAGCCCTTT GACTTTTTC CCCTCTCCCT CCCCAATGGC 60
 TGTGTAGCAA ACATCCCTGG CGATACCTTG GAAAGGACGA AGTTGGTCTG CAGTCGCAAT 120
 TTCGTGGGTT GAGTTCACAG TTGTGAGTGC GGGGCTCGGA GATGGAGCCG TGGTCCCTCTA 180
 GGTGGAAAAC GAAACGGTGG CTCTGGGATT TCACCGTAAC AACCTCGCA TTGACCTTCC 240
 TCTTCCAAGC TAGAGAGGTC AGAGGAGCTG CTCCAGTTGA TGTACTAAAA GCACTAGATT 300
 TTCACAATTC TCCAGAGGGA ATATCAAAAA CAACGGGATT TTGCACAAAC AGAAAGAATT 360
 CTAAAGGCTC AGATACTGCT TACAGAGTTT CAAAGCAAGC ACAACTCAGT GCCCAACAA 420
 AACAGTTATT TCCAGGTGGA ACTTTCCAG AAGACTTTTC AATACTATTT ACAGTAAAAAC 480
 CAAAAAAGG AATTCACTCT TCCCTTTTAT CTATATATAA TGAGCATGGT ATTCAGCAAA 540
 TTGGTGTGTA GTTGGGAGTA TCACCTGTTT TTCTGTTTGA AGACCACACT GGAACACCTG 600
 CCCGGAAGA CTTCCCTCCT TTCAGAACTG TTAACATCGC TGACGGGAAG TGGCATCGGG 660
 TAGCAATCAG CGTGGAGAAG AAAACTGTGA CAATGATTGT TGATTGTAAG AAGAAAACCA 720
 CGAAACCACT TGATAGAAGT GAGAGAGCAA TTGTGTATAC CAATGGAATC ACGGTTTTTG 780
 GAACAAGGAT TTTGGATGAA GAAGTTTTTG AGGGGACAT TCAGCAGTTT TTGATCACAG 840
 GTGATCCCAA GGCAGCATAT GACTACTGTG AGCATTATAG TCCAGACTGT GACTCTTCAG 900
 CACCCAGGCG TCCTCAAGCT CAGGAACCTC AGATAGATGA GTATGCACCA GAGGATATAA 960
 TCGAATATGA CTGATAGTAT GGGGAAGCAG AGTATAAAGA GGCTGAAAGT GTAAACAGAGG 1020
 GACCCACTGT AACTGAGGAG ACAATAGCAC AGACGGAGGC AAACATCGTT GATGATTTTC 1080
 AAGAATACAA CTATGGAAAC ATGGAAAGTT ACCAGACAGA AGCTCCTAGG CATGTTTCTG 1140
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 CAGAACTGTA TATTACAGAA ACAAGCATAA ATGGCCATGG TGCATATGGA GAGAAAGGAC 1440
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 GTCCCTCTGG TACTATGTTG ATGTTACCGT TCCGTTATGG TGGTGATGGT TCCAAAGGAC 1680
 CAACCATCTC TGCTCAGGAA GCTCAGGCTC AAGCTATTCT TCAGCAGGCT CGGATTGCTC 1740
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 GTTCATCTGG GGCCAAAGGT GAGAGTGGTG ATCCAGGTCC TCAGGGCCCT CGAGGCGTCC 1860
 AGGGTCCCCC TGGTCCAACG GGAACACCTG GAAAAAGGGG TCGTCCAGGT GCAGATGGAG 1920
 GAAGAGGAAT GCCAGGAGAA CCTGGGCAAA AGGGAGATCG AGGGTTTGAT GGACTTCCGG 1980
 GTCTGCCAGG TGACAAAGGT CACAGGGGTG AACGAGGTCC TCAGGTCTCT CCAGGTCTCT 2040
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 AAGCTGGCCC ACGAGGTTTG CTGGGTCCAA GGGGAACCTC AGGAGCTCCA GGGCAGCCTG 2160
 GTATGGCAGG TGTAGATGGC CCCCAGGAG CAAAGGGGAA CATGGGTCCT CAAGGGGAGC 2220
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 AAGGTGCACG GGGAGTAGCT GGCACACCA GGCCTCGGGG TCAGCGTGGT CCAACGGGTC 2820
 CTCGAGGTTT AAGAGGTGCA AGAGGTCCCA CTGGGAAACC TGGGCCAAAG GGCACCTTCC 2880
 GTGGCGATGG CCTCTCTGGC CCTCCAGGTG AAAGAGGTCC TCAAGGACCT CAGGGTCCAG 2940
 TTGGATTCCC TGGACCAAAA GGCCCTCCTG GACCACAGG AAGGATGGGC TGCCACAGGAC 3000
 ACCCTGGGCA ACGTGGGGAG ACTGGATTTC AAGGCAAGAC CGGCCCTCCT GGGCCAGGGG 3060
 GAGTGGTTGG ACCACAGGGA CCAACCGGTG AGACTGGTCC AATAGGGGAA CGTGGGTATC 3120
 CTGGTCTCTC TGCCCTCTCT GGTGAGCAAG GTCTTCTCTG TGCTGCAGGA AAAGAAAGGT 3180
 CAAAGGGTGA TCCAGGTCTC CAAGGTATCT CAGGGAAGA TGGAACAGCA GGATTACGTG 3240
 GTTTCCACAG GGAAGAGAGT CTTCTGGAG CTAGGGTGC ACCTGGACTG AAAGGAGGGG 3300
 AAGGTCCCCA GGGCCACCA GGTCCAGTTG GCTCACCAGG AGAACGTGGG TCAGCAGGTA 3360
 CAGCTGGCCC AATTGGTTTA CGAGGGCGCC CGGACCTCA GGGTCTCTCT GTCCAGCTG 3420
 GAGAGAAAGT TGCTCTTGA GAAAAAGGTC CCCAAGGGCC TGACGGGAGA GATGGAGTTT 3480
 AAGTCTCTGT TGGTCTCCCA GGGCCAGCTG GTCCTGCCGG CTCCTTGGG GAAGACGGAG 3540
 ACAAGGGTGA AATTGGTGAG CCGGGACAAA AAGGCAGCAA GGGTGGCAAG GGAGAAAATG 3600
 GCCCTCCCCG TCCCCCAGGT CTTCAAGGAC CAGTTGGTGC CCTTGGAAAT GCTGGAGGTG 3660
 ATGGTGAACC AGTCTCTAGA GGCAGCAGG GATGTTTGG GCAAAAGGT GATGAGGGTG 3720
 CCAGAGGCTT CCTTGGACCT CTTGGTCCAA TAGGTCTTCA GGTCTGCCA GGCCACCTG 3780
 GTGAAAAAGG TGAATAATGG GATGTTGGTC CATGGGGGCC ACCTGGTCTC CCAGGCCCAA 3840

	GAGGCCCTCA	AGGTCCCAAT	GGAGCTGATG	GACCACAAGG	ACCCCCAGGT	TCTGTTGGTT	3900
	CAGTTGGTGG	TGTTGGAGAA	AAGGGTGAAC	CTGGAGAAGC	AGGAAACCCA	GGGCCCTCCTG	3960
	GGGAAGCAGG	TGTAGGCGGT	CCCAAAGGAG	AAAGAGGAGA	GAAAGGGGAA	GCTGGTCCAC	4020
5	CTGGAGCTGC	TGGACCTCCA	GGTGCCAAGG	GGCCGCCAGG	TGATGATGGC	CCTAAGGGTA	4080
	ACCCGGGTCC	TGTTGGTITT	CCTGGAGATC	CTGGTCTCTC	TGGGGAACCT	GGCCCTGCAG	4140
	GTCAAGATGG	TGTTGGTGGT	GACAAGGGTG	AAGATGGAGA	TCCTGGTCAA	CCGGGTCTCTC	4200
	CTGGCCCATC	TGGTGAAGGT	GGCCCAACAG	GTCTCTCTGG	AAACACGAGT	CCTCTCTGGAG	4260
	CTGCAGGTGC	AGAGGGTAGA	CAAGGTGAAA	AAGGTGCTAA	GGGGGAAGCA	GGTGCAAGAG	4320
10	GTCTCTCTGG	AAAAACCGGC	CCAGTCGGTC	CTCAGGGACC	TGCAGGAAAG	CCTGGTCCAG	4380
	AAGGTCTTCG	GGGCATCCCT	GGTCTGTGG	GAGAACAAGG	TCTCCCTGGA	GCTGCAGGCC	4440
	AAGATGGACC	ACCTGGTCCT	ATGGGACCTC	CTGGCTTACC	TGGTCTCAAA	GGTGACCCCTG	4500
	GCTCCAAGGG	TGAAAAGGGA	CATCTGGTT	TAATTTGGCT	GATTGGTCTC	CCAGGAGAAC	4560
	AAGGGGAAAA	AGGTGACCGA	GGGCTCCCTG	GAATCAAGG	ATCTCCAGGA	GCAAAAGGGG	4620
15	ATGGGGGAAT	TCCTGGTCTC	GCTGGTCCCT	TAGGTCCACC	TGGTCTCTCA	GGCTTACCAG	4680
	GTCTCTCAAG	CCCAAAGGGT	AACAAAGGCT	CTACTGGACC	CGCTGGCCAG	AAAGGTGACA	4740
	GTGGTCTTCC	AGGGCCTCCT	GGGCTCCAG	GTCCACCTGG	TGAAGTCATT	CAGCCTTTAC	4800
	CAATCTTTGC	CTCCAAAAAA	ACGAGAAGAC	ATACTGAAGG	CATGCAAGCA	GATGCAGATG	4860
	ATAATATTCT	TGATTACTCG	GATGGAATGG	AAGAAATATT	TGGTCTCCCTC	AATTCCTTGA	4920
20	AACAAGACAT	CGAGCATATG	AAATTTCCAA	TGGGTACTCA	GACCAATCCA	GCCCGAAGCTT	4980
	GTAAGACCT	GCAAGTCAGC	CATCTGACT	TCCCAGATGG	TGAATATTGG	ATTGATCCTA	5040
	ACCAAGGTTG	CTCAGGAGAT	TCCTTCAAAG	TTTACTGTAA	TTTCACATCT	GGTGGTGAGA	5100
	CTTGCAATTA	TCCAGACAAA	AAATCTGAGG	GAGTAAGAAT	TTCATCATGG	CCAAGGAGAG	5160
	AACCAAGAAC	TTGTTTTAGT	GAATTTAAGA	GGGGAAAACT	GCTTTCATAC	TTAGATGTTG	5220
25	AAGGAAATTC	CATCAATATG	GTGCAAAATG	CATTCTGTAA	ACTTCTGACT	GCCTCTGCTC	5280
	GGCAAAATTT	CACCTACCAC	TGTATCATGT	CAGCAGCCTG	GTATGATGTG	TCATCAGGAA	5340
	GTTATGACAA	AGCACTTCGC	TTCCTGGGAT	CAAAATGATG	GGAGATGTCC	TATGACAATA	5400
	ATCCCTTTTAT	CAAAACACTG	TATGATGGTT	GTACGTCCAG	AAAAGGCTAT	GAAAAAACTG	5460
	TCATTGAAAT	CAATACACCA	AAAATTGATC	AAGTACCTAT	TGTTGATGTC	ATGATCAGTG	5520
30	ACTTTGGTGA	TCAGAAATCAG	AAGTTCGGAT	TTGAAGTTGG	TCCTGTTTGT	TTTCTTGGCT	5580
	AAGATTAAAG	CAAAGAACAT	ATCAAATCAA	CAGAAAATGT	ACCTTGGTGC	CACCAACCCA	5640
	TTTTGTGCCA	CATGCAAGTT	TTGAATAAGG	ATGTATGGAA	AACAACGCTG	CATATACAGG	5700
	TACCATTTAG	GAATACCGA	TGCCTTTGTG	GGGGCAGAA	CACAGACAAA	AGCTTTGAAA	5760
	ATCATAAAGA	TATAAGTTGG	TGTGGCTAAG	ATGGAAACAG	GGCTGATTCT	TGATTCCTCA	5820
35	TTCTCAACTC	TCCTTTTCTC	ATTTGAATTT	CTTTGGTGCT	GTAGAAAACA	AAAAAAGAAA	5880
	AATATATATT	CATAAAAAAT	ATGGTGCTCA	TTCTCATCCA	TCCAGGATGT	ACTAAAAACAG	5940
	TGTGTTTAAT	AAATTTGTAAT	TATTTGTGT	ACAGTTCTAT	ACTGTTATCT	GTGTCCATT	6000
	CCAAAACFTG	CACGTGTCC	TGAATTCGC	TGACTCTAAT	TTATGAGGAT	GCCGAAGCTT	6060
40	GATGGCAATA	ATATATGTAT	TATGAAAATG	AAGTTATGAT	TTCCGATGAC	CCTAAGTCCC	6120
	TTTCTTTGGT	TAATGATGAA	ATTCCTTTGT	GTGTGTTT			

Seq ID NO: 361 Protein sequence
Protein Accession #: NP_001845

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45	MEPWSSRWKT	KRWLWDFTVT	TLALTFLFQA	REVRGAAPVD	VLKALDFHNS	PEGISKTTGF	60
	CTNRKNSKGS	DTAYRVSKQA	QLSAPTKQLF	PGGTFFPEDFS	ILFTVKPKKG	IQSFLLSIYN	120
	EHGIQQIGVE	VGRSPVFLFE	DHTGKPAPED	YPLFRTVNIA	DGKWHRVAS	VEKKTVMIV	180
50	DCKKKTTKPL	DRSERAIVDT	NGITVFGTRI	LDEEVFEGDI	QQFLITGDPK	AAYDYCEHYS	240
	PDCDSSAPKA	AQAQEPQIDE	YAPEDIIEYD	YEYGEAEYKE	AESVTEGPTV	TEETIAQTEA	300
	NIVDDFQEYN	YGTMESYQTE	APRHVSGTNE	PNPVEEITFE	EYLTGEDYDS	QRKNSDITLY	360
	ENKEIDGRDS	DLLVDGDLGE	YDFYKEYEY	DKPTSPFPNEE	FQPGVPAETD	ITETSINGHG	420
	AYGEKGQKGE	PAVVEPGLMV	EGPPPGPAGPA	GIMGPPGLQG	PTGPPGDFGD	RGPPGRPGLP	480
55	GADGLPGPPG	TMLMLPFRYG	GDGSKGPTIS	AQEAQAQAIL	QQAIALRGF	PGPMGLTRFP	540
	GPVGGPGSSG	AKGESGDPGP	QGPGRVQGGP	GPTGKPKKRG	RPGADGGGRM	PGEPGAKGDR	600
	GFDGLPLGLP	DKGHRGERGP	QGPFGPPGDD	GMRGEDGEIG	PRGLPGEAGP	RGLLGPRTGP	660
	GAPGQPGMAG	VDGPPPGPKGN	MGPQGEPPGP	GQQGNFPGQG	LPGPQGPPIG	PGEKGPQKGP	720
	GLAGLPGADG	PPCHPGKEQG	SGEKGALGPP	GPQGPIGXPG	PRGVKADGV	RGLKGSKEGK	780
60	GEDGFPFGFK	DMGLKDRGE	VQIGPRGXG	GPEGPKGRAG	PTGDPGSPSG	AGEKGLGVLP	840
	GLPGYFGRQG	PKGSTGFPGF	PGANGEKGAR	GVAGKFPGRG	QRGPTGPRGS	RGARGPTGKP	900
	GPKGTSGGDD	PGPPGGERGP	QGPQGPVGF	GPKPPPGPPG	RMGCPGHFGQ	RGETGFQKGT	960
	GPPGPGGVVG	PQGPTGETGP	IGERGYPPGP	GPPGEGQLPG	AAGKEGAKGD	PGPQGISGKD	1020
	GPAGLRGFP	ERGLPGAQGA	PGLKGEGEPQ	GPPGPGVSPG	ERGSAGTAGP	IGLRGRPGPQ	1080
65	GPPGPAGEKG	APGEKGPQGP	AGRDGVQGPV	GLPGPAGPAG	SPGEDGDKGE	IGEPGQKGSK	1140
	GGKGENGPPG	PPGLQGPVGA	PGIAGGDGEP	GPRGQGMFG	QKGDGARGF	PGPPGPIGLQ	1200
	GLPFPPEKEG	ENGDVGPWGP	PGPPGPRGPQ	GPNGADGPQG	PPGSGVSGVG	VGEKGEPEGE	1260
	GNPFPPEEAG	VGGPKGERGE	KGEAGPPGAA	GPPGAKGPPG	DDGPKGNPGP	VGFPDGPDPG	1320
	GELGPAGQDG	VGGDKGEDGD	PQPGPPPGPS	GEAGPPGPPG	KRGPPGAAGA	EGRQGEKGA	1380
70	GEAGEGPPG	KTGPVPGQGP	AGKPGPEGLR	GIPGPVGEQG	LPGAAGQDGP	PGPMGPPGLP	1440
	GLKGDGPGSK	EKGHPGLIGL	IGPPGEQGEK	GDRGLPGTQG	SPGAKGDGGI	PGPAGPLGFP	1500
	GPPGLPGPQG	PKGNKGSTGP	AGQKGDGSLP	GPPGPPGPPG	EVIQPLPILS	SKKTRRHTEG	1560
	MQADADDNII	DYSDGMEEIF	GSLNSLKQDI	EHMKFPMGTQ	TNPARTCKDL	QLSHPDFFDG	1620
	EWIDPNQGC	SGDSFKVYCN	FTSGGETCIY	PDKKSEGVRI	SSWPKEKPGS	WFSEFKRGKL	1680
75	LSYLDVEGNS	INMVQMTFLK	LLTASARQNF	TYHCHQSAAW	YDVSSGSYDK	ALRFLGSNDE	1740
	EMSYDNPPFI	KTYLDGCTSR	KGYEKTIVIEI	NTPKIDQVPI	VDVMISDFGD	QNQKFGFEVG	1800
	PVCFLG						

Seq ID NO: 362 DNA sequence
Nucleic Acid Accession #: NM_003107
Coding sequence: 351-1775

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85	TTCCCCAGCA	TTCGAGAAAC	TCCTCTCTAC	TTTAGCACGG	TCTCCAGACT	CAGCCGAGAG	60
	ACAGCAAAC	GCAGCGCGGT	GAGAGAGCGA	GAGAGAGGGA	GAGAGAGACT	CTCCAGCCTG	120
	GGAACATATA	CTCTCTGCG	AGAGGCGGAG	AACTCCTTCC	CCAAATCTTT	TGGGGACTTT	180

	TCTCTCTTTA	CCACCTCTCG	CCCCTGCGAG	GAGTTGAGGG	GCCAGTTCGG	CCGCGCGCGG	240
	CGTCTTCCCG	TTCCGCGTGT	GCTTGGCCCG	GGGAACCGGG	AGGGCCCGGC	GATCGCGCGG	300
	CGGCGCGCGG	GAGGGTGTGA	GCGCGCGTGG	GCGCCCGCCG	AGCCGAGGCC	ATGGTGCAGC	360
5	AAACCAACAA	TGCGGAGAAC	ACGGAAGCGC	TGCTGGCCCG	CGAGAGCTCG	GACTCGGGCG	420
	CCGCGCTCGA	GCTGGGAATC	GCCTCTCTCC	CCACGCGCGG	CTCCACCGCC	TCCACGGGCG	480
	GCAAGGCCGA	CGACCCGAGC	TGGTGCAAGA	CCCCGAGTGG	GCACATCAAG	CGACCCATGA	540
	ACGCCTTCAT	GCTGTGTGTC	CAGATCGAGC	GCGCAAGAT	CATGGAGCAG	TCGCCCCACA	600
	TGCACAACGC	CGAGATCTCC	AAGCGGCTGG	GCAAAACGCTG	GAAGCTGCTC	AAAGACAGCG	660
10	ACAAGATCCC	TTTCATTCTGA	GAGGCGGAGC	GGCTGCGCCT	CAAGCACATG	GCTGACTACC	720
	CCGACTACAA	GTACCGGCCC	AGGAAGAAGG	TGAAGTCCGG	CAACGCCAAC	TCCAGCTCCT	780
	CGGCGCGCGC	CTCCTCCAAG	CCGCGGAGGA	AGGGAGACAA	GGTCGGTGGC	AGTGGCGGGG	840
	CGGCGCATGG	GGGCGGCGGC	GGCGGCGGGA	GCAGCAACGC	GGGGGAGGGA	GGCGGCGGTG	900
	CGAGTGGCGG	CGGCGCCAAC	TCCAAACCGG	CGCAGAAAAA	GAGCTGCGGC	TCCAAAGTGG	960
15	CGGGCGGCGC	GGGCGGTGGG	GTTAGCAAAAC	CGCACGCCAA	GCTCATCCTG	GCAGGCGGCG	1020
	GCGGCGGCGG	GAAAGACAGC	GCTGCGCGCG	CCGCCTCCTT	CGCCGCCGAA	CAGGCGGGGG	1080
	CCGCGCGCCT	GCTGCCCTTG	GGCGCGCGCG	CCGACCACTA	CTCGCTGTAC	AAGGCGCGGA	1140
	CTCCACGCGC	CTCGGCTCTC	GCCTCTCTCG	CAGCCTCGGC	CTCCGAGCGC	CTCGCGGCC	1200
	CGGGCAAGCA	CCTGGCGGAG	AAGAAGGTGA	AGCGCGTCTA	CCTGTTCTGG	GGCCTGGGCA	1260
20	CGTCGTCTGC	CCCGCTGGGC	GGCGTGGGCG	CGGGAGCCGA	CCCCAGCGAC	CCCCTGGGCC	1320
	TGTACGAGGA	GGAGGGCGCG	GGCTGCTCGC	CCGACGCGCC	CAGCCTGAGC	GGCCGCGAGC	1380
	GCGCGCGCTC	GTCCCGCGCC	GCGGCGCGCT	CGCCCGCGGA	CCACCGCGGC	TACGCCAGCC	1440
	TGCGCGCGCG	CTCGCGCGCC	CCGTCCAGCG	CGCCCTCGCA	CGCGTCTCTC	TCGCGCTCGT	1500
	CCCACTCTCT	CTCTTCTCTC	TCCTCGGGCT	CCTCGTCTCT	CGACGACGAG	TTGGAAGACG	1560
25	ACCTGCTCGA	CCTGAACCCC	AGCTCAAACT	TTGAGAGCAT	GTCCCTGGGC	AGCTTCAGTT	1620
	CGTCGTCTGC	GCTCGACCGG	GACCTGGATT	TTAACTTCGA	GCCCGGCTCC	GGCTCGCACT	1680
	TCGAGTTCCC	GGACTACTGC	ACGCCCAGAG	TGAGCGAGAT	GATCTCGGGA	GACTGGCTCG	1740
	AGTCCAGCAT	CTCCAACCTG	GTTTTCACCT	ACTGAAGGGC	GCGCAGGCAG	GGAGAAGGGC	1800
	CGGGGGGGGT	AGGAGAGGAG	AAAAAAAAGG	TGAAAAAAGG	AAACGAAAAA	GACAGACGAA	1860
30	GAGTTTAAAG	AGAAAAGGGA	AAAAAGAAAG	AAAAAGTAAG	CAGGGCTCGT	TCGCCCCCGT	1920
	TCTCGTCTGC	GGATCAAGGA	GCGCGGCGGC	GTTTGTGACC	CGCGCTCCCA	TCCCCACCT	1980
	TCCCGGGCGG	GGGACCCACT	CTGCCCAGCC	GGAGGGAGCG	GGAGGAGGAA	GAGGGTAGAC	2040
	AGGGCGGAGC	TGTGATTGTT	GTTATTGATG	TTGTTGTGTA	TGGCAAAAAA	AAAAAGCGAC	2100
	TTGAGTTTTC	CTCCCCCTTG	CTTGAAGAGA	CCCCCTCCCC	CTTCCAACGA	GCTTCCGGAC	2160
35	TTGCTCTGAC	CCCCAGCAAG	AAGCGAGTTT	AGTTTTCTAG	AGACTTGAAG	GAGTCTCCCC	2220
	CTTCTCTGAT	CACCACTTTG	GTTTTGTTTC	ATTTTGCTTC	TTGGTCAAGA	AAGGAGGGGA	2280
	GAAACCAAGC	CACCCCTCCC	CCCCCTTTTT	TAAACGCGTG	ATGAAGACAG	AAGGCTCCGG	2340
	GGTGACGAAT	TTGGCCGATG	GCAGATGTTT	TGGGGGAACG	CCGGGACTGA	GAGACTCCAC	2400
40	GCAGGCGAAT	TCCCGTTTGG	GGCCTTTTTT	TCCTCCCTCT	TTTCCCTTGG	CCCCCTCTGC	2460
	AGCCGAGGGA	GGAGATGTTG	AGGGGAGGAG	GCCAGCCAGT	GTGACCGGCG	CTAGGAAATG	2520
	ACCCGAGAAG	CCCGTTGGAA	GCGCAGCAGC	GGGAGCTAGG	GGCGGGGGCG	GAGGAGGACA	2580
	CGAACTGGAA	GGGGGTTTCA	GGTCAAACTG	AAATGGATTT	GCACGTTGGG	GAGCTGGCGG	2640
	CGGCGGCTGC	TGGGCCTCCG	CCTTCTTTTC	TACGTGAAAT	CAGTGAGGTG	AGACTTCCCA	2700
45	GACCCGCGAG	CGGTGGAGGA	GAGGAGACTG	TTTGATGTGG	TACAGGGGGA	GTCAGTGGAG	2760
	GGCGAGTGGT	TTCGGAAAAA	AAAAAAGAAA	AAAAGGG			

Seq ID NO: 363 Protein sequence
Protein Accession #: NP_003098

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50	MVQQTNNAE	TEALLAGESS	DSGAGLELGI	ASSPTPGSTA	STGGKADDP	WCKTPSGHIK	60
	RPNNAFMVWS	QIERRKIMEQ	SPDMHNAEIS	KRLGKRWLK	KDSDKIPFIR	EAERLRLKHM	120
	ADYDQKYRYP	RKKVKSGNAN	SSSSAAASSK	PGEKGDVGG	SGGGHGGGG	GGSSNAGGG	180
55	GGGASGGGAN	SKPAQKKSCG	SKVAGGAGGG	VSKPHAKLIL	AGGGGGGKAA	AAAAAFFAAE	240
	QAGAAALLPL	GAAADHHSLY	KARTPSASAS	ASSAASASAA	LAAPGKHLAE	KKVKRVYLP	300
	GLTSSSPFVG	ATTCAGGTTG	PLGLYEEEGA	GCSFDAPSL	GRSSAASSPA	AGRSPADHRG	360
	YASLRAASPA	PSSAPSHASS	SASSHSSSSS	SSGSSSSDDE	FEDDLLDLNP	SSNFESMSLG	420
	SFSSSSALDR	DLDFNFEPGS	GSHPFEPDYC	TPEVSEMISG	DWLESSISNL	VFTY	

Seq ID NO: 364 DNA sequence
Nucleic Acid Accession #: U10860
Coding sequence: 123-2204

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65	TGCCGGCTGC	TCCTCGACCA	GGCCTCCTTC	TCAACCTCAG	CCCGCGGCGC	CGACCCCTTC	60
	GGCACCCCTC	CGCCCCGTCT	CGTACTGTCT	CCGTCAACGC	CGCGGCTCCG	GCCTTGGCCC	120
	CGATGGCTCT	GTGCAACGGA	GACTCCAAGC	TGGAGAATGC	TGGAGGAGAC	CTTAAGGATG	180
70	GCCACCACCA	CTATGAAGGA	GCTGTTGTCA	TTCTGGATGC	TGGTGCTCAG	TACGGGAAAG	240
	TCATAGACCG	AAGAGTGAGG	GAAGTGTTCG	TGCAGTCTGA	AATTTTCCCC	TTGGAAACAC	300
	CAGCATTTGC	TATAAAGGAA	CAAGGATTCC	GTGCTATTAT	CATCTCTGGA	GGACCTAATT	360
	CTGTGTATGC	TGAAGATGCT	CCCTGGTTTG	ATCCAGCAAT	ATTCACTATT	GGCAAGCCTG	420
75	TTCTTGAAT	TTGCTATGGT	ATGCAGATGA	TGAATAAGGT	ATTGGAGGT	ACTGTGCACA	480
	AAAAAAGTGT	CAGAGAAGAT	GGAGTTTTC	ACATTAGTGT	GGATAATACA	TGTTTATTAT	540
	TCAGGGGCGC	TCAGAAAGGA	GAAAGTGTTC	TGCTTACACA	TGGAGATAGT	GTAGACAAAG	600
	TAGCTGATGG	ATTCAAGGTT	GTGGCAGGTT	CTGGAACAT	AGTAGCAGGC	ATAGCAAATG	660
	AATCTAAAAA	GTTATATGGA	GCACAGTTCC	ACCCTGAAGT	TGGCCTTACA	GAAATGGAA	720
	AAGTAATACT	GAAGAATTTT	CTTTATGATA	TAGCTGGATG	CAGTGGAAAC	TTACCCGTGC	780
80	AGAACAGAGA	ACTTGAGTGT	ATTGAGAGAG	TCAAAGAGAG	AGTAGGCACG	TCAAAAGTTT	840
	TGGTTTTACT	CAGTGGTGGG	GTAGACTCAA	CAGTTTGTAC	AGCTTTGCTA	AATCGTGCTT	900
	TGAACCAAGA	ACAAGTCATT	GCTGTGCACA	TTGATAATGG	CTTTATGAGA	AAACGAGAAA	960
	GCCAGTCTGT	TGAAGAGGCC	CTCAAAAGC	TTGGAATTCA	GGTCAAAGTG	ATAAATGCTG	1020
85	CTCATTCTTT	CTACAAATGA	ACAACAACCC	TACCAATATC	AGATGAAGAT	AGAACCCAC	1080
	GGAAAAGAA	TAGCAAAACG	TTAAATATGA	CCCAAGTCC	TGAAGAGAAA	AGAAAAATCA	1140
	TTGGGGATAC	TTTTGTTAAG	ATTGCCAATG	AAGTAATTGG	AGAAATGAAC	TTGAAACCCG	1200
	AGGAGGTTTT	CCTTGCCCAA	GGTACTTTAC	GGCCTGATCT	AATTGAAAGT	GCATCCCTTG	1260

TTGCAAGTGG CAAAGCTGAA CTCATCAAAA CCCATCAGAG CTCATCAGAA 1320
 AGTTGAGAGA GGAGGGAAAA GTAATAGAAC CTCTGAAAGA TTTTCATAAA GATGAAGTGA 1380
 GAATTTTGGG CAGAGAACTT GGACTTCCAG AAGAGTTAGT TTCCAGGCAT CCATTTCCAG 1440
 5 GTCTCTGGCCT GGCATACAGA GTAATATGTG CTGAAGAACC TTATATTGT AAGGACTTTC 1500
 CTGAAACCAA CAATATTTTG AAAATAGTAG CTGATTTTTC TGCAAGTGTT AAAAGCCAC 1560
 ATACCCCTATT ACAGAGAGTC AAAGCCTGCA CAACAGAAGA GGATCAGGAG AAGCTGATGC 1620
 AAATACACAG TCTGCATTCA CTGAATGCCT TCTTGCTGCC AATTAAAACT GTAGGTGTGC 1680
 10 AGGGTGACTG TCGTTCCCTAC AGTTACGTGT GTGGAATCTC CAGTAAAGAT GAACCTGACT 1740
 GGGAACTACT TATTTTCTG GCTAGGCTTA TACCTCGCAT GTGTCAACAC GTTAACAGAG 1800
 TTGTTTATAT ATTTGGCCCA CCAGTTAAAG AACCTCTTAC AGATGTTACT CCCACTTTCT 1860
 TGACAACAGG GGTGCTCAGT ACTTTACGCC AAGCTGATTT TGAGGCCCAT AACATTCTCA 1920
 GGGAGTCTGG GTATGCTGGG AAAATCAGCC AGATGCCGGT GATTTTGACA CCATTACATT 1980
 15 TTGATCGGGA CCCACTCAA AAGCAGCCTT CATGCCAGAG ATCTGTGGTT ATTCGAACCT 2040
 TTATTACTAG TGACTTCATG ACTGGTATAC CTGCAACACC TGGCAATGAG ATCCCTGTAG 2100
 AGGTGGTATT AAAAGTGGTC ACTGAGATTA AGAAGATTCC TGGTATTCT CGAATTATGT 2160
 ATGACTTAAC ATCAAAGCCC CCAGGAACCTA CTGAGTGGGA GTAATAAACT TC

Seq ID NO: 365 Protein sequence
 Protein Accession #: AAA60331

1 11 21 31 41 51
 MALCNGDSKL ENAGGDLKDG HHHYEGAVVI LDAGAQYGVK IDRRVRELFV QSEIFPLETP 60
 25 AFAIKEQGFR AIIISGGPNS VYAEADPWFD PAIFTIGKPV LGICYGMQMM NKVFGGTVHK 120
 KSVREDGVFN ISVDNTCSLF RGLQKEEVVL LTHGSDVDKV ADGFKVVARV GNIVAGIANE 180
 SKKLYGAQFH PEVLGTENGK VILKNFLYDI AGCSGTFTVQ NRELECI REI KERVGTSKVL 240
 VLLSGGVDST VCTALLNRAL NQEQVIAVHI DNGFMRKRES QSVEEALKKL GIQVKVINAA 300
 HSFYNGTTTL PISDEDRTPR KRISKTLNMT TSPEKRII GDTFVKIANE VIGEMNLKPE 360
 30 EVFLAQGTLR PDLIESASLV ASGKAELIKT HHNDTELIRK LREEGKVIEP LKDFHKDEVR 420
 ILGRELGLEPE ELVSRHPPFG PGLAIRVICA EEPYICKDFP ETNNILKIVA DFSASVKKPH 480
 TLLQRVKACT TEEDEKLMQ ITSLSHSLNLF LLPIKTVGVQ GDCRSYSYVC GISSKDEPDW 540
 BSLIFLARLI PRMCHNVNRV VYIFGPPVKE PPTDVTPTFL TTGVLSTLRQ ADFAHNILR 600
 35 ESGYAGKISQ MPVILTPLEH DRDPLQKQPS QRSVVIRTF ITSDFMTGIP ATPGNEIPVE 660
 VVLKNVTEIK KIPGISRMY DLTSKPPGTT EWE

Seq ID NO: 366 DNA sequence
 Nucleic Acid Accession #: NM_004219
 Coding sequence: 46-654

1 11 21 31 41 51
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 45 TATGTTGATA AGGAAAAATGG AGAACCCAGC ACCCGTGTGG TTGCTAAGGA TGGGCTGAAG 120
 CTGGGGTCTG GACCTTCAAT CAAAGCCTTA GATGGGAGAT CTCAGTTTC AACACCACT 180
 TTTGGCAAAA CGTTCGATGC CCCACCAGCC TTACCTAAAG CTACTAGAAA GGCTTTGGGA 240
 ACTGTCAACA GAGCTACAGA AAAGTCTGTA AAGACCAAGG GACCCCTCAA AAAAAACAG 300
 CCAAGCTTTT CTGCCAAAAA GATGACTGAG AAGACTGTTA AAGCAAAAAG CTCTGTTTCT 360
 50 GCCTCAGATG ATGCCTATCC AGAAATAGAA AAATCTTTC CCTTCAATCC TCTAGACTTT 420
 GAGAGTTTTG ACCTGCCTGA AGAGCACCAG ATTGCGCACC TCCCCTTGAG TGGAGTGCCT 480
 CTCATGATCC TTGACGAGGA GAGAGAGCTT GAAAAGCTGT TTCAGCTGGG CCCCCTTCA 540
 CCTGTGAAGA TGCCCTCTCC ACCATGGGAA TCCAATCTGT TGCAGTCTCC TTCAGCATT 600
 CTGTGCAACC TGGATGTTGA ATTGCCACCT GTTTGCTGTG ACATAGATAT TTAATTTCT 660
 55 TAGTGCTTCA GAGTTTGTGT GTATTGTGAT TAATAAGCA TTCTTCAACA GAAAAAATA 720
 AAAAAA

Seq ID NO: 367 Protein sequence
 Protein Accession #: NP_004210

1 11 21 31 41 51
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 65 RKALGTVNRA TEKSVKTKGP LKQKQPSFSA KKMTEKTVKA KSSVPASDDA YPEIEKFFPF 120
 NPLDFESFDL PEEHQIAHLP LSGVPLMILD EERELEKLFQ LGPPSPVKMP SPPWESNLLQ 180
 SPSSILSTLD VELPPVCCDI DI

Seq ID NO: 368 DNA sequence
 Nucleic Acid Accession #: NM_000597
 Coding sequence: 118-1104

1 11 21 31 41 51
 75 ATTCGGGGCG AGGGAGGAGG AAGAAGCGGA GGAGGCGGCT CCCGCTCGCA GGGCGGTGCA 60
 CCGCCCGGCC CGCCGCTCGC CTCGCTCGCC CGCCGCGCCG CGCTGCCGAC CGCCAGCATG 120
 CTGCGGAGAG TGGGCTGCCG CGCGCTGCCG CTGCGCGCCG CGCCGCTGCT GCCGCTGCTG 180
 CGCGTGTCTG TGCTGCTACT GGGCGCGAGT GCGGCGGCGG GCGGGGCGCG CGCGGAGGTG 240
 CTGTTCCGCT GCCCGCCCTG CACACCCGAG CGCCTGGCCG CCTGCGGGCC CCCGCGGTT 300
 80 GCGCCGCGCC CGCGGCTGCG CGCAGTGGCC GGAGGCGCCC GCATGCCATG CGCGGAGCTC 360
 GTCCGGGAGC CGGGCTGCGG CTGCTGCTCG GTGTGCGCCC GGCTGGAGGG CGAGGCGTGC 420
 GCGGTCTACA CCCCAGCTG GCGCCAGGGG CTGCGCTGCT ATCCCCACCC GGGCTCCGAG 480
 CTGCCCCCTG AGCGCTGTGT CATGGGCGAG GGCATTGTG AGAAGCGCCG GGACGCGAG 540
 TATGCGCCCA GCGCGGAGCA GGTTCAGAC AATGGCGATG ACCACTCAGA AGGAGGCTG 600
 GTGGAGAAC AGTGGACAT CACCATGAAC ATGTTGGGCG GGGGAGGAGG TGCTGGCCGG 660
 85 AAGCCCTCA AGTCCGGTAT GAAGGAGCTG GCCGTGTTCC GGGAGAAGGT CACTGAGCAG 720
 CACCGGCAGA TGGGCAAGGG TGGCAAGCAT CACCTTGGCC TGGAGGAGCC CAAGAAGCTG 780
 CGACCACCCC CTGCCAGGAC TCCCTGCCAA CAGGAAGTGG ACCAGGTCCT GGAGCGGATC 840

5
10

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TCCACCATGC GCCTTCGCGA TGAGCGGGGC CCTCTGGAGC ACCTCTACTC CCTGCACATC 900
CCCAACTGTG ACAAGCATGG CCTGTACAAC CTCAAACAGT GCAAGATGTC TCTGAACGGG 960
CAGCGTGGGG AGTGCTGGTG TGTGAACCCC AACACCGGGA AGCTGATCCA GGGAGCCCCC 1020
ACCATCCGGG GGGACCCCGA GTGTCACTCT TTCTACAATG AGCAGCAGGA GGGTTGCGGG 1080
GTGCACACCC AGCGGATGCA GTAGACGCGA GCCAGCCGGT GCCTGGCGCC CCTGCCCCCC 1140
GCCCTCTCC AAACACCGGC AGAAAACGGA GAGTGTCTGG GTGGTGGGTG CTGGAGGATT 1200
TTCCAGTTCT GACACACGTA TTTATATTGG GAAAGAGACC AGCACCGAGC TCGGCACCTC 1260
CCCGCCCTCT CTCTTCCAG CTGCAGATGC CACACCTGCT CCTTCTTGCT TTCCCGGGG 1320
GAGGAAGGGG GTTGTGTCG GGGAGCTGGG GTACAGGTTT GGGGAGGGGG AAGAGAAATT 1380
TTTATTTTGG AACCCCTGTG TCCCTTTTGC ATAAGATTAA AGGAAGGAAA AGT

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Seq ID NO: 369 Protein sequence
Protein Accession #: NP_000588

15
20

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1      11      21      31      41      51
|      |      |      |      |      |
MLPRVGCPL PLPPPLLLPL LPLLLLLLGA SGGGGGARAE VLFRCPPCTP ERLAACGPPP 60
VAPPAVAAV AGGARMPCAE LVREPGCGCC SVCARLEGEA CGVYTPRCGQ GLRCYPHPGS 120
ELPLQALVMG EGTCEKRRDA EYGASPEQVA DNGDDHSEGG LVENHVDSTM NMLGGGGSAG 180
RKPLKSGMKE LAVFREKVTE QHRQMGKGGK HHLGLEBPKK LRPPPARTPC QQELDQVLER 240
ISTMRLPDER GPLEHLYSLH IPNCDKHGLY NLKQCKMSLN GQRGECNCVN PNTGKLIQGA 300
PTIRGDPECH LFNQEQQEAC GVHTQRMQ

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25
Seq ID NO: 370 DNA sequence
Nucleic Acid Accession #: NM_004264
Coding sequence: 6-440

30
35
40

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1      11      21      31      41      51
|      |      |      |      |      |
GGAACATGGC GGATCGGCTC ACGCAGCTTC AGGACGCTGT GAATTCGCTT GCAGATCAGT 60
TTTGTAATGC CATTGGAGTA TTGCAGCAAT GTGGTCCTCC TGCCTCTTTC AATAATATTC 120
AGACAGCAAT TAACAAAGAC CAGCCAGCTA ACCCTACAGA AGAGTATGCC CAGCTTTTTG 180
CAGCACTGAT TGCACGAACA GCAAAAGACA TTGATGTTTT GATAGATTCC TTACCCAGTG 240
AAGATCTAC AGTCTCTTTA CAGGCTGCTA GCTTGTATAA GCTAGAAGAA AAAAACCATG 300
AAGCTGCTAC ATGTGTGGAG GATGTTGTTT ATCGAGGAGA CATGCTTCTG GAGAAGATAC 360
AAAGCGCACT TGCTGATATT GCACAGTCAC AGCTGAAGAC AAGAAGTGGT ACCCATAGCC 420
AGTCTCTTCC AGACTCATAG CATCAGTGGG TACCATGTGG CTGAGAAAAG AACTGTTTGA 480
GTGCCATTAA GAATCTGCA TCAGACTTAG ATACAAGCCT TACCAACAAT TACAGAAACA 540
TTAAACACTA TGACACATTA CCTTTTAGC TATTTTAAAT AGTCTTCTAT TTCACTCTT 600
GATAAGCTTA TAAATCATGA TTGAATCAGC TTTAAAGCAT CATACCATCA TTTTTTAACT 660
GAGTGAAATT ATTAAGGCAT GTAATACATT AATGAACATA ATATAAGGAA ACATATGTAA 720
AATTCTGTTA TGACATAATT TATGTCTCCA TTTGTTGTA TTGCCAGTA CTTTACAAT 780
C

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45
Seq ID NO: 371 Protein sequence
Protein Accession #: NP_004255

50

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1      11      21      31      41      51
|      |      |      |      |      |
MADRLTLQLD AVNSLADQFC NAIGVLQCGG PPASFNNIQT AINKDQPANP TEEYAQLFAA 60
LIARTAKDID VLIDSLPSEE STAALQAASL YKLEENHEA ATCVEDVVYR GDMLEKIQS 120
ALADIAQSQL KTRSGTHSQS LPDS

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55
Seq ID NO: 372 DNA sequence
Nucleic Acid Accession #: AJ271091
Coding sequence: 1-1113

60
65
70
75

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1      11      21      31      41      51
|      |      |      |      |      |
ATGGAGAATC AGGTGTTGAC GCCGCATGTC TACTGGGCTC AGCGACACCG CGAGCTATAT 60
CTGCGCGTGG AGCTGAGTGA CGTACAGAAC CCTGCCATCA GCATCACTGA AAACGTGCTG 120
CATTTCAAAG CTCAGGACA TGGTGCCAAA GGAGACAATG TCTATGAATT TCACCTGGAG 180
TTCTTAGACA TTGTGAAACC AGAGCCTGTT TACAACTGA CCCAGAGGCA GGTAAACATT 240
ACAGTACAGA AGAAAGTGAG TCAGTGGTGG GAGAGACTCA CAAAGCAGGA AAAGCGACCA 300
CTGTTTTTGG CTCTGACTT TGATCGTTGG CTGGATGAAT CTGATGCGGA AATGGAGCTC 360
AGAGCTAAGG AAGAAGAGCG CCTAAATAAA CTCCGACTGG AAAGCGAAGG CTCTCCTGAA 420
ACTCTTACAA ACTTAAGGAA AGGATACCTG TTTATGTATA ATCTTGTGCA ATTCTTGGGA 480
TTCTCCTGGA TCTTTGTCAA CCTGACTGTG CGATTCTGTA TCTTGGGAAA AGAGTCCCTT 540
TATGACACAT TCCATACTGT GGCTGACATG ATGTATTCTT GCCAGATGCT GGCAGTTGTG 600
GAAACTATCA ATGCAGCAAT TGGAGTCACT ACGTCACCGG TGCTGCCTTC TCTGATCCAG 660
CTTCTTGGA GAAATTTTAT TTTGTTTATC ATCTTTGGCA CCATGGAAGA AATGCAGAAC 720
AAAGCTGTGG TTTTCTTTGT GTTTTATTTG TGGAGTGCAA TTGAAATTTT CAGGTACTCT 780
TTCTACATGC TGACGTGCAT TGACATGGAT TGGAAAGTGC TCACATGGCT TCGTTACACT 840
CTGTGGATTG CCTTATATCC ACTGGGATGT TTGGCGGAAG CTGTCTCAGT GATTCACTCC 900
ATTCCAATAT TCAATGAGAC CGGACGATTC AGTTTCACAT TGCCATATCC AGTGAAAATC 960
AAAGTTAGAT TTTCTTTTTT TCTTCAGATT TATCTTATAA TGATATTTTT AGGTTTATAC 1020
ATAAATTTTC GTCACTTTTA TAAACAGCGC AGACTGAAAA TGAGGGCAGG CGCAGTGGCT 1080
CATGCCTGTG ATCCACGCGC TTTGGGAGGC TGA

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80
Seq ID NO: 373 Protein sequence
Protein Accession #: CAB69070

85

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1      11      21      31      41      51
|      |      |      |      |      |
MENQVLTPHV YWAQRHRELY LRVELSDVQN PAISITENVL HFKAQGHGAK GDNVYEFHLE 60
FLDLVKPEPV YKLTRQVNI TVQKVSQWW ERLTKQEKRP LFLAPDFDRW LDESDAEMEL 120
RAKEERLNK LRLSEGSPE TLNLRKGYL FMYNLVQFLG FSWIFVNLTV RFCILGKESF 180

```

YDTFHTVADM MYFCQMLAVV ETINAAIGVT TSPVLPSLIQ LLGRNFILFI IFGTMEEMQN 240
KAVVFFVFYL WSAIEIFRYS FYMLTICIDMD WKVLTWLRYT LWIPLYPLGC LAEAVSVIQS 300
IPIFNETGRF SFTLPYPVKI KVRFSFFLQI YLIMIFLGLY INFRHLYKQR RLKMRAGAVA 360
HACDPSALGG

Seq ID NO: 374 DNA sequence
Nucleic Acid Accession #: NM_016395
Coding sequence: 1-1113

1 11 21 31 41 51
| | | | | |
ATGGAGAATC AGGTGTTGAC GCCGCATGTC TACTGGGCTC AGCGACACCG CGAGCTATAT 60
CTGCGCGTGG AGCTGAGTGA CGTACAGAAC CCTGCCATCA GCATCACTGA AACCTGCTG 120
CATTTCAAAG CTCACAGACA TGGTGCCAAA GGAGACAATG TCTATGAATT TCACCTGGAG 180
TTCTTAGACC TTGTGAAACC AGAGCCTGTT TACAAACTGA CCCAGAGGCA GGTAACATT 240
ACAGTACAGA AGAAGGTGAG TCAGTGGTGG GAGAGACTCA CAAAGCAGGA AAAGCGACCA 300
CTGTTTTTGG CTCCTGACTT TGAATCGTTG CTGGATGAAT CTGATGCGGA AATGGAGCTC 360
AGAGCTAAGG AAGAAGAGCG CCTAAATAAA CTCCGACTGG AAAGCGAAGG CTCTCCTGAA 420
ACTCTTACAA ACTTAAGGAA AGGATACCTG TTTATGTATA ATCTTGTGCA ATTCTTGGGA 480
TTCTCCTGGA TCTTTGTCAA CCTGACTGTG CGATTCTGTA TCTTGGGAAA AGAGTCCTTT 540
TATGACACAT TCCATACTGT GGCTGACATG ATGTATTTCT GCCAGATGCT GGCAGTTGTG 600
GAAACTATCA ATGACAGCAAT TGGAGTCACT ACGTCACCGG TGCTGCCTTC TCTGATCCAG 660
CTTCTTGGAA GAAATTTTAT TTTGTTTATC ATCTTTGGCA CCATGGAAGA AATGCAGAAC 720
AAAGCTGTGG TTTTCTTTGT GTTTTATTTG TGGAGTGCAA TTGAAATTTT CAGGTACTCT 780
TTCTACATGC TGACGTGCAT TGACATGGAT TGGAGGTGCT TCACATGGCT TCGTTACACT 840
CTGTGGATTC CCTTATATCC ACTGGGATGT TTGGCGGAAG CTGTCTCAGT GATTCACTCC 900
ATTCCAATAT TCAATGAGAC CGGACGATTC AGTTTCACAT TGCCATATCC AGTGAAAATC 960
AAAGTTAGAT TTTCTTTTAT TCTTCAGATT TATCTTATAA TGATATTTT AGGTTTATAC 1020
ATAAATTTTC GTACCTTTTA TAAACAGCGC AGACTGAAAA TGAGGGCAGG CGCAGTGGCT 1080
CATGCCTGTG ATCCACGCGC TTTGGGAGGC TGA

Seq ID NO: 375 Protein sequence
Protein Accession #: NP_057479

1 11 21 31 41 51
| | | | | |
MENQVLTPHV YWAQRHRELY LRVELSDVQN PAISITENVL HFKAQGHGAK GDNVVEPHLE 60
FLDLVKPEPV YKLTQRQVNI TVQKKVSQWW ERLTKQEKRP LFLAPDFDRW LDESDAEMEL 120
RAKEEERLNK LRLESEGSPE TLTNLRKGYL FMYNLVQFLG FSWIFVNLTV RFCILKESF 180
YDTFHTVADM MYFCQMLAVV ETINAAIGVT TSPVLPSLIQ LLGRNFILFI IFGTMEEMQN 240
KAVVFFVFYL WSAIEIFRYS FYMLTICIDMD WKVLTWLRYT LWIPLYPLGC LVEAVSVIQS 300
IPIFNETGRF SFTLPYPVKI KVRFSFFLQI YLIMIFLGLY INFRHLYKQR RRRYGGKKRK 360
STKKKDLDFG LPV

Seq ID NO: 376 DNA sequence
Nucleic Acid Accession #: NM_005987
Coding sequence: 1-270

1 11 21 31 41 51
| | | | | |
ATGAATTCCTC AGCAGCAGAA GCAGCCTTGC ACCCCACCCC CTCAGCCTCA GCAGCAGCAG 60
GTGAAACAAC CTTGCCAGCC TCCACCCAG GAACCATGCA TCCCCAAAC CAAGGAGCCC 120
TGCCAACCCA AGGTGCCTGA GCCCTGCCAC CCCAAAGTGC CTGAGCCCTG CCAGCCCAAG 180
ATTCAGAGC CCGCCAGGCC CAAGGTGCCT GAGCCCTGCC CTTCAACGGT CACTCCAGCA 240
CCAGCCAGC AGAAGACCAA GCAGAAGTAA

Seq ID NO: 377 Protein sequence
Protein Accession #: NP_005978

1 11 21 31 41 51
| | | | | |
MNSQQQKQPC TPPPQPPQQQ VKQPCQPPFQ EPCIPKTKEP CQPKVPEPCH PKVPEPCQPK 60
IPEPCQPKVP EPCPSTVTPA PAQQTQKQK

Seq ID NO: 378 DNA sequence
Nucleic Acid Accession #: NM_002105
Coding sequence: 74-505

1 11 21 31 41 51
| | | | | |
ACAGCAGTTA CACTGCGGCG GCGCTCTGTT CTAGTGTTTG AGCCGTCGTG CTTACCCGGT 60
CTACCTCGCT AGCATGTGCG GCCGCGGCAA GACTGGCGGC AAGGCCCGCG CCAAGGCCAA 120
GTCGCGCTCG TCGCGCGCGG GCCTCCAGTT CCCAGTGGGC CGTGACACC GGCTGCTGCG 180
GAAGGGCCAC TACGCCGAGC GCGTTGGCGC CGGCGCGCCA GTGTACCTGG CGGCAGTGCT 240
GGAGTACCTC ACCGCTGAGA TCCTGGAGCT GGCGGCAAT GCGGCCCGCG ACAACAAGAA 300
GACGCGAATC ATCCCCCGCC ACCTGCAGCT GGCCATCCGC AACGACGAGG AGCTCAACAA 360
GCTGCTGGGC GCGCTGACGA TCGCCAGGG AGGCGTCCTG CCCAACATCC AGGCCGTGCT 420
GCTGCCAAG AAGACCAGCG CCACCGTGGG GCCGAAGCG CCCTCGGGCG GCAAGAAGGC 480
CAGCCAGGCC TCCAGGAGT ACTAAGAGGG CCCGCGCGCG GCGCGCGCGC CCCAGCTCCC 540
CATGCCACCA CAAAGGCCCT TTTAAGGGCC ACCACGCGCC TCATGGAAGG AGCTGAGCCG 600
CTTCAGACTG CGGGCAAGC GGGCGCGCGC TCCCTTCCCC TCCCCCTCCC TCGCCCGCCT 660
TCGCGCGCGG GCGTGCAGTC CCGCCCGGCC CCGCTTCCCG TCCCGCACCG CCGTCCCGCT 720
CGGCCTCGGG CCTGCCTGT CCGCCGTCCG CCCTCCGGTA GGGTTCGGGC CTTCCGGATG 780
CGCTTGGGC GCTCTTCGGG GACCTCCGTG GCGCGGAAGA CCGGAGCCTG CCGGGGGGAG 840

GCCGGCGGCG CCGCACCTGC CCGCCTCGGC GTTCGTGACT CAGCCGCCCC ATCCCGAGTC 900
 GCTAAGGGGC TGGCGGGAGG CCGCAGCACC TTCTGGAAGA CTTGGCCTTC CGCTCTGACG 960
 CAGGGCCGAG GTGGGCGACT CAGGCGGAGA GCCGGCGGCC CTGAAGGTGA GTGAGGCCCT 1020
 CGGCAGCTGC AGCCGGGGTG TCTGGTACCC CCCCAGCGTG GTGCTTAGCC CAGGACTTTC 1080
 AGACGGCCGC TGGCCGGGAG GCTTTGGTGG GAGAGACGCG ATCGCCGATT TCGGTCTGGC 1140
 GCCCCTTCTG CCGCCGGGAC CCAGGCCTTT CACATCAGCT CTCCCTCCAT CTTCATTTCAT 1200
 AGGTCTGCGC TGGGGCCGGG ACGAAGCACT TGGTAACAGG CACATCTTCC TCCCGAGTGA 1260
 CTGCCTCCTA GGAGGACAT TTAGGGGAGG CAGAGGCCTG CAGTTTGGCT TCACGGCTGG 1320
 CTATGTGGAC AGCAAGAGTC GTTTTGCGGA ACGCGACTGG CAGCCAGGCC TGTGCGGCC 1380
 CCGACGCCGC CCCATTTCCT TTCCAGCAA CTCAACTCGG CAATCCAAGC ACCTAGATAC 1440
 CAGCACAACT CGTTAATCC CTGTCTGGAC TGAGCCTCCG TTGGCTTCTG AACTGGAATT 1500
 CTGCAGCTAA CCCTTCCACG ACTAGAACCT TAGGCATTGG GGAGTTTATG ATGGACTAAT 1560
 TTTATTAAAG GATTGTTTTT TTTT

Seq ID NO: 379 Protein sequence
 Protein Accession #: NP_002096

1 11 21 31 41 51
 | | | | | |
 MSGRGKTGGK ARAKAKSRSS RAGLQFPVGR VHRLLRKHY AERVGAGAPV YLAADVLEYLT 60
 AEILELAGNA ARDNKKTRII PRHLQLAIRN DEELNKLGG VTIAQGGVLP NIQAVLLPKK 120
 TSATVGPAPK SGGKKATQAS QEY

Seq ID NO: 380 DNA sequence
 Nucleic Acid Accession #: AL136942
 Coding sequence: 184-864

1 11 21 31 41 51
 | | | | | |
 ACGCGTCCCG CAGAAGCTCG GAGCTCTCGG GGTATCGAGG AGGCAGGCC GCGGGCGCAC 60
 GGGCGAGCGG CCGGGGAGCC GGAGCGCGCG AGGAGCCGCG AGCAGCGGCG CCGCGGGCTC 120
 CAGGCGAGGC GGTGACGCT CCGTAAACT TGCGCGCGCG CTCGCGCCAC TCGCGCCGGA 180
 GCGATGAAGA TGGTCGCGCC CTGGACGCGG TTCTACTCCA ACAGCTGCTG CTTGTGCTGC 240
 CATGTCCGCA CCGGACCAT CCGTCTCGG GTCTGGTATC TGATCATCAA TGCTGTGGTA 300
 CTGTGATTTT TATTGAGTGC CCGGCTGAT CCGGATCAGT ATAACTTTTC AAGTTCTGAA 360
 CTGGGAGGTG ACTTTGAGTG CATGGATGAT GCCAACATGT GCATTGCCAT TCGGATTTC 420
 CTTCTCATGA TCCTGATATG TGCTATGGCT ACTTACGGAG CGTACAAGCA ACGCGCAGCC 480
 TGGATCATCC CATCTTCTCG TTACCAGATC TTTGACTTTG CCTGAACAT GTTGGTTGCA 540
 ATCACTGTGC TTATTTATCC AAATCCATT CAGGAATACA TACGGCAACT GCCTCCTAAT 600
 TTTCCCTACA GAGATGATGT CATGTCAAGT AATCCTACCT GTTTGGTCTT TATTATCTT 660
 CTGTTTATTA GCATTATCTT GACTTTTAA GGTACTTGA TTAGCTGTGT TTGAACTGC 720
 TACCGATACA TCAATGTAG GAATCCTCT GATGTCCTGG TTTATGTTAC CAGCAATGAC 780
 ACTACGGTGC TGCTACCCCG GTATGATGAT GCCACTGTGA ATGGTGTGCG CAAGGAGCCA 840
 CCGCCACCTT ACGTGTCTGC CTAAGCCTTC AAGTGGGCGG AGCTGAGGGC AGCAGCTTGA 900
 CTTTGCAGAC ATCTGAGCAA TAGTCTGTGT ATTTCACTTT TGCCATGAGC CTCTCTGAGC 960
 TTGTTTGTGG CTGAAATGCT ACTTTTAAA ATTTAGATGT TAGATTGAAA ACTGTAGTTT 1020
 TCAACATATG CTTTGTCTGA ACATGTGAT AGATTAACTG TAGAATTCCT CCGTACGAT 1080
 TGGGATATA ACGGCTTCA CTAACCTTCC CTAGGCATTG AAATCTCCCC CAAATCTGAT 1140
 GGACCTAGAA GTCTGCTTTT GTACCTGCTG GGGCCCAAAG TTGGGCATT TTTCTCTGT 1200
 TCCCTCTCTT TTGAAATGT AAAATAAAAC CAAAAATAGA CAATTTTTC TTCAGCCATT 1260
 CAGCATAGA GAACAAACCT TTATGGAAC AGGAATGTCA ATTTGTGAAT CATTTGTTCTA 1320
 ATTAGGTAAA TAGAAGTCTT TAGTATGTG TTACAAGAA TTCCCCCACA ACATCCTTTA 1380
 TGAAGTAAAG TCAATGACAG TTTGTGTTG GTGGTAAAG ATTTCTCTCA TGGCTGAAT 1440
 TAAGACCAT AGAAAGCACC AGGCGGTGG AGCAGTGACC ATCTACTGAC TGTCTTGTG 1500
 GATCTTGTGT CAGGGGACAT GGGGTGACAT GCCTCGTATG TGTAGAGGG TGAATGGAT 1560
 GTGTTGGCG CTGCATGGGA TCTGGTCCCC CTCTCTCTCT GGATTCACAT CCCCACCCAG 1620
 GGCCCGCTTT TACTAAGTGT TCTGCCCTAG ATTTGGTTCAA GGAGGTCATC CAACTGACTT 1680
 TATCAAGTGG AATTGGGATA TATTGTATAT ACTTCTGCCT AACAACATGG AAAAGGGTTT 1740
 TCTTTTCCCT CCAAGTACA TCCTACTGCT TTGAACCTCC AAGTATGTCT AGTCACTTT 1800
 TAAATGTAA ACATTTTTCAG AAAATGAGG ATTGCCTTCC TTGTATGCGC TTTTACCTT 1860
 GACTACCTGA ATTGCAAGGG ATTTTATAT ATTCATATGT TACAAAGTCA GCACTCTCC 1920
 TGTGGTTCA TTATTGAATG TGCTGTAAT TAAGTCGTTT GCAATTAATA CAAGGTTTGC 1980
 CCACATCCAA AAAAAAATA AAAAA

Seq ID NO: 381 Protein sequence
 Protein Accession #: CAB66876

1 11 21 31 41 51
 | | | | | |
 MKMVPWTRF YSNSCLCCH VRTGTILLGV WYLIINAVVL LILLSALADP DQYNFSSSEL 60
 GGDFEFMDDA NMCIAIAISL LMILICAMAT YGAYKQRAAW IIPFFCYQIF DFALNMLVAI 120
 TVLIYPNSIQ EYIRQLPPNF PYRDDVMSVN PTCLVLIILL FISIIILTFKG YLISCVWNCY 180
 RYINGRNSSD VLVVYISNDT TVLLPPYDDA TVNGAAKEPP PPVYSA

Seq ID NO: 382 DNA sequence
 Nucleic Acid Accession #: NM_002510
 Coding sequence: 92-1774

1 11 21 31 41 51
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 CAGATGCCAG AAGAACAACCT TTGCTCTTGG TGGACGGGCC CAGAGGAATT CAGAGTTAAA 60
 CCTTGAGTGC CTGCGTCCGT GAGAATTCAG CATGGAATGT CTCTACTATT TCCTGGGATT 120
 TCTGCTCTG CTTGCAAGAT TGCCACTTGA TGCCGCCAAA CGATTTTCATG ATGTGCTGGG 180
 CAATGAAAGA GCTTCTGCTT ACATGAGGGA GCACAATCAA TTAAATGGCT GGTCTTCTGA 240
 TGAATGAC TGAATGAAA AACTCTACCC AGTGTGGAAG CGGGAGACA TGAGGTGGAA 300
 AAATCTCTGG AAGGAGGCC GTGTGCAGGC GGTCTGACC AGTGACTCAC CAGCCCTCGT 360

	GGGCTCAAAAT	ATAACATTTTG	CGGTGAACCT	GATATTCCCT	AGATGCCAAA	AGGAAGATGC	420
	CAATGGCAAC	ATAGTCTATG	AGAAGAACTG	CAGAAATGAG	GCTGGTTTAT	CTGCTGATCC	480
	ATATGTTTAC	AACCTGGACAG	CATGGTCAGA	GGACAGTGAC	GGGGAAAAATG	GCACCGGCCA	540
	AAGCCATCAT	AACGCTCTTCC	CTGATGGGAA	ACCTTTTTCCT	CACCACCCCG	GATGGAGAAG	600
5	ATGGAATTTT	ATCTACGTCT	TCCACACACT	TGGTCAGTAT	TTCAGAAAT	TGGGACGATG	660
	TTCAGTGAGA	GTTTCTGTGA	ACACAGCCAA	TGTGACACTT	GGGCCCTCAAC	TCATGGAAGT	720
	GACTGTCTAC	AGAAGACATG	GACGGGCATA	TGTTCCCATC	GCACAAGTGA	AAGATGTGTA	780
	CGTGGTAACA	GATCAGATTTC	CTGTGTTTGT	GACTATGTTC	CAGAAGAAACG	ATCGAAATTC	840
10	ATCCGACGAA	ACCTTCTCTCA	AAGATCTCCC	CATTATGTTT	GATGTCTCTGA	TTCATGATCC	900
	TAGCCACTTC	CTCAATTATT	CTACCATTAA	CTACAAGTGG	AGCTTCGGGG	ATAATACTGG	960
	CCTGTTTGT	TCCACCAATC	ATACTGTGAA	TCACACGTAT	GTGCTCAATG	GAACCTTCAG	1020
	CCTTAACCTC	ATGTGAAAG	CTGCAGCACC	AGGACCTTGT	CCGCCACCCG	CACCACCACC	1080
	CAGACCTTCA	AAACCCACCC	CTTCTTTAGG	ACCTGCTGGT	GACAACCCCG	TGGAGCTGAG	1140
15	TAGGATTCTC	GATGAAACT	GCCAGATTAA	CAGATATGGC	CACCTTCAAG	CCACCATCAC	1200
	AATTGTAGAG	GGAATCTTAG	AGGTTAACAT	CATCCAGATG	ACAGACGTCC	TGATGCCGGT	1260
	GCCATGGCCT	GAAAGCTCCC	TAATAGACTT	TGTCGTGACC	TGCCAAGGGA	GCATTCCAC	1320
	GGAGGTCTGT	ACCATCATTT	CTGACCCAC	CTGCGAGATC	ACCCAGAACA	CAGTCTGCAG	1380
	CCCTGTGGAT	GTGGATGAGA	TGTGTCTGCT	GACTGTGAGA	CGAACCTTCA	ATGGGTCTGG	1440
20	GACGTACTGT	GTGAACCTCA	CCCTGGGGGA	TGACACAAGC	CTGGCTCTCA	CGAGCACCCT	1500
	GATTTCTGTT	CCTGACAGAG	ACCCAGCCTC	GCCTTTAAGG	ATGGCAAAACA	GTGCCCTGAT	1560
	CTCCGTTGGC	TGCTTGGCCA	TATTTGTCAC	TGTGATCTCC	CTCTTGGTGT	ACAAAAAACA	1620
	CAAGGAATAC	AACCCAATAG	AAAATAGTCC	TGGGAATGTG	GTGAGAAGCA	AAGGCTGAG	1680
	TGCTTTTCTC	AACCGTGCAA	AAGCCGTGTT	CTTCCCGGGA	AACCAGGAAA	AGGATCCGCT	1740
25	ACTCAAAAAC	CAAGAATTTC	AAGGAGTTTC	TTAAATTTCC	ACCTTGTTC	TGAAGCTCAC	1800
	TTTTCAAGTC	CATTGATGTG	AGATGTGCTG	GAGTGGCTAT	TAACCTTTT	TTCTTAAAGA	1860
	TTATTGTTAA	ATAGATATTG	TGGTTTGGGG	AAGTTGAATT	TTTTATAGGT	TAAATGTCAT	1920
	TTTAGAGATG	GGGAGAGGGA	TTATACTGCA	GGCAGCTTCA	GCCATGTTGT	GAAACTGATA	1980
	AAAGCAACTT	AGCAAGGCTT	CTTTTCATTA	TTTTTTATGT	TTCACTTATA	AAGTCTTAGG	2040
30	TAACATAGT	GATAGAATCA	CTGTGCTCCG	AGAGTAAGGA	GAGAAGCTAC	TATTGATTAG	2100
	AGCCTAACCC	AGGTAACTG	CAAGAAGAGG	CGGATACTTT	TCAGCTTTCC	ATGTAAGTGT	2160
	ATGCATAAAG	CCAATGTAGT	CCAGTTTCTA	AGATCATGTT	CCAAGCTAAC	TGAATCCAC	2220
	TTCAATACAC	ACTCATGAAC	TCCTGATGGA	ACAATAACAG	GCCCAAGCCT	GTGGTATGAT	2280
	GTGCACACTT	GCTAGACTCA	GAAAAAATAC	TACTCTCATA	AATGGGTGGG	AGTATTTTGG	2340
35	TGCAACCTTA	CTTTGCTTGG	CTGAGTGAAG	GAATGATATT	CATATATTCA	TTTATTCCAT	2400
	GGACATTTAG	TTAGTGCTTT	TTATATACCA	GGCATGATGC	TGAGTGACAC	TCTTGTGTAT	2460
	ATTTCCAAAT	TTTTGTATAG	TCGCTGCACA	TATTTGAAAT	CATATATTAA	GACTTTCCAA	2520
	AGATGAGGTC	CCTGGTTTTT	CATGGCAACT	TGATCAGTAA	GGATTTTACC	TCTGTTTGTA	2580
	ACTAAAACCA	TCTACTATAT	GTTAGACATG	ACATTCTTTT	TCTCTCTTTC	CTGAAAAATA	2640
40	AAGTGTGGGA	AGAGACAAAA	AAAAAATAA				

Seq ID NO: 383 Protein sequence
Protein Accession #: NP_002501

45	1	11	21	31	41	51	
	MECLYYFLGF	LLLAARLPLD	AAKRFHDLVG	NERPSAYMRE	HNQLNGWSSD	ENDWNEKLYP	60
	VWKRQDMRWK	NSWKGRVQA	VLTSDSPALV	GSNITFAVNL	IFPRCQKEDA	NGNIVYEKNC	120
	RNEAGLSADP	YVYNWTAWSE	DSGGENGTGQ	SHHNVPDGGK	PPPHHPGWR	WNFIYVFHTL	180
50	GQYFQKLGR	SVRVSVNTAN	VTLGPPQLMEV	TVYRRHGRAY	VPIAQVKDVY	VVDQIPVVFV	240
	TMFQKNDRNS	SDETFLLKDL	IMFDVLHDP	SHFLNYSTIN	YKWSFGDNTG	LFVSTNHTVN	300
	HTVYLVNGTFS	LNLITVKAAP	GPCPPPPPPP	RPSKPTPSLG	PAGDNPLELS	RIPDENCQIN	360
	RYGHFQATIT	IIVGILEVNI	IQMTDVLMPV	PWPESLIDF	VVTCQGSIPT	EVCTIISDPT	420
	CETIQNTVCS	PVDVDEMCLL	TVRRTFNGSG	TYCVNLTLGD	DTSLALSTSL	ISVPDRDPAS	480
55	PLRMANSALI	SVGCLAIFVT	VISLLVYKXH	KEYNPIENSP	GNVVRSKGLS	VFLNRKAVF	540
	FPGNQEKDPL	LKNQEFKGV					

Seq ID NO: 384 DNA sequence
Nucleic Acid Accession #: NM_001134
Coding sequence: 48-1877

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	AATCAATTTT	TTTAATTTTC	CTACTAAATT	TTACTGAATC	CAGAACACTG	CATAGAAATG	120
65	AATATGGAAT	AGCTTCCATA	TTGGATTCTT	ACCAATGTAC	TGCAGAGATA	AGTTTAGCTG	180
	ACCTGGCTAC	CATATTTTTT	GCCAGTTTG	TTCAAGAAGC	CACCTTCAAG	GAGTAAGCA	240
	AAATGGTGAA	AGATGCATTG	ACTGCAATTG	AGAAACCCAC	TGGAGATGAA	CAGTCTTCAG	300
	GGTGTTTAGA	AAACCGACTA	CCTGCCTTTC	TGGAAGAAGT	TTGCCATGAG	AAAGAAATTT	360
70	TGGAGAAGTA	CGGACATTTA	GACTGCTGCA	GCCAAAGTGA	AGAGGGAAGA	CATAACTGTT	420
	TTCTTGACAC	CAAAAAGCCC	ACTCCAGCAT	CGATCCCACT	TTTCCAAGTT	CCAGAACCTG	480
	TCACAAGCTG	TGAAGCATAT	GAAGAAGACA	GGGAGACATT	CATGAACAAA	TTCAATTATG	540
	AGATAGCAAG	AAGGCATCCC	TTCTGTATG	CACCTACAAT	TCTTCTTTGG	GCTGCTCGCT	600
	ATGACAAAAT	AATTCCATCT	TGCTGCAAAG	CTGAAAATGC	AGTTGAATGC	TTCCAAACAA	660
75	AGGCAGCAAC	AGTTACAAAA	GAATTAAAG	AAAGCAGCTT	GTTAAATCAA	CATGCATGTG	720
	CAGTAATGAA	AAATTTTGGG	ACCCGAACCT	TCCAAGCCAT	AACTGTTACT	AAACTGAGTC	780
	AGAAGTTTAC	CAAAGTTAAT	TTTACTGAAA	TCCAGAAACT	AGTCCCTGGAT	GTGGCCCATG	840
	TACATGAGCA	CTGTTGCAGA	GGAGATGTGC	TGGATTGTCT	GCAGGATGGG	GAAAAAATCA	900
	TGTCCTACAT	ATGTTCTCAA	CAAGCACTC	TGTCAAACAA	AATAACAGAA	TGCTGCAAAC	960
80	TGACCACGCT	GGAACGTGGT	CAATGTATAA	TTTATGACAGA	AAATGATGAA	AAACCTGAAG	1020
	GTCTATCTCC	AAATCTAAAC	AGGTTTTTAG	GAGATAGAGA	TTTTAACCAA	TTTTCTTCAG	1080
	GGGAAAAAAA	TATCTTCTTG	GCAAGTTTTG	TTTATGAATA	TTCAAGAAGA	CATCCTCAGC	1140
	TTGCTGTCTC	AGTAATTCTA	AGAGTTGCTA	AAGGATACCA	GGAGTTATTG	GAGAAGTGT	1200
	TCCAGACTGA	AAACCTCTT	GAATGCCAAG	ATAAAGGAGA	AGAAGAATTA	CAGAAATACA	1260
85	TCCAGGAGAG	CCAAGCATTT	GCAAAGCGAA	GCTGCGGCCT	CTTCCAGAAA	CTAGGAGAAT	1320
	ATTACTTACA	AAATGCGTTT	CTCGTTGCTT	ACACAAAGAA	AGCCCCCAG	GACCTCTCGT	1380
	CGGAGCTGAT	GGCCATCACC	AGAAAAATGG	CAGCCACAGC	AGCCACTTGT	TGCCAACTCA	1440
	GTGAGGACAA	ACTATTGGCC	TGTGGCGAGG	GAGCGGCTGA	CATTATTATC	GGACACTTAT	1500

GTATCAGACA TGAATGACT CCAGTAAACC CTGGTGTGG CCAGTGTGC ACTTCTTCAT 1560
 ATGCCAACAG GAGGCCATGC TTCAGCAGCT TGGTGGTGA TGAACATAT GTCCCTCCTG 1620
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 TGCAAAACGAT GAAGCAAGAG TTTCTCATTA ACCTTGTGAA GCAAAAGCCA CAAATAACAG 1740
 AGGAACAACT TGAGGCTGTC ATTGCAGATT TCTCAGGCCT GTTGGAGAAA TGCTGCCAAG 1800
 GCCAGGAACA GGAAGTCTGC TTTGCTGAAG AGGGACAAAA ACTGATTTCA AAAACTCGTG 1860
 CTGCTTTGGG AGTTTAAATT ACTTCAGGGG AAGAGAAGAC AAAACGAGTC TTTTCATTCG 1920
 TGTGAACCTT TCTCTTTAAT TTTAACTGAT TTAACACTTT TTGTGAATTA ATGAAATGAT 1980
 AAAGACTTTT ATGTGAGATT TCCTTATCAC AGAAATAAAA TATCTCCAAA TG

Seq ID NO: 385 Protein sequence
 Protein Accession #: NP_001125

1 11 21 31 41 51
 MKWVESIFLI FLNFTESRT LHRNEYGIAS ILDSYQCTAE ISLADLATIF FAQFVQEATY 60
 KEVSKMVKDA LTAIEKPTGD EQSSGCGLENO LPAFLEELCH EKEILEKYGH SDCCSQSEEG 120
 RHNCFLAHKK PTPASIPLFQ VPEPVTSCEA YEEDRETFFM KFIYEIARRH PFLYAPTILL 180
 WAARYDKIIP SCCKAENAVE CFQTKAATVT KELRESSLLN QHACAVMKNF GTRTFQAITV 240
 TKLSQKFTKV NFTBIQKLV DVAHVHEHCC RGDVLDCLQD GEKIMSYICS QQDTLSNKIT 300
 ECCKLTTLER QCIIHAEND EKPEGLSPNL NRFLGDRDFN QFSSGEKNIF LASFVHEYSR 360
 RHPQLAVSVI LRVAKGYQEL LEKCFQTENP LECQDKGEE LQKYIQESQA LAKRSCGLFQ 420
 KLGEYLLQNA FLVAYTKKAP QLTSSSELMAI TRKMAATAAT CCQLSEDKLL ACREGAADI 480
 IGHLCIRHEM TPNVPGVQC CTSSYANRRP CFSSLVVDET YVPPAFSDDK FIFHKDLQCA 540
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 SKTRAAALGV

Seq ID NO: 386 DNA sequence
 Nucleic Acid Accession #: NM_002205.1
 Coding sequence: 1..3149

1 11 21 31 41 51
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 GGCTTCAACT TAGACGCGGA GGCCTCAGCA GTACTCTCGG GGCCTCCGCG CTCCTTCTTC 180
 GGATTCTCAG TGGAGTTTTA CCGCCCGGGA ACAGACGGGG TCAGTGTGCT GGTGGGAGCA 240
 CCCAAGGCTA ATACCAGCCA GCCAGGAGTG CTGCAGGGTG GTGCTGTCTA CCTCTGTCTC 300
 TGGGGTGCCA GCCCCACACA GTGCACCCCC ATTGAATTG ACAGCAAAGG CTCCTCGGCTC 360
 CTGGAGTCCCT CACTGTCCAG CTACAGAGGA GAGGAGCCTG TGGAGTACAA GTCCTTGACG 420
 TGGTTCGGGG CAACAGTTCG AGCCCATGGC TCCTCCATCT TGGCATGCGC TCCACTGTAC 480
 AGCTGGCGCA CAGAGAAGGA GCCACTGAGC GACCCCGTGG GCACCTGCTA CCTCTCCACA 540
 GATAACTTCA CCCGAATTCT GGAGTATGCA CCTGCGCGCT CAGATTTTCA CTGGGCAGCA 600
 GGACAGGGTT ACTGCCAAGG AGGCTTCAGT GCCAGATTCA CCAAGACTGG CCGTGTGGTT 660
 TTAGGTGGAC CAGGAAGCTA TTTCTGGCAA GGCCAGATCC TGTCTGCCAC TCAGGAGCAG 720
 ATTGCAGAA CTATTATCCC CGAGTACCTG ATCAACCTGG TTCAGGGGCA GCTGCAGACT 780
 CGCCAGGCCA GTTCCATCTA TGATGACAGC TACCTAGGAT ACTCTGTGGC TGTGTGGTGA 840
 TTCACTGGTG ATGACACAGA AGACTTTGTT GCTGGTGTGC CCAAGGGGAA CCTCACTTAC 900
 GGCTATGTCA CCATCCTTAA TGGCTCAGAC ATTCGATCCC TCTACAACCT CTCAGGGGAA 960
 CAGATGGCCT CCTACTTTGG CTATGCAATG GCCGCCACAG ACGTCAATGG GGACGGGCTG 1020
 GATGACTTGC TGGTGGGGGC ACCCTGTCTC ATGGATCGGA CCCCTGACGG GCGGCCTCAG 1080
 GAGGTGGGCA GGGTCTACGT CTACCTGCAG CACCCAGCCG GCATAGAGCC CACGCCACCC 1140
 CTTACCCTCA CTGGCCATGA TGAGTTTGGC CGATTGGGCA GCTCCTTGAC CCCCTGGGG 1200
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 GGTTTTACAG TGGAACTTGT GCTGGACTGG CAGAAGCAGA AGGGAGGGGT ACGGCGGGCA 1680
 CTGTTCTCTG CCTCCAGGCA GGCAACCCTG ACCCAGACCC TGCTCATCCA GAATGGGGCT 1740
 CGAGAGGATT GCAGAGAGAT GAAGATCTAC CTCAGGAACG AGTCAGAAAT TCGAGACAAA 1800
 CTCTCGCCGA TTCACATCGC TCTCAACTTC TCCTTGGACC CCAAGCCCC AGTGGACAGC 1860
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 ATCCAGTTTG ACTTCCAGAT CCTCAGCAAG AATCTCAACA ACTCGCAAAG CGACGTGGTT 2340
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 GAGGCAGTGC TATTCCAGT AAGCGACTGG CATCCCCGAG ACCAGCCTCA GAAGGAGGAG 2460
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 AGCCAGGGTG TTCTGGAACT CAGCTGTCCC CAGGCTCTGG AAGGTCAAGC GCTCCTATAT 2580
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 GAGTTGGATC CCGAGGGTTC CCTGCACCAC CAGCAAAAAC GGGAGCTCC AAGCCGAGC 2700
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 TACAAAGCCC TGAAGATGCC CTACCGAATC CTGCTCGGC AGCTGCCCA AAAAGAGCGT 2940
 CAGGTGGCCA CAGCTGTGCA ATGGACCAAG GCAGAAGGCA GCTATGGCGT CCCACTGTG 3000
 ATCATCATCC TAGCCATCCT GTTTGGCCTC CTGCTCCTAG GTCTACTCAT CTACATCCTC 3060
 TACAAGCTTG GATTCTTCAA ACGTCCCTC CCATATGGCA CCGCATGGA AAAAGCTCAG 3120
 CTCAGCCTC CAGCCACCTC TGATGCTGTA

Seq ID NO: 387 Protein sequence
Protein Accession #: NP_002196.1

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GFSVEFYRPG TDGVSVLVGA PKANTSQPGV LQGGAVYLCF WGASPTQCTP IEFDSKGSRL 120
LESSLSSESG EEPVEYKSLQ WFGATVRAHG SSILACAPLY SWRTEKEPLS DPGVTCYLSL 180
10     DNFTRILEYA PCRSDFSWAA GQGYCQGGFS AEFTKTGRVV LGGPGSYFWQ GQILSATQEQ 240
IAESYYPEYL INLVQGGQQT RQASSIYDDS YLGYSVAVGE FSGDDTDFV AGVPKGNLTY 300
GYVTILNGSD IRSLYNFSGE QMASYFGYAV AATDVNGDGL DDLVVGAPLL MDRTPDGRPQ 360
EVGRVYVYLQ HPAGIEPTPT LTLTGHDEFG RFGSSLTPLG DLDQDGYNDV AIGAPFGGET 420
15     QQGVVVFVPG GPGLGSKPS QVLQPLWAAS HTPDFFGSAL RGGRLDNGG YPDIVGSFG 480
VDKAVVYRGR PIVSASASLT IFPAMFNPEE RSCSLEGNPV ACINLSFCLN ASGKHVADSI 540
GFTVELQLDW CDLGNPMKAG ASLWGGLRFT VPHLRDTKKT IQPDFQILSK NLNNSQSDVV 600
LSPHIALNF SLDPQAPVDS HGLRPAHLYQ SKSRIEDKAO ILLDCGEDNI CVPDLQLEVF 660
GEQNHVYLG D KNALNLTFHA QNVGEGGAYE AELRVLTAPPE AEYSGLVHRP GNFSLSLSDY 720
20     FAVNQSRLLV CDLGNPMKAG ASLWGGLRFT VPHLRDTKKT IQPDFQILSK NLNNSQSDVV 780
SFRLSVEAQA QVTLNGVSKP EAVLFPVSDW HPRDQPKKEE DLGPAVHHVY ELINQGPSSI 840
SQGVLELSCP QALGGLQLLY VTRVTGLNCT TNHPINPKGL ELDPGSLHH QKREAPSR 900
SASSGPQILK CPEAECFRLR CELGPLHQE SQSLQLHFRV WAKTFLOREH QPFSLQCEAV 960
YKALKMPYRI LPRQLPQKER QVATAVQWTK AEGSYGVPLW IITLAILFGL LLLGLLIYIL 1020
25     YKLGFKKRSL PYGTAMEKAQ LKPPATSDA

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Seq ID NO: 388 DNA sequence
Nucleic Acid Accession #: NM_002425
Coding sequence: 26..1453

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35     TGCCACAGCA TACCTAGAAA AGTACTACAA CCTCGAAAAG GATGTGAAAC AGTTTAGAAG 180
AAAGGACAGT AATCTCATTT TTAATAAAT CCAAGGAATG CAGAAGTTCC TTGGGTGGGA 240
GGTGACAGGG AAGCTAGACA CTGACACTCT GGAGGTGATG CGCAAGCCCA GGTGTGGAGT 300
TCTTGAGGTT GGTCACTTCA GCTCCTTTCC TGGCATGCCG AAGTGGAGGA AAACCCACCT 360
TACATACAGG ATTGTGAATT ATACACCAGA TTTGCCAAGA GATGCTGTTG ATTCTGCCAT 420
40     TGAGAAAGCT CTGAAAGTCT GGGAGAGGTT GACTCCACTC ACATTCCTCA GGTGTATAGA 480
AGGAGAGGCT GATATAATGA TCTCTTTCGC AGTTAAAGAA CATGGAGACT TTTACTCTTT 540
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TATTCACTTT GATGATGATG AAAAATGGAC AGAAGATGCA TCAGGCACCA ATTTATTCTT 660
CGTTGCTGCT CATGAACCTG GCCACTCCCT GGGGCTCTTT CACTCAGCCA ACACCTGAAGC 720
45     TTTGATGTAC CCACCTCTACA ACTCATTAC AGAGCTCGCC CAGTTCGCCC TTTCGCAAGA 780
TGATGTGAAT GGCATTACGT CTCTCTACGG ACCTCCCTCT CCCTCTACTG AGGAACCCCT 840
GGTGCCCAACA AAATCTGTTC CTTCGGGATC TGAGATGCCA GCCAAGTGTG ATCCTGCTTT 900
GTCCTTCGAT GCCATCAGCA CTCTGAGGGG AGAATATCTG TTCTTTAAAG ACAGATATTT 960
TTGGCGAAGA TCCCACTGGA ACCCTGAACC TGAATTTTCA TTGATTTCTG CATTTTGGCC 1020
50     CTCTCTTCCA TCATATTGGG ATGCTGCATA TGAAGTTAAG AGCAGGGACA CCGTTTTTAT 1080
TTTTAAAGGA AATGAGTTCT GGGCCATCAG AGSAAATGAG GTACAAGCAG GTTATCCAAG 1140
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CAAGGAAAAA AAGAAAAACT ACTCTTTTGC AGCGGACAAA TACTGGAGAT TTGATGAAAA 1260
TAGCCAGTCC ATGGAGCAAG GCTTCCCTAG ACTAATAGCT GATGACTTTC CAGGAGTTGA 1320
55     GCCTAAGGTT GATGCTGTAT TACAGGCATT TGGATTTTTC TACTTCTTCA GTGGATCATC 1380
ACAGTTTGAG TTTGACCCCA ATGCCAGGAT GGTGACACAC ATATTAAAGA GTAACAGCTG 1440
GTTACATTGC TAGGCGAGAT AGGGGGAAGA CAGATATGGG TGTTTTAAAT AAATCTAATA 1500
ATTATTCATC TAATGTATTA TGAGCCAAAA TGGTTAATTT TTCCTGCATG TTCTGTGACT 1560
GAAGAAGATG AGCCTTGCA GATATCTGCAT GTGTATGAA GAATGTTTCT GGAATCTTTC 1620
60     ACTTGCTTTT GAATTGCACT GAACAGAATT AAGAAATACT CATGTGCAAT AGGTGAGAGA 1680
ATGTATTTTC ATAGATGTGT TATTACTTCC TCAATAAAAA GTTTTATTTT GGGCCTGTTC 1740
CTT

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Seq ID NO: 389 Protein sequence
Protein Accession #: NP_002416

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KIQGMQKFLG LEVTGKLDTD TLEVMRKPRC GVPDVGHFSS FPGMPKWRKT HLTYYRIVNYT 120
70     PDLPRDAVDS AIEKALKVWE EVTPLTF SRL YEGEADIMIS FAVKEHGDY SFDGPGHSLA 180
HAYPPGGLY GDIHFDDDEK WTEDASGTLN FLVAHAELGH SLGLFHSANT EALMYPLYNS 240
FTELAQFRLS QDDVNGIQSL YGPPPASTEE PLVPTKSVPS GSEMPAKCDP ALSFDAISTL 300
RGEYLFKDR YFWRSSHWNP EPEFHLSAF WPSLPSYLD AYEVSNDTV FIFKGNFNA 360
75     IRGNEVQAGY PRGIHTLGF PTIRKIDAAV SDKEKKTYF FAADKYWRF ENSQSMQGF 420
PRLIADDFPG VEPKVDVQLQ AFGFFYFSSG SSQFEFDPNA RMVTHILKSN SWLHC

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Seq ID NO: 390 DNA sequence
Nucleic Acid Accession #: NM_002421.2
Coding sequence: 1..1409

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85     TACTACAAAC TGAAGCAATGA TGGGAGGCAA GTTGAAAGC GGAGAAATAG TGGCCAGTGT 180
GTTGAAAAAT TGAAGCAAT GCAGGAATTC TTTGGGCTGA AAGTACTGGG GAAACCAGAT 240
GCTGAAACCC TGAAGGTGAT GAAGCAGCCC AGATGTGGAG TGCCTGATGT GGCTCAGTTT 300

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5 GTCCTCACTG AGGGGAAACCC TCGCTGGGAG CAAACACATC TGACCTACAG GATTGAAAAAT 360
 TACACGCCAG ATTTGCCAAG AGCAGATGTG GACCATGCCA TTGAGAAAGC CTTCCAACCTC 420
 TGGAGTAATG TCACACCTCT GACATTCACC AAGGTCTCTG AGGGTCAAGC AGACATCATG 480
 ATATCTTTTG TCAGGGGAGA TCATCGGGAC AACTCTCCTT TTGATGGACC TGGAGGAAAT 540
 CTTGCTCATG CTTTTCACCC AGGCCCAGGT ATTGGAGGGG ATGCTCATT TTATGAAGAT 600
 GAAAGGTGGA CCAACAATTT CAGAGAGTAC AACTTACATC GTGTTGCGGC TCATGAACTC 660
 GGCCATTCTC TTGGACTCTC CCATTCTACT GATATCGGGG CTTTGATGTA CCTTAGCTAC 720
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 10 GGACGTTCCC AAAATCCTGT CCAGCCCATC GGGCCACAAA CCCCAAAAGC ATGTGACAGT 840
 AAGCTAACCT TTGATGCTAT AACTACGATT CGGGGAGAAG TGATGTTCTT TAAAGACAGA 900
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 15 CCCAAGGACA TCTACAGCTC CTTTGGCTTC CCTAGAACTG TGAAGCATAT CGATGCTGCT 1140
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 GATGAATATA AACGATCTAT GGATCCAGGT TATCCCAAAA TGATAGCACA TGACTTTCCT 1260
 GGAATTGGCC ACAAAGTTGA TGCAGTTTTC ATGAAAGATG GATTTTCTA TTTCTTTCAT 1320
 20 GGAACAAGAC AATACAAATT TGATCCTAAA ACGAAGAGAA TTTTGACTCT CCAGAAAGCT 1380
 AATAGCTGGT TCAACTGCAG GAAAAATTAG

Seq ID NO: 391 Protein sequence
 Protein Accession #: NP_002412.1

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 VEKLKQMQEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTEGNPRWE QTHLTYRIEN 120
 YTPDLPRADV DHAIEKAPQL WSNVPLTFT KVSSEGQADIM ISFVRGDHRD NSPFDGPGGN 180
 30 LAHAFFQPGPG IGGDAHFDED ERWTNNFREY NLHRVAAHEL GHSGLGSHST DIGALMYPST 240
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 FYMRTNPFYP EVELNFISVF WPQLPENGLEA AYEFAADRDEV RFFKGNKYWA VQGNVHLHG 360
 PKDIYSSFGF PRTVKHIDAA LSEENTGKTY FVANKYWR YDEYKRSMDPG YPKMIAHDFP 420
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35 Seq ID NO: 392 DNA sequence
 Nucleic Acid Accession #: NM_002421.2
 Coding sequence: 1..1409

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 45 GTTGAAAAAT TGAAGCAATC GCAGGAATTC TTTGGGCTGA AAGTGACTGG GAAACAGAT 240
 GCTGAAACCC TGAAGGTGAT GAAGCAGCCC AGATGTGGAG TGCTGATGT GGCTCAGTTT 300
 GTCCTCACTG AGGGGAAACCC TCGCTGGGAG CAAACACATC TGACCTACAG GATTGAAAAAT 360
 TACACGCCAG ATTTGCCAAG AGCAGATGTG GACCATGCCA TTGAGAAAGC CTTCCAACCTC 420
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 50 ATATCTTTTG TCAGGGGAGA TCATCGGGAC AACTCTCCTT TTGATGGACC TGGAGGAAAT 540
 CTTGCTCATG CTTTTCACCC AGGCCCAGGT ATTGGAGGGG ATGCTCATT TTATGAAGAT 600
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 GGCCATTCTC TTGGACTCTC CCATTCTACT GATATCGGGG CTTTGATGTA CCTTAGCTAC 720
 ACCTTCACTG GTGATGTTCA GCTAGCTCAG GATGACATTG ATGGCATCCA AGCCATATAT 780
 55 GGACGTTCCC AAAATCCTGT CCAGCCCATC GGGCCACAAA CCCCAAAAGC ATGTGACAGT 840
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 60 CCCAAGGACA TCTACAGCTC CTTTGGCTTC CCTAGAACTG TGAAGCATAT CGATGCTGCT 1140
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 GATGAATATA AACGATCTAT GGATCCAGGT TATCCCAAAA TGATAGCACA TGACTTTCCT 1260
 GGAATTGGCC ACAAAGTTGA TGCAGTTTTC ATGAAAGATG GATTTTCTA TTTCTTTCAT 1320
 65 GGAACAAGAC AATACAAATT TGATCCTAAA ACGAAGAGAA TTTTGACTCT CCAGAAAGCT 1380
 AATAGCTGGT TCAACTGCAG GAAAAATTAG

Seq ID NO: 393 Protein sequence
 Protein Accession #: NP_002412.1

70 1 11 21 31 41 51
 | | | | | |
 MHSFPPLLLL LFWGVVSHSF PATLETQEQD VDLVQKYLEK YYNLKNDGRQ VEKRRNSGPV 60
 VEKLKQMQEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTEGNPRWE QTHLTYRIEN 120
 YTPDLPRADV DHAIEKAPQL WSNVPLTFT KVSSEGQADIM ISFVRGDHRD NSPFDGPGGN 180
 75 LAHAFFQPGPG IGGDAHFDED ERWTNNFREY NLHRVAAHAL GHSGLGSHST DIGALMYPST 240
 TFSGDVQLAQ DDIDIGIAIY GRSQNPVQPI GPQTPKACDS KLTFDATTTI RGEVMFFKDR 300
 FYMRTNPFYP EVELNFISVF WPQLPENGLEA AYEFAADRDEV RFFKGNKYWA VQGNVHLHG 360
 PKDIYSSFGF PRTVKHIDAA LSEENTGKTY FVANKYWR YDEYKRSMDPG YPKMIAHDFP 420
 GIGHKVDVAV MKDGFFFFFFH GTRQYKFDPK TKRILTLQKA NSWFNCRKN

85 Seq ID NO: 394 DNA sequence
 Nucleic Acid Accession #: NM_014331.2
 Coding sequence: 1..1506

1 11 21 31 41 51
 | | | | | |

	ATGGTCAGAA	AGCCTGTGT	GTCCACCATC	TCCAAAGGAG	GTTACCTGCA	GGGAAATGTT	60
	AACGGGAGGC	TGCCTTCCT	GGGCAACAAG	GAGCCACCTG	GGCAGGAGAA	AGTGCAGCTG	120
	AAGAGGAAAG	TCACCTTTACT	GAGGGGAGTC	TCCATTATCA	TTGGCACCAT	CATTGGAGCA	180
5	GGAACTCTTCA	TCTCTCCTAA	GGGCGTGCTC	CAGAACACGG	GCAGCGTGGG	CATGCTCTCG	240
	ACCATCTGGA	CGGTGTGTGG	GGTCTGTCA	CTATTGGAG	CTTTGTCTTA	TGCTGAATTG	300
	GGAACAACATA	TAAAGAAATC	TGGAGGTGAT	TACACATATA	TTTTGGAAGT	CTTTGGTCCA	360
	TTACCAGCTT	TTGTACGAGT	CTGGGTGGAA	CTCCTCATAA	TACGCCCTGC	AGCTACTGCT	420
	GTGATATCCC	TGGCATTGG	ACGCTACATT	CTGGAACCAT	TTTTTATTCA	ATGTGAAATC	480
10	CCTGAACCTT	CGATCAAGCT	CATTACAGCT	GTGGGCATAA	CTGTAGTGAT	GGTCTTAAAT	540
	AGCATGAGTG	TCAGCTGGAG	CGCCCGGATC	CAGATTTTCT	TAACCTTTTG	CAAGCTCACA	600
	GCAATTCTGA	TAATTATAGT	CCCTGGAGTT	ATGCAGCTAA	TAAAGGTCA	AACGCAGAAC	660
	TTTAAAGACG	CGTTTTCAGG	AAGAGATTCA	AGTATTACGC	GGTTGCCACT	GGCTTTTAT	720
	TATGGAATGT	ATGCATATGC	TGGCTGGTTT	TACCTCAACT	TTGTTACTGA	AGAAGTAGAA	780
15	AACCCGTAAG	AAACCATTCC	CCTTGCAATA	TGTATATCCA	TGGCCATTGT	CACCATTGGC	840
	TATGTGCTGA	CAATGTGGC	CTACTTTACG	ACCATTAATG	CTGAGGAGCT	GCTGCTTTCA	900
	AATGCAGTGG	CAGTGCCTT	TTCTGAGCGG	CTACTGGGAA	ATTCTCATT	AGCAGTTCCG	960
	ATCTTTGTGT	CCCTCTCCTG	CTTTGGCTCC	ATGAACGGTG	GTGTGTTTGC	TGTCTCCAGG	1020
	TTATTCTATG	TTGCGTCTCG	AGAGGGTCAC	CTTCCAGAAA	TCCTCTCCAT	GATTCAATGC	1080
20	CGCAAGCACA	CTCCTCTACC	AGCTTTTATT	GTTTGTGACC	CTTTGACAA	GATAATGCTC	1140
	TTCTCTGGAG	ACCTCGACAG	TCTTTTGAAT	TTCTTCAGTT	TTGCCAGGTG	GCTTTTATTT	1200
	GGGCTGGCAG	TTGCTGGGCT	GATTTATCTT	CGATACAAAT	GCCAGATAT	GCATCGTGAT	1260
	TTCAAGGTGC	CACGTGTCAT	CCCAGCTTTG	TTTTCTTTCA	CATGCCCTCT	CATGGTTGCC	1320
	CTTTCCCTCT	ATTCCGACCC	ATTTAGTACA	GGGATTTGGT	TCGTCTCAC	TCTGACTGGA	1380
25	GTCCCTGCGT	ATTATCTCTT	TATTATATGG	GACAAGAAAC	CCAGGTGGTT	TAGAATAATG	1440
	TCAGAGAAAA	TAACCAGAAC	ATTACAAATA	ATACTGGAAG	TTGTACCAGA	AGAAGATAAG	1500
	TTATGAACATA	ATGGACTTGA	GATCTTGCCA	ATCTGCCCAA	GGGGAGACAC	AAAATAGGGA	1560
	TTTTTACTTC	ATTTTCTGAA	AGTCTAGAGA	ATTACAACCT	TGGTGATAAA	CAAAAGGAGT	1620
	CAGTTATTTT	TATTCATATA	TTTTAGCATA	TTTCAACTAA	TTTCTAAGAA	ATTTAGTTAT	1680
30	AACCTATGT	AGTTATAGAA	AGTGAATATG	CAGTTATTCT	ATGAGTCGCA	CAATTCTTGA	1740
	GTCTCTGATA	CCTACCTATT	GGGGTTAGGA	GAAAAGACTA	GACAATTACT	ATGTGGTCAT	1800
	TCTCTACAA	ATATGTTAGC	ACGGCAAAGA	ACCTTCAAA	TGAAGACTGA	GATTTTCTG	1860
	TATATATGGG	TTTTGTAAAG	ATGGTTTAC	ACACTACAGA	TGCTATACT	GTGAAAAGTG	1920
	TTTTCAATTC	TGAAAAAAG	CATACATCAT	GATTATGGCA	AAGAGGAGAG	AAAGAAATTT	1980
35	ATTTTACATT	GACATTGCAT	TGCTTCCCTT	TAGATACCAA	TTTAGATAAC	AAACACTCAT	2040
	GCTTTAATGG	ATTATACCCA	GAGCACTTTG	AACAAAGGTC	AGTGGGGATT	AGTGAATACA	2100
	TTAAAGAAAG	GTTTCTAGGG	GCTACTGTTT	ATGAGACACA	TCCAGGAGTT	ATGTTTAAAT	2160
	AAAAATCCTT	GAGAACTTAT	TATGTCAGAT	GTTTTTTCAT	TCATATCAG	GAAGTTTATG	2220
	TTATCTGTCA	TTTTTTTTTT	TCACATCAGT	TTGATCAGGA	AAGTGTATAA	CACATCTTAG	2280
40	AGCAAGAGTT	AGTTTGGTAT	TAAATCCCTA	TTAGAACAAC	CACCTGTTC	ACTAATAACT	2340
	TACCCCTGAT	GAGTCTATCT	AAACATATGC	ATTTTAAAGC	TTCAAATTAC	ATTATCAACA	2400
	TGAGAGAAAT	AACCAACAAA	GAAGATGTTC	AAAAATAATG	TCCATATCT	GTAATCATAT	2460
	CTACATGCAA	TGTTAGTAAT	TCTGAAGTTT	TTTAAATTTA	TGGCTATTTT	TACACGATGA	2520
	TGAATTTTGA	CAGTTTGTGC	ATTTCTTTTA	TACATTTTAT	ATTCTTCTGT	TAAAATATCT	2580
45	CTTCAGATGA	AAGTGTCCAG	ATTAATTAGG	AAAAGGCATA	TATTAACATA	AAAATTGCAA	2640
	AAGAAATGTC	GCTGTAAATA	AGATTTACAA	CTGATGTTTC	TAGAAAAATT	CCACTTCTAT	2700
	ATCTAGGCTT	TGTCAGTAAT	TTCCACACCT	TAATTATCAT	TCAACTTGCA	AAAGAGACAA	2760
	CTGATAAGAA	GAAAAATTGAA	ATGAGAACT	GTGGATAAGT	GTTTGTGTTC	AGAAGATGTT	2820
	GTTTTGCCAG	TATTAGAAAA	TACTGTGAGC	CGGGCATGGT	GGCTTACATC	TGTAATCCCA	2880
50	GCACTTTGGG	AGGCTGAGGG	GGTGGATCAC	CTGAGGTCCG	GAGTCTAGAA	CCAGCCTGAC	2940
	CAACATGGAG	AAACCCCATC	TCTACTAAAA	ATACAAAAAT	AGCTGGGCAT	GGTGGCACAT	3000
	GCTGGTAATC	TCAGCTATTG	AGGAGGCTGA	GGCAGGAGAA	TTGCTTGAAC	CCGGGAGGCG	3060
	GAGGTTGCAG	TGAGCCAAAG	TTGCACCACT	GTACTCCAGC	CTGGGTGACA	AAGTCAGACT	3120
	CCATCTCCAA	AAAAAAAAAA	AAAA				

Seq ID NO: 395 Protein sequence
Protein Accession #: NP_055146.1

	1	11	21	31	41	51	
60	MVRKPVVSTI	SKGGYLQGNV	NGRLPSLGNK	EPFGQEKVQL	KRKVTLRLGV	SIIIGTIIGA	60
	GIFISPKGVL	QNTGSVGMSL	TIWTVCGVLS	LFGALSYAEL	GTTIKKSGGH	YTYLLEVFGP	120
	LPAFVRVWVE	LLIIRPAATA	VISLAFGRYI	LEPFFIQCEI	PELAIKLITA	VGITVVMVLN	180
	SMSVSWSARI	QIFLTFCKLT	AILIIIVPGV	MQLIKGQTQN	FKDAFSGRDS	SITRLPLAFY	240
65	YGMVAYAGWF	YLFNVTEEVE	NPEKTIPLAI	CISMAITIGV	YVLNVAYFT	TINAEELLS	300
	NAVAVTFSE	LLGNFSLAVP	IFVALSCFGS	MNGGVFAVSR	LFYVASREBH	LPEILSMIHV	360
	RKHTPLPAVI	VLHPLTMIML	PSGDLDSLNL	FLSFARWLFI	GLAVAGLIYL	RYKCPDMHRP	420
	FKVPLFIPAL	FSFTCLFMVA	LSLYSDPFST	GIGFVITLTG	VPAYYLFIIW	DKKPRWFRIM	480
	SEKTRTLQI	ILEVVPEEDK	L				

Seq ID NO: 396 DNA sequence
Nucleic Acid Accession #: NM_006528
Coding sequence: 57..764

	1	11	21	31	41	51	
75	GCCGCCAGCG	GCTTCTCGG	ACGCCTTGCC	CAGCGGGCCG	CCCGACCCCC	TGCACCATGG	60
	ACCCCGCTCG	CCCCCTGGGG	CTGTGCAATC	TGCTGCTTTT	CCTGACGGAG	GCTGCACTGG	120
	GCGATGCTGC	TCAGGAGCCA	ACAGGAAATA	ACGCGGAGAT	CTGTCTCCTG	CCCCTAGACT	180
80	ACGGACCTGT	CCGGGCCCTA	CTTCTCCGTT	ACTACTACGA	CAGGTACACG	CAGAGCTGCC	240
	GCCAGTTCTT	GTACGGGGGC	TGCGAGGGCA	ACGCCAACAA	TTTCTACACC	TGGGAGGCTT	300
	GCGACGATGC	TTGCTGGAGG	ATAGAAAAAG	TTCCCAAAGT	TTGCCGGCTG	CAAGTGAGTG	360
	TGGACGACCA	GTGTGAGGGG	TCCACAGAAA	AGTATTTCTT	TAATCTAAGT	TCCATGACAT	420
	GTGAAAAATT	CTTTTCCGGT	GGGTGTCAAC	GGAACCGGAT	TGAGAACAGG	TTTCCAGATG	480
85	AAGCTACTTG	TATGGGCTTC	TGCGCACCAA	AGAAAATTCC	ATCATTTTTC	TACAGTCCAA	540
	AAGATGAGGG	ACTGTGCTCT	GCCAAATGTA	CTCGCTATTA	TTTTAATCCA	AGATACAGAA	600
	CCTGTGATGC	TTTCACTTAT	ACTGGCTGTG	GAGGGAATGA	CAATAACTTT	GTTAGCAGGG	660

AGGATTGCAA ACGTGCATGT GCAAAAGCTT TGAAAAAGAA AAAGAAGATG CCAAAGCTTC 720
 GCTTTGCCAG TAGAATCCGG AAAATTCGGA AGAAGCAATT TTAACATTC TTAATATGTC 780
 ATCTTGTGTTG TCTTTATGCG TATTTTGCCCT TTATGGTTGT ATCTGAAGAA TAATATGACA 840
 GCATGAGGAA ACAAATCATT GGTGATTTAT TCACCAGTTT TTATTAATAC AAGTCACTTT 900
 TTTCAAAATTT TGGATTTTAT TATATATAAC TAGCTGCTAT TCAAAATGTGA GTCTACCAT 960
 TTTAATTTAT GGTCAACTG TTTGTGAGAC GAATTCTTGC AATGCATAAG ATATAAAAGC 1020
 AAATATGACT CACTCATTTC TTGGGGTTCG ATTCTGATT TCAGAAGAGG ATCATAACTG 1080
 AAACAACATA AGACAATATA ATCATGTGCT TTTAACATAT TTGAGAATAA AAAGGACTAG 1140
 CC

Seq ID NO: 397 Protein sequence
 Protein Accession #: NP_006519

1 11 21 31 41 51
 MDPARPLGLS ILLFLTEAA LGDAAQEPTG NNAEICLLPL DYGPCCRALLL RYYYDRYTQS 60
 CRQFLYGGGE GNANNFYWE ACDDACWRIE KVPKVCRLQV SVDDQCEGST EKYFFNLSSM 120
 TCEKFFSGGC HLRNRIENRFP DEATCMGFCA PKKIPSFYCS PKDEGLCSAN VTRYFNPFRY 180
 RTCDAPTYTG CGGNDNNFVS REDCKRACAK ALKKKKKMPK LRFASRIRKI RKKQF

Seq ID NO: 398 DNA sequence
 Nucleic Acid Accession #: NM_001508.1
 Coding sequence: 1..1361

1 11 21 31 41 51
 ATGGCTTCAC CCAGCCTCCC GGGCAGTGAC TGCTCCCAAA TCATTGATCA CAGTCATGTC 60
 CCCGAGTTTG AGGTGGCCAC CTGGATCAAA ATCACCCTTA TTCTGGTGTA CCTGATCATC 120
 TTCTGATAGG GCCTTCTGGG GAACAGCGTC ACCATTCGGG TCACCCAGGT GCTGCAGAAG 180
 AAAGGATACT TGCAGAAGGA GGTGACAGAC CACATGGTGA GTTTGGCTTG CTCGGACATC 240
 TTGGTGTTC TCATCGGCAT GCCATGGAG TTCTACAGCA TCATCTGGAA TCCCTGACC 300
 ACGTCCAGCT ACACCTCTGT CTGCAAGCTG CACACTTTCC TCTTCGAGGC CTGCAGCTAC 360
 GCTACGCTGC TGCACGTGCT GACGCTCAGC TTTGAGCGCT ACATCGCCAT CTGTCAACCC 420
 TTTCAAGTACA AGGCTGTGTC GGGACCTTGC CAGGTGAAGC TGCTGATTGG CTTCTCTG 480
 GTCACTCTCG CCCTGGTGGC ACTGCCCTTG CTGTTTGCCA TGGGTACTGA GTACCCCTG 540
 GTGAACGTGC CCAGCCACCG GGGTCTCACT TGCAACCGCT CCAGCACCAG CCACCCAGG 600
 CAGCCCGAGA CTTCAATAT GTCCATCTGT ACCAACCTCT CCAGCCGCTG GACCGTGTTC 660
 CAGTCCAGCA TCTTCGGCGC CTTCTGTGTC TACCTCGTGG TCCTGCTCTC CGTAGCCTTC 720
 ATGTGCTGGA ACATGATGCA GTGCTCATG AAAAGCCAGA AGGGCTCGCT GGCCGGGGGC 780
 ACGCGGCCTC CGCAGCTGAG GAAGTCCGAG AGCGAAGAGA GCAGGACCGC CAGGAGGCAG 840
 ACCATCATCT TCCTGAGGCT GATTGTTGTG ACATTGGCCG TATGCTGGAT GCCCAACAG 900
 ATTTCGGAGA TCATGCTGTC GGCCAAACCC AAGCACGACT GGACGAGGTC CTACTTCCGG 960
 GCGTACATGA TCCTCTCTCC CTTCTCGGAG ACGTTTTTCT ACCTCAGCTC GGTCAATCAAC 1020
 CCGCTCCTGT ACACGGTGTG CTGCGAGCAG TTTCGGCGGG TGTTCTGTGCA GGTGCTGTG 1080
 TGCCGCTGTG CGCTGCAGCA CGCCAAACCC GAGAAGCGCC TGCGCGTACA TGCGCACTCC 1140
 ACCACCGACA GCGCCCGCTT TGTGACGCGC CCGTTGCTCT TCGCGTCCCG GCGCCAGTCC 1200
 TCTGCAAGGA GAACTGAGAA GATTTTCTTA AGCACTTTTC AGAGCGAGGC CGAGCCCCAG 1260
 TCTAAGTCCC AGTCATTGAG TCTCGAGTCA CTAGAGCCCA ACTCAGGCGC GAAACCAGCC 1320
 AATTCTGCTG CAGAGAATGG TTTTCAGGAG CATGAAGTTT GA

Seq ID NO: 399 Protein sequence
 Protein Accession #: NP_001499.1

1 11 21 31 41 51
 MASPSPLPGSD CSQIIDHSHV PEFEVATWIK ITLILVYLII FVMGLLGNV TIRVTQVLQK 60
 KGYLQKEVTD HMVSLACSDI LVFLIGMPME FYSIIWNPLT TSSYTLSCKL HTFLFEACSY 120
 ATLLHLVLTLS FERYIAICHP FRYKAVSGPC QVKLLIGFVW VTSALVALPL LFAAMGTEYPL 180
 VNYPSHRGLT CNRSSTRHHE QPETSNSMIC TNLSSRWTVF QSSIIFGAFV YLVVLLSVAF 240
 MCWNMMQVLM KSQKGLSLAG TRPFLRKSE SEESRTARRQ TIIFLRLIVV TLAVCWMPNQ 300
 IRRIMAAAKP KHDWTRSYFR AYMILLPFSE TFFYLSVIN PLRYTVSSSQ FRRRVFQVLC 360
 CRLSLQHANH EKRLRVHAHS TTDSAREVQR PLLFASRRQS SARRTKIFL STFQSEAE PQ 420
 SKSQSLSLLES LEPNSGAKPA NSAAENGFOE HEV

Seq ID NO: 400 DNA sequence
 Nucleic Acid Accession #: NM_006475.1
 Coding sequence: 28..2538

1 11 21 31 41 51
 AACAGAACTG CAACGGAGAG ACTCAAGATG ATTCCCTTTT TACCCATGTT TTCTCTACTA 60
 TTGCTGCTTA TTGTTAACCCT TATAAAGGCC AACAATCATT ATGACAAGAT CTGGCTCAT 120
 AGTCGTATCA GGGGTCCGGG CCAAGGCCCA AATGTCTGTG CCCTTCAACA GATTTTGGGC 180
 ACCAAAAAGA AATACTTCAG CACTTGTAAG AACTGGTATA AAAAGTCCAT CTGTGGACAG 240
 AAAACGACTG TTTTATATGA ATGTTGCCCT GGTATATGA GAATGGAAGG AATGAAAGGC 300
 TGCCCGACAG TTTTGCCCAT TGACCATGTT TATGGCACTC TGGGCATCGT GGGAGCCACC 360
 ACAACGCAGC GCTATTCTGA CGCCTCAAAA CTGAGGGAGG AGATCGAGGG AAAGGGATCC 420
 TTCACTTACT TTGCACCGAG TAATGAGGCT TGGGCAACT TGGAATTCTGA TATCCGTAGA 480
 GGTTTGAGGA GCAACGTGAA TGTGAATTA CTGAATGCTT TACATAGTCA CATGATTAAT 540
 AAGAGAAATG TGACCAAGGA CTTAAAAAAT GGCAATGATTA TTCCTTCAAT GTATAACAAT 600
 TTGGGGCTTT TCATTAAACCA TTATCCTAAT GGGGTGTGCA CTGTTAATTG TGCTCGAATC 660
 ATCCATGGGA ACCAGATTGC AACAATGGT GTTGTCATG TCATTGACCG TGTGCTTACA 720
 CAAATTGGTA CCTCAATTCA AGACTTCATT GAAGCAGAAG ATGACCTTTC ATCTTTTAGA 780
 GCAGCTGCCA TCACATCGGA CATATTGGAG GCCCTTGGA GAGACGGTCA CTTCACTC 840
 TTTGCTCCCA CCAATGAGGC TTTTGAGAAA CTTCCACGAG GTGTCCTAGA AAGGTTTCATG 900
 GGAGACAAAG TGCTTCCGA AGCTCTTATG AAGTACCACA TCTTAAATAC TCTCCAGTGT 960
 TCTGAGTCTA TTATGGGAGG AGCAGTCTTT GAGACGCTGG AAGGAAATAC AATTGAGATA 1020

	GGATGTGACG	GTGACAGTAT	AACAGTAAAT	GGAATCAAAA	TGGTGAACAA	AAAGGATATT	1080
	GTGACAAATA	ATGGTGTGAT	CCATTTGATT	GATCAGGTCC	TAATTCCTGA	TTCTGCCAAA	1140
	CAAGTTATTG	AGCTTGGCTGG	AAAAACAGCAA	ACCACCTTCA	CGGATCTTGT	GGCCCAATTA	1200
	GGCTTGGCAT	CTGCTCTGAG	GCCAGATGGA	GAATACACTT	TGCTGGCACC	TGTGAATAAT	1260
5	GCATTTTCTG	ATGATACTCT	CAGCATGGTT	CAGCGCCTCC	TTAAATTAAT	TCTGCAGAA	1320
	CACATATTGA	AAGTAAAAGT	TGGCCTTAAT	GAGCTTTACA	ACGGGCAAAT	ACTGGAACCC	1380
	ATCGGAGGCA	AACAGCTCAG	AGTCTTCGTA	TATCGTACAG	CTGTCTGCAT	TGAAAAATCA	1440
	TGCGATGGAGA	AAGGGAGTAA	GCAAGGGAGA	AACGGTGCAG	TTACATATTT	CCGCGAGATC	1500
10	ATCAAGCCAG	CAGAGAAATC	CCTCCATGAA	AAGTTAAATC	AAGATAAGCG	CTTTAGCACC	1560
	TTCCTCAGCC	TACTTGAAGC	TGCAGACTTG	AAAGAGCTCC	TGACACAACC	TGGAGACTGG	1620
	ACATTATTTG	TGCCAACCAA	TGATGCTTTT	AAGGGAATGA	CTAGTGAAGA	AAAAGAAATT	1680
	CTGATACGGG	ACAAAAATGC	TCTTCAAATC	ATCATTCTTT	ATCACCTGAC	ACCAGGAGTT	1740
	TTCATTGGAA	AAGGATTTGA	ACCTGGTGTT	ACTAACATTT	TAAAGACCAC	ACAAGGAAGC	1800
15	AAAATCTTTC	TGAAGAAGT	AAATGATACA	CTTCTGGTGA	ATGAATTGAA	ATCAAAAGAA	1860
	TCTGACATCA	TGACAAACAA	TGGTGTAATT	CATGTTGTAG	ATAAACTCCT	CTATCCAGCA	1920
	GACACACCTG	TTGGAATGTA	TCAACTGCTG	GAAATACTTA	ATAAATTAAT	CAAATACATC	1980
	CAAATTAAGT	TTGTTCGTGG	TAGCACCTTC	AAAGAAATCC	CCGTGACTGT	CTATACAAC	2040
	AAAATTATAA	CCAAAGTTGT	GGAACCAAAA	ATTAAAGTGA	TTGAAGGCAG	TCTTCAGCCT	2100
20	ATTATCAAAA	CTGAAGGAGC	CACACTAACA	AAAGTCAAAA	TTGAAGGTGA	ACCTGAATTC	2160
	AGACTGATTA	AAGAAGGTGA	AACAATAACT	GAAGTGATCC	ATGGAGAGCC	AATTATTAAA	2220
	AAATACACCA	AAATCATTTG	TGGAGTGCCT	GTGGAATAAA	CTGAAAAAGA	GACACGAGAA	2280
	GAACGAATCA	TTACAGGTCC	TGAATAAAAA	TACACTAGGA	TTTCTACTGG	AGGTGGAGAA	2340
	ACAGAAAGAA	CTCTGAAGAA	ATTGTTACAA	GAAGAGGTCA	CCAAGGTCAC	CAAATTCATT	2400
25	GAAGGTGGTG	ATGTGTCATT	ATTGTAAGAT	GAAGAAATTA	AAAGACTGCT	TCAGGGAGAC	2460
	ACACCCGTGA	GGAAGTTGCA	AGCCAAACAA	AAAGTTCAAG	GTTCCTAGAA	ACGATTAAAG	2520
	GAAGGTGCTT	CTCAGTGAAA	ATCCAAAAAC	CAGAAAAAAA	TGTTTATACA	ACCCTAAGTC	2580
	AAATAACCTGA	CCTTAGAAAA	TTGTGAGAGC	CAAGTTGACT	TCAGGAACTG	AAACATCAGC	2640
	ACAAAGAGC	AATCATCAAA	TAATTTCTGAA	CACAAATTTA	ATATTTTTTT	TTCTGAATGA	2700
30	GAACATGAG	GAATCATTTG	GAGTTAGCCT	CCTGTGGTAA	AGGAATTGAA	GAAAAATATA	2760
	CACCTTACAC	CCTTTTTTCAT	CTTGACATTA	AAAGTTCTGG	CTAACTTTGG	AATCCATTAG	2820
	AGAAAAATCC	TTTGTCACCG	ATTCAATTACA	ATTCAAATCG	AAGAGTTGTG	AACTGTTATC	2880
	CCATTGAAAA	GACCGAGCCT	TGTATGTATG	TTATGGATAC	ATAAAATGCA	CGCAAGCCAT	2940
35	TATCTCTCCA	TGGGAAGCTA	AGTTATAAAA	ATAGGTGCTT	GGTGACAAA	ACTTTTTTATA	3000
	TCAAAAGGCT	TTGCACATTT	CTATATGAGT	GGGTTTACTG	GTAATTTATG	TTATTTTTTA	3060
	CAACTAATTT	TGTACTCTCA	GAATGTTTGT	CATATGCTTC	TTGCAATGCA	TATTTTTTAA	3120
	TCTCAACGTT	TTCAATAAAA	CCATTTTTC	GATATAAAGA	GAATTACTTC	AAATTGAGTA	3180
	ATTCAGAAAA	ACTCAAGATT	TAAGTTAAAA	AGTGGTTTGG	ACTTGGGAA		

Seq ID NO: 401 Protein sequence
Protein Accession #: NP_006466.1

	1	11	21	31	41	51	
45	MIPFLPMFSL	LLLLIVNPIN	ANNHYDKILA	HSRIRGRDQG	PNVCLQQL	GTKKKYFSTC	60
	KNWYKKSICG	QKTVLYEBC	PGYMRMEGMK	GCPAVLPIDH	VYGTGLIVGA	TTTQRYSDAS	120
	KLREEIEGKG	SFTYFAPSNE	AWDNLDSDIR	RGLESNVNVE	LLNALHSHMI	NKRMLTKDLK	180
	NGMIIPSMYN	NLGLFINHYP	NGVVTVNCAR	IIHGNQIATN	GVVHVIVDRVL	TQIGTSIQDF	240
	IEAEDDLSSF	RAAAATSDIL	EALGRDGHFT	LFAPTNEAFE	KLPRGVLERF	MGDKVASEAL	300
50	MKYHILNLTQ	CSESIMGAV	FETLEGNTIE	IGCDGDSITV	NGIKMVNKKD	IVTNNGVIHL	360
	IDQVLIPDSA	KQVIELAGKQ	QTTFTDLVAQ	LGLASALRPD	GEYTLAPVN	NAFSDDTLSM	420
	VORLLKLILQ	NHILKVKVGL	NELYNGQILE	TIGGKQLRVF	VYRTAVCIEN	SCMEKSGKQG	480
	RNGAIHIFRE	IIKPAEKSILH	EKLQDKRFS	TFLSLLEAAD	LKELLTPQPD	WTLFVPTNDA	540
	FKGMTSEEKE	ILIRDKNALQ	NIIILYHLTPG	VFIGKGFEPG	VTNLIKTTQG	SKIFLKEVND	600
55	TLLVNLKSKS	ESDIMTTNGV	IHVVDKLLYP	ADTPVGNLQ	LEILNKLIK	IQIKFVRGST	660
	FKEIPVTYVT	TKIITKVVEP	KIKVIEGSLQ	PIIKTEGPTL	TKVKIEGEPE	FRLIKEGETI	720
	TEVIHGEPII	KKYTKIIDGV	PVEITEKETR	EERIITGPEI	KYTRISTGGG	ETEBTLKLL	780
	QEEVTKVTKF	IEGGDGLHFE	DEEIKRLLQG	DTPVRKLQAN	KKVQGSRRRL	REGRSQ	

Seq ID NO: 402 DNA sequence
Nucleic Acid Accession #: NM_002416
Coding sequence: 40..417

	1	11	21	31	41	51	
65	ATCCAATACA	GGAGTGACTT	GGAATCCCAT	TCTATCACTA	TGAAGAAAAG	TGGTGTCTTT	60
	TTCCTCTTGG	GCAATCATCT	GCTGGTTCTG	ATTGGAGTGC	AAGGAACCCC	AGTAGTGAGA	120
	AAGGGTCGCT	GTTCTCTGAT	CAGCACCAAC	CAAGGGACTA	TCCACCTACA	ATCCTTGAAA	180
	GACCTTAAAC	AATTTGCCCC	AAGCCCTTCC	TGCGAGAAAA	TTGAAATCAT	TGCTACACTG	240
70	AAGAATGGAG	TTCAAACTAG	TCTAAACCCA	GATTACAGCAG	ATGTGAAGGA	ACTGATTAAA	300
	AAGTGGGAGA	AACAGGTCAG	CCAAAAGAAA	AAGCAAAAGA	ATGGGAAAAA	ACATCAAAAA	360
	AAGAAAGTTC	TGAAAGTTTC	AAAATCTCAA	CGTTCTCGTC	AAAAGAAGAC	TACATAAGAG	420
	ACCACTTCAC	CAATAAGTAT	TCTGTGTTAA	AAATGTTCTA	TTTAAATTAT	ACCGCTATCA	480
	TTCCAAAGGA	GGATGGCATA	TAATACAAAG	GCTTATTAAT	TTGACTAGAA	AATTTAAAC	540
75	ATTACTCTGA	AATTGTAAC	AAAGTTAGAA	AGTTGATTTT	AAGAATCCAA	ACGTTAAGAA	600
	TTGTTAAAGG	CTATGATTGT	CTTTGTTCTT	CTACCACCCA	CCAGTTGAAT	TTTCATCATGC	660
	TTAAGGCCAT	GATTTTAGCA	ATACCCATGT	CTACACAGAT	GTTCAACCAA	CCCATCCCA	720
	CTCAACACAG	CTGCTTGAAA	GAGCAGCCCT	AGGCTTCCAC	GTACTGCAGC	CTCCAGAGAG	780
	TATCTGAGGC	ACATGTCAGC	AAGTCTTAAG	CCTGTTAGCA	TGCTGGTGAG	CCAAGCAGTT	840
80	TGAAATTGAG	CTGGACCTCA	CCAAGCTGCT	GTGGCCATCA	ACCTCTGTAT	TTGAATCAGC	900
	CTACAGGCCT	CACACACAAT	GTGCTGAGA	GATTCATGCT	GATTGTTATT	GGGTATCACC	960
	ACTGGAGATC	ACCAAGTGTG	GGCTTTCAGA	GCCTCCTTTC	TGGCTTTGGA	AGCCATGTGA	1020
	TTCCATCTTG	CCCCTCAGG	CTGACCACCT	TATTTCTTTT	TGTTCCCTTT	TGCTTCATTC	1080
	AAGTCAGCTC	TTCTCCATCC	TACCACAATG	CAGTGCCTTT	CTTCTCTCCA	GTGCACCTGT	1140
	CATATGCTCT	GATTTATCTG	AGTCAACTCC	TTTCTCATCT	TGTCCCCAAC	ACCCACAGA	1200
85	AGTGCTTTCT	TCTCCCAATT	CATCTCACT	CAGTCCAGCT	TAGTTCAAGT	CTCGCTCTTT	1260
	AAATAAACCT	TTTTGGACAC	ACAAATTATC	TTAAACTCC	TGTTTCACTT	GGTTCAGTAC	1320
	CACATGGGTG	AACACTCAAT	GGTTAACTAA	TTCTTGGGTG	TTTATCTTAT	CTCTCCAAAC	1380

AGATTGTCTAG CTCCTTGAGG GCAAGAGCCA CAGTATATTT CCCTGTTTCT TCCACAGTGC 1440
 CTAATAATAC TGTGGAACCTA GGTTTTAATA ATTTTAAAT TGATGTTGTT ATGGGCAGGA 1500
 TGGCAACCAG ACCATTGTCT CAGAGCAGGT GCTGGCTCTT TCCTGGCTAC TCCATGTTGG 1560
 CTAGCCTCTG GTAACCTCTT ACTTATTATC TTCAGGACAC TCACTACAGG GACCAGGGAT 1620
 GATGCAACAT CCTTGTCTTT TTATGACAGG ATGTTTGCTC AGCTTCTCCA ACAATAAGAA 1680
 GCACGTGGTA AAACACTTGC GGATATTCTG GACTGTTTTT AAAAAATATA CAGTTTACCG 1740
 AAAATCATAT AATCTTACAA TGAAAAGGAC TTTATAGATC AGCCAGTGAC CAACCTTTTC 1800
 CCAACCATAC AAAAATTCTT TTTCCGAAAG GAAAAGGGCT TTCTCAATAA GCCTCAGCTT 1860
 TCTAAGATCT AACAAGATAG CCACCGAGAT CCTTATCGAA ACTCATTTTA GGCAAAATATG 1920
 AGTTTTATTG TCCGTTTACT TGTTCAGAG TTTGTATTGT GATTATCAAT TACCACACCA 1980
 TCTCCCATGA AGAAAGGGAA CGGTGAAGTA CTAAGCGCTA GAGGAAGCAG CCAAGTCGGT 2040
 TAGTGGAAAGC ATGATTGGTG CCCAGTTAGC CTCTGCAGGA TGTGGAACCC TCCTTCCAGG 2100
 GGAGGTTTCA TGAATTGTGT AGGAGAGGTT GTCTGTGGCC AGAATTTAAA CCTTACTTCA 2160
 CTTTCCCAAA TTGAATCACT GCTCACACTG CTGATGATTT AGAGTGCTGT CCGGTGGAGA 2220
 TCCCAACCGA ACGTCTTATC TAATCATGAA ACTCCCTAGT TCCTTCATGT AACTTCCCTG 2280
 AAAAATCTAA GTGTTCATA AATTTGAGAG TCTGTGACCC ACTTACCTTG CATCTCACAG 2340
 GTAGACAGTA TATACTAAC AACCAGAGAC TACATATTGT CACTGACACA CAGTTTATAA 2400
 TCATTATCA TATATATACA TACATGCATA CACTCTCAA GCAATAATT TTTCACTTCA 2460
 AAACAGTATT GACTTGTATA CTTTGTAAAT TGAAATATTT TCTTTGTTAA AATAGAAATG 2520
 TATCAATAAA TAGACCATTA ATCAG

Seq ID NO: 403 Protein sequence

Protein Accession #: NP_002407

1 11 21 31 41 51
 MKKSGVLFLI GIIILLVLIGV QGTPVVRKGR CSCISTNQGT IHLQSLKDLK QFAPSPSCEK 60
 IBIIATLKNQ VQTCNLNPSA DVKELIKKWE KQVSQKKKQK NGKKHQKKKV LKVRKSQRSR 120
 QKKRTT

Seq ID NO: 404 DNA sequence

Nucleic Acid Accession #: NM_006670

Coding sequence: 85..1347

1 11 21 31 41 51
 CCGGCTCGCG CCCTCCGGGC CCAGCCTCCC GAGCCTTCGG AGCGGGCGCC GTCCCAGCCC 60
 AGCTCCGGGG AAACGCGAGC CGCGATGCCT GGGGGGTGCT CCCGGGGCCC CGCGCCGGG 120
 GACGGGCGTC TCGGGCTGGC GCGACTAGCG CTGGTACTCC TGGGCTGGGT CTCCTCGTCT 180
 TCTCCACCTT CCTCGGCATC CTCTTCTCC TCCTCGGCGC CGTTCCTGGC TTCGCGCGTG 240
 TCCGCCCAGC CCCGCTGCC GGACCACTGC CCCGCGCTGT GCGAGTGTCT CGAGGCAGCG 300
 CGCACAGTCA AGTGCCTTAA CCGCAATCTG ACCGAGGTGC CCACGGACCT GCCCGCCTAC 360
 GTGCGCAACC TCTTCCTTAC CGGCAACCAG CTGGCCGTGC TCCCTGCGCG CGCCTTCGCC 420
 CGCGGGCGCG CGCTGGCGGA GCTGGCGCGC CTCACCTTCA GCGGCAGCCG CCTGGACGAG 480
 GTGCGCGCGG GCGCCTTCGA GCATCTGCC AGCCTGCGCC AGCTCGACCT CAGCCACAAC 540
 CCACTGGCGG ACCTCAGTCC CTTGCTTTC TCGGGCAGCA ATGCCAGCGT CTCGCCCCCC 600
 AGTCCCTTTG TGGAACTGAT CCTGAACAC ATCGTGCCCC CTGAAGATGA GCGGCAGAAC 660
 CGGAGCTTCG AGGGCATGGT GGTGGCGGCC CTGCTGGCGG GCCGTGCACT GCAGGGGCTC 720
 CGCGCTTTGG AGCTGGCCAG CAACCACTTC CTTTACCTGC CGCGGGATGT GCTGGCCCAA 780
 CTGCCCCAGC TCAGGCACCT GGACTTAAAT AATAATTGCG TGGTGAGCCT GACCTACGTG 840
 TCCTTCCGCA ACCTGACACA TCTAGAAAGC CTCACCTGG AGGACAATGC CCTCAAGTTC 900
 CTTCAACAAT GCACCTGGC TGAGTTGCAA GGTCTACCCC ACATTAGGGT TTTCTTGGAC 960
 AACAACTCCT GGGTCTGCGA CTGCCACATG GCAGACATGG TGACCTGGCT CAAGGAAACA 1020
 GAGGTAGTGC AGGGCAAAGA CCGGCTCACC TGTGCATATC CGGAAAAAAT GAGGAATCGG 1080
 GTCCTCTTGG AACTCAACAG TGCTGACCTG GACTGTGACC CGATTCTTCC CCCATCCCTG 1140
 CAAACCTCTT ATGTCTTCTT GGGTATTGTT TTAGCCCTGA TAGGCGCTAT TTTCTCTCTG 1200
 GTTTTGTATT TGAACCGCAA GGGGATAAAA AAGTGGATGC ATAACATCAG AGATGCCCTG 1260
 AGGGATCACA TGGAAAGGTA TCATTACAGA TATGAAATCA ATGCGGACCC CAGATTAACA 1320
 AACCTCAGTT CTAACCTCGA TGTCTGAGAA ATATTAGAGG ACAGACCAAG GACAACTCTG 1380
 CATGAGATGT AGACTTAAGC TTTATCCCTA CTAGGCTTGC TCCACTTTCA TCCTCCACTA 1440
 TAGATACAA GACCTTTTGC TAAAGCAGT GAAGGGGATT TGCTTCTTGT TTATGTAAAG 1500
 TTTCTCGGTG TGTCTGTTA ATGTAAGACG ATGAACAGTT GTGTATAGTG TTTTACCTTC 1560
 TTCTTTTCTT TGGAACTCCT CAACACGTAT GGAGGGATTT TTCAGGTTTC AGCATGAACA 1620
 TGGGCTTCTT GCTGTCTGTC TCTCTCTCAG TACAGTTCAA GGTGTAGCAA GTGTACCCAC 1680
 ACAGATAGCA TTCAACAAAA GCTGCCTCAA CTTTTTCGAG AAAAAACTT TATTATATAA 1740
 TATCAGTTT ATTCTCATGT ACCTAAGTTG TGGAGAAAAA AATTGCATCC TATAAACTGC 1800
 CTGCAGACGT TAGCAGGCTC TTCAAATAA CTCCATGGTG CACAGGAGCA CCTGCATCCA 1860
 AGAGCATGCT TACATTTTAC TGTCTGTCAT ATTACAAAAA ATAACCTGCA ACTTCATAAC 1920
 TTCTTTGACA AAGTAAATTA CTTTTTTGAT TGCAGTTTAT ATGAAAAATG ACTGATTTT 1980
 TTTTAATAAA CTGCATCGAG ATCCAACCGA CTGAATTGTT AAAAAAATAA AAAAAATAAG 2040
 ATTCTTAAAA GAA

Seq ID NO: 405 Protein sequence

Protein Accession #: NP_006661

1 11 21 31 41 51
 MPGGCSRGP AAGDRLRLAR LALVLLGWVS SSSPTSSASS FSSSAPFLAS AVSAQPPLED 60
 QCPALCECSE AARTVKCVNR NLTEVPTDLP AYVRNLFLTG NQLAVLPAGA FARRPPLAEL 120
 AALNLSGSR LDEVAGAFEH LPSLRQLDLS HNPDLADLSPF AFSGSNASVS APSPLVELIL 180
 NHIVPEPDER QNRSEFEGMVV AALLAGRALQ GLRRLLELASN HFLYLPRLDV LQPLSLRHL 240
 LSNLSVSLT YVSRNLTHL ESHLEDNAL KVLHNGTLAE LQGLPHIRVF LDNNPWCDC 300
 HMDMVTWLK ETEVVQKDR LTCAYPEKMR NRVLLELNSA DLDLDPILPP SLQTSYVFLG 360
 IVLALIGAI FLLVLYLNRK IKKMMHNI RDACRDHMEGYH YRYEINADPR LTNLSSNSDV

Seq ID NO: 406 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..927

1	11	21	31	41	51	
5	ATGCTGCGGG	GGTGTCCCG	GGGCCCCGCC	GCCGGGGACG	GGCGTCTGCG	GCTGGCGCGA 60
	CTAGCGCTGG	TACTCCTGGG	CTGGGTCTCC	TCGTCTTCTC	CCACCTCCTC	GGCATCCTCC 120
	TTCTCCTCCT	CGGCGCCGTT	CCTGGCTTCC	GCCGTGTCCG	CCCAGCCCCC	GCTGCCGGAC 180
	CAGTGCCCCG	CGCTGTGCGA	GTGCTCCGAG	GCAGCGCGCA	CAGTCAAGTG	CGTTAACCGC 240
	AATCTGACCG	AGGTGCCCCAC	GGACTGCCCC	GCCTACGTGC	GCAACCTCTT	CCTTACCGGC 300
10	AACCAGCTGG	CCAGCAACCA	CTTCCTTTAC	CTGCCGCGGG	ATGTGCTGSC	CCAACTGCCC 360
	AGCCTCAGGC	ACCTGGACTT	AAGTAATAAT	TCGCTGGTGA	GCCTGACCTA	CGTGCTCTTC 420
	CGCAACCTGA	CACATCTAGA	AAGCTCCAC	CTGGAGGACA	ATGCCCTCAA	GGTCCTTCAC 480
	AATGGCACCC	TGGCTGAGTT	GCAAGGTCTA	CCCCACATTA	GGGTTTTCCT	GGACAACAAT 540
	CCCTGGGTCT	GCGACTGCCA	CATGGCAGAC	ATGGTGACCT	GGCTCAAGGA	AACAGAGGTA 600
15	GTGCAAGGCA	AAGACCGGCT	CACCTGTGCA	TATCGGAAA	AAATGAGGAA	TCCGGTCTCT 660
	TTGGAAGTCA	ACAGTGCTGA	CCTGGACTGT	GACCCGATTC	TTCCCCATC	CCTGCAAAAC 720
	TCTTATGTCT	TCCTGGGTAT	TGTTTTAGCC	CTGATAGGCG	CTATTTTCCT	CCTGGTTTTC 780
	TATTTGAACC	GCAAGGGGAT	AAAAAGTGG	ATGCATAACA	TCAGAGATGC	CTGCAGGGAT 840
20	CACATGGAAG	GGTATCATT	CAGATATGAA	ATCAATGCGG	ACCCAGATT	AACAAACCTC 900
	AGTTCTAACT	CGGATGTCT	CGAGTGA			

Seq ID NO: 407 Protein sequence
Protein Accession #: Eos sequence

25	1	11	21	31	41	51	
	MPGGCSRGP	AGDGRRLAR	LALVLLGWVS	SSSPTSSASS	FSSSAPFLAS	AVSAQPPLPD	60
	QCPALCECE	AARTVKCNVR	NLTVPTDLP	AYVRNLFITG	NQLASNHFLY	LPRDVLQALP	120
	SLRHLDLN	SLVSLTVYSF	RNLTHLESLH	LEDNALKVLH	NGTLAELOGL	PHIRVFLDNN	180
30	PWVCDCHMAD	MVTWLKETE	VQKDRILTCA	YPEKMRNRVL	LELNSADLDC	DPILPPLSLQ	240
	SYVFLGIVLA	LIGAILFLVL	YLNKRGIKKW	MHNIRDACRD	HMEGYHYRYE	INADPRLTNL	300
	SSNSDVLE						

35 Seq ID NO: 408 DNA sequence
Nucleic Acid Accession #: NM_000095.1
Coding sequence: 26..2299

40	1	11	21	31	41	51	
	CAGCACCCAG	CTCCCCGCCA	CCGCCATGGT	CCCCGACACC	GCCTGCGTTC	TTCTGCTCAC	60
	CCTGGCTGCC	CTCGCGCGGT	CCGGACAGGG	CCAGAGCCCC	TTGGGCTCAG	ACCTGGGCCC	120
	GCAGATGCTT	CGGGAACATG	AGGAACACAA	CGCGGCGCTG	CAGGACGTGC	GGGACTGGCT	180
	GCGGCAGCAG	GTGAGGGAGA	TCACGTTTCT	GAAAAACACG	GTGATGGAGT	GTGACGCGTG	240
	CGGATGACAG	CAGTCAGTAC	GCACCGGCTT	ACCCAGCGTG	CGGCCCCGTC	TCCACTGCGC	300
45	GCCCGGCTTC	TGCTTCCCCG	GCGTGCGCTG	CATCCAGACG	GAGAGCGGCG	GCCGCTGCGG	360
	CCCCTGCCCC	GCGGGCTTCA	CGGGCAACGG	CTCGCACTGC	ACCGACGTCA	ACGAGTGCAA	420
	CGCCACCCCC	TGCTTCCCCC	GAGTCCGCTG	TATCAACACC	AGCCCGGGGT	TCCGCTGCGA	480
	GGCTTGCCCC	CCGGGGTACA	GCGGCCCCAC	CCACCAGGGC	GTGGGGCTGG	CTTTGCGCAA	540
	GGCCAACAAG	CAGGTTTGCA	CGGACATCAA	CGAGTGTGAG	ACCGGGCAAC	ATAACTGCGT	600
50	CCCCAACTCC	GTGTGCATCA	ACACCCGGGG	CTCCTTCCAG	TGCGGCCCGT	GCCAGCCCGG	660
	CTTCGTGGGC	GACCAAGCGT	CCGGCTGCCA	GCGCGGCGCA	CAGCGCTTCT	GCCCCGACGG	720
	CTCGCCACAG	GAGTGCCACG	AGCATGCAGA	CTGCGTCTTA	GAGCGCGATG	GCTCGCGGTC	780
	GTGCGTGTGT	GCGCTGGCTT	GGGCGGCAAA	CGGGATCCTC	TGTGGTCCGG	ACACTGACCT	840
	AGACGGCTTC	CCGGACGAGA	AGCTGCGCTG	CCCCGAGCCG	CAGTGCCGTA	AGGACAACCTG	900
55	CGTGACTGTG	CCCAACTCAG	GGCAGGAGGA	TGTGGACCGC	GATGGCATCG	GAGACGCTCG	960
	CGATCCGGAT	GCCGACGGGG	ACGGGGTCCC	CAATGAAAAG	GACAACCTGC	CGTGGTGCG	1020
	GAACCCAGAC	CAGCGCAACA	CGGACGAGGA	CAAGTGGGGC	GATGCGTGCG	ACAACCTGCC	1080
	GTCCCAAGAG	AACGACGACC	AAAGGACAC	AGACCAGGAC	GGCCGGGGCG	ATGCGTGCGA	1140
	CGACGACATC	GACGGCGACC	GGATCCGCAA	CCAGGCCGAC	AACTGCCCTA	GGGTACCCAA	1200
60	CTCAGACACG	AAGGACAGTG	ATGGCGATGG	TATAGGGGAT	GCCTGTGACA	ACTGTCCCCA	1260
	GAAGAGCAAC	CCGATCAGG	CGGATGTGGA	CCACGACTTT	GTGGGAGATG	CTTGTGACAG	1320
	CGATCAAGAC	CAGGATGGAG	ACGGACATCA	GGACTCTCGG	GACAACTGTC	CCACGCTGCC	1380
	TAACAGTGCC	CAGGAGGACT	CAGACCACGA	TGGCCAGGGT	GATGCCTGCG	ACGACGACGA	1440
	CGACAATGAC	GGAGTCCCTG	ACAGTCCGGA	CAACTGCCGC	CTGGTGCCCTA	ACCCCGGCCA	1500
65	GGAGGACGCG	GACAGGGACG	GCGTGGGCGA	CGTGTGCCAG	GACGACTTTG	ATGCAGACAA	1560
	GGTGGTAGAC	AAGATCCGAG	TGTGTCCGGA	GAACGCTGAA	GTCACGCTCA	CCGACTTCAG	1620
	GGCCTTCCAG	ACAGTCTGTC	TGGACCCGGA	GGGTGACGCG	CAGATTGACC	CCAACTGGGT	1680
	GGTGTCAAC	CAGGGAAGGG	AGATCGTGCA	GACAATGAAC	AGCGACCCAG	GCCTGGCTGT	1740
	GGGTACACT	GCCTTCAATG	GCGTGGACTT	CGAGGGCACG	TTCCATGTGA	ACACGGTCAC	1800
70	GGATGACGAC	TATGCGGGCT	TCATCTTTGG	CTACCAGGAC	AGCTCCAGCT	TCTACGTGGT	1860
	CATGTGGAAG	CAGATGGAGC	AAACGTATTG	GCAGGCGAAC	CCCTTCCGTG	CTGTGGCCGA	1920
	GCCTGGCATC	CAACTCAAGG	CTGTGAAGTC	TTCCACAGGC	CCCGGGGAAC	AGCTGCGGAA	1980
	CGCTCTGTGG	CATACAGGAG	ACACAGAGTC	CCAGGTGCGG	CTGCTGTGGA	AGGACCCGCG	2040
	AAACGTGGGT	TGGAAGGACA	AGAAGTCCTA	TCGTTGGTTC	CTGCAGCACC	GGCCCCAAGT	2100
75	GGGCTACATC	AGGGTGCGAT	TCTATGAGGG	CCCTGAGCTG	GTGGCCGACA	GCAACGTGGT	2160
	CTTGAGACCA	ACCATGCGGG	GTGGCCGCTT	GGGGTCTTTC	TGCTTCTCCC	AGGAGAACAT	2220
	CATCTGGGCC	AACCTGCGTT	ACCGCTGCAA	TGACACCATC	CCAGAGGACT	ATGAGACCCA	2280
	TCAGTGTGCG	CAAGCCTAGG	GACCAGGGTG	AGGACCCGCC	GGATGACAGC	CACCTCACCC	2340
	GCGGCTGGAT	GGGGGCTCTG	CACCCAGCCC	AAGGGGTGGC	CGTCTGAGG	GGGAAGTGAG	2400
80	AAGGCTCAG	AGAGGACAAA	ATAAGTGTG	TGTGCAGGG			

Seq ID NO: 409 Protein sequence
Protein Accession #: NP_000086.1

85	1	11	21	31	41	51	
	MVPDTACVLL	LTLAALGASG	QQQSPLGSDL	GPQMLRELQE	TNAALQDVDR	WLRQQVREIT	60

FLKNTVMEDC ACGMQQSVRT GLPSVRPLLH CAPGFCFFGV ACIQTESGGR CGPCPAGFTG 120
NGSHCTDVNE CNAHPCFPRV RCINTSPGFR CEACPPGYSG PTHQGVGLAF AKANKQVCTD 180
INECETGQHN CVPNSVCINT RGSFQCGPCQ PGFVGDQASG CQRGAQRFCP DGSPSECHEH 240
ADCVLERDGS RSCVCRVQWA GNGILCGRDT DLDGFPDEKL RCPEPQCRKD NCVTVPNNSGQ 300
EDVDRDGGID ACDPDADGDG VPNEKDNCPV VRNPDQRNTD EDKWDGACDN CRSQKNDQDK 360
5 DTDQDGRGDA CDDIDIDGRI RNQADNCPRV PNSDQKSDSG DGIGDACDNC PQKSNPDQAD 420
VDHDFVGDAC DSDQDQDGDG HQDSRDNCPT VPNSAQEDSD HDGQGDACDD DDDNDGVPPDS 480
RDNCRLVPNP GQEDADRDGV GDVCQDDFDA DKVVDKIDVC PENAETVLTID FRAFQTVVLD 540
10 PEGDAQIDPN WVVLNQGREI VQTMNSDPGL AVGYTAFNGV DFEGTFHVNT VTDDDYAGFI 600
FGYQSSSFY VVMWQMEQY YWQANPFRAV AEPGIQLKAV KSSTGPGEQL RNALWHTGDT 660
BSQVRLWKD PRNVGWKDKK SYRWFLQHRP QVGYIRVRFY EGPELVADSN VVLDTTMRGG 720
RLGVFCFSQE NIIWANLRYR CNDTIPEDYE THQLRQA

Seq ID NO: 410 DNA sequence
Nucleic Acid Accession #: NM_001565.1
Coding sequence: 67..363

1 11 21 31 41 51
| | | | | |
20 GAGACATTCC TCAATTGCTT AGACATATTC TGAGCCTACA GCAGAGGAAC CTCCAGTCTC 60
AGACCATGGA ATCAAACTGC GATTCGTATT TGCTGCCTTA TCTTCTGAC TCTAAGTGGC 120
ATTCAAGGAG TACCTCTCTC TAGAACCGTA CGCTGTACCT GCATCAGCAT TAGTAATCAA 180
CCTGTAAATC CAAGGTCTTT AGAAAACTT GAAATTATTC CTGCAAGCCA ATTTTGTCCA 240
25 CGTGTGAGA TCATTGTCTAC AATGAAAAAG AAGGGTGAGA AGAGATGTCT GAATCCAGAA 300
TCGAAGGCCA TCAAGAATTT ACTGAAAGCA GTTAGCAAGG AAATGTCTAA AAGATCTCCT 360
TAAACCAGGA GGGGAGCAGAA ATCGATGCAG TGCTTCCAAG GATGGACCAC ACAGAGGCTG 420
CCTCTCCCAT CACTTCCCTA CATGGAGTAT ATGTCAAGCC ATAATTGTTC TTAGTTTGCA 480
GTTACACTAA AAGGTGACCA ATGATGGTCA CCAATCAGC TGCTACTACT CCTGTAGGAA 540
GGTTAATGTT CATCATCCTA AGCTATTGAG TAATAACTCT ACCCTGGCAC TATAATGTAA 600
30 GCTCTACTGA GGTCTATGT TCTTAGTGA TGTCTGACC CTGCTTCAA TATTTCCCTC 660
ACCTTTCCCA TCTTCCAAAG GTACTAAGGA ATCTTCTCG TTTGGGGTTT ATCAGAATTC 720
TCAGAATCTC AAATAACTAA AAGGTATGCA ATCAAATCTG CTTTTTAAAG AATGCTCTTT 780
ACTTCATGGA CTTCCACTGC CATCTCCCA AGGGGCCCAA ATTCTTTCAG TGGCTACCTA 840
CATACAATTC CAAACACATA CAGGAAGGTA GAAATATCTG AAAATGTATG TGTAAAGTAT 900
35 CTTATTTAAT GAAAGACTGT ACAAAGTATA AGTCTTAGAT GTATATATTT CCTATATGT 960
TTTCAGTGT CATGGAATA CATGTAATTA AGTACTATGT ATCAATGAGT AACAGGAAAA 1020
TTTAAAAAT ACAGATAGAT ATATGCTCTG CATGTTACAT AAGATAAATG TGCTGAATGG 1080
TTTTCAAATA AAAATGAGGT ACTCTCCTGG AAATATTAAG

Seq ID NO: 411 Protein sequence
Protein Accession #: NP_001556.1

1 11 21 31 41 51
| | | | | |
45 MNQTALICC LIFLTLGSIQ GVPLSRTVRC TCISISNQPV NPRSLEKLEI IPASQFCPRV 60
ELIATMKKKK EKRLCLNPESK AIKLLKAVS KEMSKRSP

Seq ID NO: 412 DNA sequence
Nucleic Acid Accession #: XM_057014
Coding sequence: 143..874

1 11 21 31 41 51
| | | | | |
55 GGGAGGGGAGA GAGGCGCGCG GGTGAAAGGC GCATTGATGC AGCCTGCGGC GGCCTCGGAG 60
CGCGGCGGAG CCAGACGCTG ACCACGTTCC TCTCCTCGGT CTCCTCGGCC TCCAGCTCCG 120
CGCTGCCCGG CAGCCGGGAG CCATGCGACC CCAGGGCCCC GCCCGCTCCC CGCAGCGGCT 180
CCGCGGCTCT CTGCTGTCTC TGCTGTCTGA GCTGCCCCGC CCGTCGAGCG CCTCTGAGAT 240
CCCCAAGGGG AAGCAAAAGG CGCAGCTCCG GCAGAGGGAG GTGGTGGACC TGTATAATGG 300
AATGTGCTTA CAAGGGCCAG CAGGAGTGCC TGGTCGAGAC GGGAGCCCTG GGGCCAATGG 360
60 CATTCGGGGT ACACCTGGGA TCCCAGGTCG GGTGAGATT AAAGGAGAAA AGGGGGAATG 420
TCTGAGGAAA AGCTTTGAGG AGTCTGGAC ACCCAACTAC AAGCAGTGTT CATGGAGTTT 480
ATTGAATTAT GGCATAGATC TTGGGAAAAT TGCGGAGTGT ACATTACAA AGATGCGTTC 540
AAATAGTGCT CTAAGAGTTT TGTTCAAGTG CTCACTTCGG CTAAAATGCA GAAATGCATG 600
CTGTGAGCGT TGGTATTTC CATTCAATGG AGCTGAATGT TCAGGACCTC TTCCCATTTA 660
65 AGCTATAATT TATTTGGACC AAGGAAGCCC TGAATGAAT TCAACAAATTA ATATTTCATC 720
CACTTCTTCT GTGGAAGGAC TTTGTGAAGG AATTGGTGCT GGATTAGTGG ATGTGCTAT 780
CTGGGTGGC ACTTGTTCAG ATTACCCAAA AGGAGATGCT TCTACTGGAT GGAATTCAGT 840
TTCTCGCATC ATTATTGAAG AACTACCAA ATAAATGCTT TAATTTTCAT TTGCTACCTC 900
70 TTTTATTATT ATGCTTGGGA ATGGTTCAC TAAATGACAT TTTAAATAAG TTTATGTATA 960
CATCTGAATG AAAAGCAAAG CTAATATGT TTACAGACCA AAGTGTGATT TCACACTGTT 1020
TTTAAATCTA GCATTATTCA TTTTGCTTCA ATCAAAAGTG GTTTCATAT TTTTTTTAGT 1080
TGGTTAGAA ACTTTCTTCA TAGTCACATT CTCTCAACCT ATAATTTGGA ATATTGTTGT 1140
GGTCTTTTGT TTTTCTCTT AGTATAGCAT TTTTAAAAAA ATATAAAAGC TACCAATCTT 1200
75 TGTACAAATT GTAAATGTTA AGAATTTTTT TTATATCTGT TAAATAAAAA TTATTTCCTA 1260
CAACCTTAAA AAAAAAAAAA AAAA

Seq ID NO: 413 Protein sequence
Protein Accession #: XP_057014

1 11 21 31 41 51
| | | | | |
80 MRPQGPAASP QLRGLLLLLL LLQLPAPSSA SEIPKQKQKA QLRQREVVDL YNGMCLQGPA 60
GVPGRDGSFG ANGIPTGPGI PGRDGFKEK GECLRESFEE SWTPNYKQCS WSSLNYGIDL 120
85 GKIAECTFTK MRSNSALRVL FSGSLRLKCR NACCQRWYFT FNGAECGSPF PIELIYLDQ 180
GSPENNSTIN IHRSSVEGL CEGIGAGLVD VAIWVGTCSD YPKGDASTGW NSVSRILIEE 240
LPK

Seq ID NO: 415 Protein sequence
Protein Accession #: XP_084007

Seq ID NO: 416 DNA sequence
Nucleic Acid Accession #: NM_015419.1
Coding sequence: 1..8487

	1	11	21	31	41	51	
5	ATGCCCAAGC	GCGCGCACTG	GGGGGCCCTC	TCCGTGGTGC	TGATCCTGCT	TTGGGGCCAT	60
	CCGCGAGTGG	CGCTGGCCCTG	CCC GCATCCT	TGTGCTCTGCT	ACGTCCCCAG	CGAGGTCCAC	120
	TGCACGTTCC	GATCCCTGGC	TTCCGTGCCC	GCTGGCATTG	CTAGACACGT	GGAAAGAATC	180
	AATTTGGGGT	TTAATAGCAT	ACAGGCCCTG	TCAGAAACCT	CATTTGCAGG	ACTGACCAAG	240
	TTGGAGCTAC	TTATGATTCA	CGGCAATGAG	ATCCCAAGCA	TCCCCGATGG	AGCTTTAAGA	300
10	GACCTCAGCT	CTCTTCAGGT	TTTCAAGTTC	AGCTACAACA	AGCTGAGAGT	GATCACAGGA	360
	CAGACCCCTCC	AGGGTCTCTC	TAACCTTAATG	AGGCTGCACA	TTGACCACAA	CAAGATCGAG	420
	TTTATCCACC	CTCAAGCTTT	CAACGGCTTA	ACGTCTCTGA	GGCTACTCCA	TTTGGAAAGGA	480
	AATCTCCTCC	ACCAGCTGCA	CCCCAGCACC	TTCTCCACGT	TCACATTTT	GGATTATTTC	540
	AGACTCTCCA	CCATAAGGCA	CCTCTACTTA	GCAGAGAAAC	TGGTTAGAAC	TCTTCTGCCC	600
15	AGCATGCTTC	GGAAACATGCC	GCTTCTGGAG	AATCTTTACT	TGCAGGGAAA	TCCGTGGACC	660
	TGCCATTGTG	AGATGAGATG	GTTTTTGGAA	TGGGATGCAA	AATCCAGAGG	AATTCTGAAG	720
	TGTAAAAAAG	ACAAAGCTTA	TGAAGGCGGT	CAGTTGTGTG	CAATGTGCTT	CAGTCCAAAG	780
	AAGTTGTACA	AACATGAGAT	ACACAAGCTG	AAGGACATGA	CTTGTCTGAA	GCCTTCAATA	840
	GAGTCCCCCTC	TGAGACAGAA	CAGGAGCAGG	AGTATTGAGG	AGGAGCAAGA	ACAGGAAGAG	900
20	GATGGTGGCA	GCCAGCTCAT	CCTGGAGAAA	TTCCAACCTGC	CCCAGTGGAG	CATCTCTTTG	960
	AATATGACCG	ACGAGCACGG	GAACATGGTG	AACCTGGTCT	GTGACATCAA	GAAACCAATG	1020
	GATGTGTACA	AGATTCACTT	GAACCAACG	GATCCTCCAG	ATATTGACAT	AAATGCAACA	1080
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Protein Accession #: NP_056234.1

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	TCGACAGAAA	TCACTGGGGT	GGAGGAGCTG	GGTTCCCGGG	AGGACTCGCC	CATGTCACCC	1260
	TCAGACACCC	AAGACCAGAA	ACGACCCCTG	AGGCCGCCAA	GTAGACACGG	CCACTCGGTG	1320
75	GTTGCTCCCG	GCAGGACTGC	AGTGAGGGCC	CGGATGCCAG	CGCTGCCCCG	AAGGGAAGGC	1380
	GTAGATAAGC	CTGGCTTTTC	CCTGGCCACG	CAGCCCGGCC	CAGGGGCGCC	CCCCTCGGCT	1440
	TCGGCCTCTC	CTGCCACCA	CGCGTCCACC	CAGGGCACCT	CTCATCGTCC	TTCCCTGCCT	1500
	GCCAGCTTGA	ATGACAACTG	CTTGGTGGAC	TCAGACGAAG	ATGAGCGCGC	TGTGGGCTCT	1560
	CTCCACCCCA	AGGGCGCCTT	CGCCAGCCCC	CGGCCAGCCC	TGTCCCCCAG	CCGCCAGTCC	1620
80	CCGTCACGCG	TTCTCCGCGT	CAGAAGCTCT	GTGCACCCCG	GCGCAAGGCC	AGCCTCGCCG	1680
	GCGCGGAGGA	CCCCCATATC	AGGGGCCGCA	GAGGAAGATT	CCAGTGCCTC	AGCCCAACCC	1740
	TCAAGACTTT	CTCCACCCCA	TGGGGGATCA	TCTCGGCTGC	TGCCACCCCA	GCCACACCTG	1800
	AGCTCTCCAC	TTTCCAAGGG	CGGGAAGGAT	GGTGAGGACG	CCCCAGCCAC	CAACTCCAAT	1860
	GCGCCATCAC	GGTCCACCAT	GTCTCTCTCT	ATCTCTCGTC	CAGGACGCAG		1920
	GTCTCTGAGG	GAGCGGAGGC	TTCTGATGGT	GAAAGCCACG	GTGACGGCGA	TAGGGAAGAC	1980
85	GGCGGAAGGC	AGGCGGAGGC	CACGGCCACG	ACGCTGCGGG	CCCGCCCTCG	CTCTGGACAC	2040
	TTCCATTTCG	TCAGACACAA	ACCCTTTGCT	GCCAAACGGA	GGTCTCCAAG	CAGGTTCAAG	2100
	ATTGGGCGGG	GACCTCGGCT	GCAGCCCTCC	AGCTCCCCAC	AGTCGACTGT	GCCCTCCCGA	2160

	GCCACCCCA	GGGTTCCTC	TCACTCTGAT	TCCCACCCTA	AGCTTAGCTC	AGGTATCCAT	2220
	GGAGACGAGG	AGGATGAGAA	GCCGCTTCCT	GCCACCGTTG	TCAATGACCA	CGTGCCTTCC	2280
	TCCTCCAGGC	AGCCCATCTC	CCGGGGCTGG	GAGGACTTAA	GGAGAAGCCC	GCAGAGAGGG	2340
	GCCAGCCTGC	ATCGGAAGGA	ACCCATCCCA	GAGAACCCCA	AATCCACAGG	GGCAGATACA	2400
5	CATCCTCAGG	GCAAGTACTC	CTCCCTGGCC	TCCAAGGCTC	AGGATGTTCA	ACAGAGCACA	2460
	GACGCGGACA	CGGAGGGTCA	TTCTCCCAAA	GCACAGCCAG	GGTCCACAGA	CCGCCACGCG	2520
	TCCCTTGCTC	GTCTCTCCGC	AGCACGGTCA	CAGCAGCATC	CCAGTGTTC	CAGAAGGATG	2580
	ACACCCGGCC	GGGCCCCAGA	ACAGCAGCCC	CCTCCTCCCG	TCGCCACGTC	CCAGCACCAC	2640
10	CCGGGACCCC	AGAGCAGAGA	CGCGGGTCGG	TCACCTTCCC	AGCCCAGGCT	CTCACTGACC	2700
	CAGGCCGGGC	GGCCCCGGCC	CACGTCGCAG	GGCCGCTCCC	ACTCCTCCTC	GGACCTTAC	2760
	ACGGCGAGCT	CCAGAGGGAT	GCTCCCCACG	GCCCTCCAGA	ACCAGGACGA	GGATGCCCAG	2820
	GGCAGCTACG	ACGACGACAG	CACAGAAATC	GAGGCCCAGG	ATGTGCGGGC	CCCCGCGCAC	2880
	GCCGCGCGCG	CCAAGGAGGC	AGCTGCGTCC	CTTCCCAAGC	ACCAGCAGGT	GGAGTCTCCC	2940
15	ACAGGCGCAG	GGGCAGGTGG	CGACCACAGG	TCCCAGCGCG	GACATGCGGC	CTCCCCCGCC	3000
	AGGCCACGAG	GACCCGGGGG	CCCCCAGTCC	CGCGCCCGGG	TCCCCAGCAG	GGCAGCGCCG	3060
	GGGAAGTCGG	AGCCTCTCTC	CAAGCGGGCC	CTGTCTCCA	AGTCCCAGCA	GTGCGTCTCA	3120
	GCCGAGGACG	AGGAGGAGGA	GGACGCGGGG	TTTTTTAAAG	GCGGGAAGA	AGACCTTCTG	3180
	TCTTCTCTG	TGCCAAAGTG	GCCCTCTTCC	TCCACTCCCA	GGGGCGGCAA	AGACGCCGAT	3240
20	GGGAGCCTCG	CCAAGGAAGA	GAGGGAGCCT	GCCATCGGCG	TTGCCCCTCG	CGGAGGGAGC	3300
	CTGGCTCTCG	TGAAGCGACC	TCTCCCCCA	CCTCCAGGCA	GCTCCCCCAG	GGCCTCCAC	3360
	GTCCCTTCCC	GACGCGCGCC	TCGCAGCGCT	GCCACCGTGA	GCCCCGTGCG	GGGCACCCAC	3420
	CCCTGGCCGC	GGTACACCAC	CGCGCGCCCV	CCTGGCCACT	TCTCCACCAC	CCCGATGCTG	3480
	TCCTTGCGCG	AGAGGATGAT	GCATGCCAGA	TTCCGTAAAC	CTCTCTCCCG	ACAGCCTGCC	3540
25	AGACCTCTT	ACAGACAAGG	TTATAATGGC	AGACCAAATG	TAGAAGGGAA	AGTCTCTCTT	3600
	GGTAGTAATG	GAAAAACCGAA	TGGACAGAGA	ATTATCAATG	GCCCTCAAGG	AACAAAGTGG	3660
	GTTGTGGACC	TTGATCGTGG	GTTAGTATTG	AATGCAGAAG	GAAGGTACCT	CCAAGATTCA	3720
	CATGGAAATC	CTCTTCGGAT	TAAACTAGGA	GGAGATGGTC	GAACCATTGT	AGATCTGGAA	3780
	GGGACCCCGG	TGGTGAGTCC	TGACGGCCCTC	CCACTCTTTG	GGCAGGGGCG	ACATGGCACA	3840
30	CCTCTGGCCA	ATGCCCAAGA	TAAGCCAATT	TTGAGTCTTG	GAGGAAAGCC	GCTGGTGGGC	3900
	TTGGAGGTCA	TCAAAAAAAC	CACCCATCCC	CCTACCACTA	CCATGCAGCC	CACCACTACT	3960
	ACGACGCCCC	TGCCTACCAC	TACAAACCCG	AGGCCCAACA	CTGCCACCAC	CATGCAGCCC	4020
	ACCACCTACTA	CGACGCCCTC	GCCTTACCCT	ACACCGAGGC	CCACCCTGTC	CACCAACCGC	4080
	CGCAGCAGCA	CCAGCGCTCC	AACAAACCACA	GTCCGAACCA	CTACGCGGAC	AACCAACCAC	4140
35	ACCACCCCA	AACCCACCAC	TCCCATCCCC	ACCTGTCCCC	CTGGGACCTT	GGAACGGCAC	4200
	GACGATGATG	GCAACCTGAT	AATGAGCTCC	AATGGGATCC	CAGAGTGCTA	CGCTGAAGAA	4260
	GATGAGTTCT	CAGGCTTGGG	GACTGACACT	GCAGTACCTA	CGGAAGAGGC	CTACGTATATA	4320
	TATGATGAAG	ATTATGAATT	TGAGACGTCA	AGGCCACCAA	CCACCCTGGA	GCCTTCGACC	4380
	ACTGCTACCA	CACCGAGGGT	GATCCAGAG	GAAGCGCCA	TCAGTTCCTT	TCCTGAAGAA	4440
40	GAATTTGATC	TGGCTGGGAG	GAAACGATTT	GTTGCTCCTT	ACGTGACGTA	CCTAAATAAA	4500
	GACCCATCAG	CCCCGTGCTG	TCTGACTGAT	GCACCTGGATC	ACTTCCAAGT	GGACAGCCTG	4560
	GATGAAATCA	TCCCCAATGA	CCTGAAGAAG	AGTGATCTGC	CTCCCCAGCA	TGCTCCCCGC	4620
	AACATCACCG	TGGTGGCCGT	GGAAGGTTGC	CACTCATTTC	TCATTGTGGA	TTGGGACAAA	4680
	GCCACCCAG	GAGATTTGGT	CACAGGTTAT	TTGGTTTACA	GTGCATCCTA	TGAAGATTTC	4740
45	ATCAGGAACA	AGTTTTCAC	TCAAGCTTCA	TCAGTAACTC	ACTTGCCCAT	TGAGAACCTA	4800
	AAGCCCAACA	CGAGGTATTA	TTTTAAAGTG	CAAGCACAAA	ATCCTCATGG	CTACGGACCT	4860
	ATCAGCCCTT	CGGTCTCAT	TGTCACCGAA	TCAGATAATC	CTCTGCTTGT	TGTGAGGCCC	4920
	CCAGGCGGTG	AGCTATCTGG	ATCCCATTCG	CTTTCAAACA	TGATCCCAGC	TACACGGACT	4980
	GCCATGGACG	GCAATATGTG	AAGCGCACGT	GGTATCGAAA	GTTTCGTGGGA	GTTGTTCTTT	5040
50	GTAATTCACT	GAGGTATAAA	ATCTACCTCA	GTGACAACTT	GAAAGATACA	TTCTACAGCA	5100
	TTGGAGACAG	CTGGGGAAGC	GGTGAAGACC	ATTGCCAATT	TGTGGATTCA	CACCTTGATG	5160
	GAAGAACAGG	GCCTCAGTCC	TATGTAGAAG	CCCTCCCTAC	TATTCAAGGC	TACTATCGCC	5220
	AGTATCGTCA	GGAGCCTGTC	AGGTTTGGGA	ACATCGGCTT	CGGAACCCCC	TACTACTATG	5280
	TGGGCTGGTA	CGAGTGTGGG	GTCTCCATCC	CTGGAAGTGG	GTAATCACAG	GACCGTCATG	5340
55	CTGCAAGCTT	GCCCTGCCCA	GCCCCACCAA	CTAAGTCGCA	CTAGGGGCTG	TGAGCAAAGA	5400
	CAGCCAGCAT	GCTCAGCCCC	GCTGCCCTAG	GTGCCAGGAA	GGTCACAGAT	GGACACTGGC	5460
	CATTCTGCTC	ATCTCAGTCT	GGAACCTCAG	CCCCTCTCTT	GGCCTGGACA	ATGAACAGGA	5520
	TTCAGTTTTC	CTGTTAATCT	TGCTTCTCTA	CTTTTCTTTG	TTTGTGTTGA	ATAGCACATC	5580
	CCAGAGACAT	CAGAAACCAG	CAACTGATTC	AGTGTGATTT	CCCAGACTTT	TTAGGCATGA	5640
60	AATTCCGACA	CTTCAGTATT	TCCAGGAATA	GCATATGCAC	GCTGTTCTTG	CTTCATGGAA	5700
	TGCTACATGC	TTTCTGTTTT	TCTCATTTTG	GATTTCCTCA	AAACTAATCT	AATTAAAGCT	5760
	TCAGGTCCTT	TTGTATGACG	TAGAAAGGAA	TTATTAATAA	CACCACCAAA	GAAATAAAT	5820
	ATATCCTACT	TGAATTTTAC	TCTATGGACT	TACCCACTGC	TAGAATAAAT	GTATCAAATC	5880
	TTATTTGTAA	ATTCTCAATT	TTGATATATA	TATGTATATA	TGCATATACA	TATCCACACT	5940
65	TGCTGCAAG	AATATTGATT	AAAATTGCTA	AATTGTACT	TGTTACCAA	AAAAAAAAA	6000
	AAAAAA						

Seq ID NO: 419 Protein sequence
Protein Accession #: Eos sequence

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	SRQYTVRYRE	KGELARWDYK	QIANRRVLIE	NLIPDTVYEF	AVRISQGERD	GKWTSTVFQR	120
	TPESAPTTAP	ENLNVWVWNG	KPTVVAASWD	ALPETEGVKV	VCLLDGTGLFS	VSSFQPSAKS	180
75	FQNTFFHTPR	LSNHLQSPS	PILETLLLPW	WMVCSLGNAI	FSKSGPQTGE	AWDLTPKPSL	240
	SLCQQBCSCT	QKDFCLAYL	IDIQTQVQNK	DPQLEGSVFG	PCFLFYFLTF	MLDIGGFSFI	300
	MCYEDPVSSL	TGNSLSKVAA	SKADVQNTTE	DNGKPEKPEP	SSPSRPAPAS	SOHPSVPASP	360
	QGRNAKDLRL	DLKNIKILANG	GAPRKPQLRA	KKAEELDLQS	TEITGEEELG	SREDSPMSPS	420
	DTQDQKRLTR	PFSRHGHSVV	APGRTAVRAR	MPALPRREGV	DKPGFSLATQ	FRPGAPPSAS	480
80	ASPAHHASTQ	GTSHRPSLPA	SLNDNDLVDS	DEDERAVGSL	HPKGAFAQPR	PALSPSRQSP	540
	SSVLDRDRSSV	HPGAKPASPA	RRTPHSGAAE	EDSSASAPPS	RLSPPHGSSS	RLLPTQPHLS	600
	SPLSKGKDKG	EDAPATNSNA	PSRSTMSSSV	SSHLSRSTOV	SEGAESADGE	SHGDGDREDG	660
	GRQAEATAQT	LRARPASGHF	HLLRHKPFPA	NGRSPSRFSI	GRGPRLQPS	SPQSTVPSRA	720
	HPRVPSHSDS	HPKLSGGIHG	DEEDEKPLPA	TVVNDHVPSS	SRQPISRGWE	DLRRSPQRGA	780
85	SLHRKEPIPE	NPKKSGDTH	PQGYSSSLAS	KAQDVQQSTD	ADTEGHSPPA	QPGSTDRHAS	840
	PARPPAARSQ	QHPSPVRMT	PGRAPEQQPF	PPVATSQHHP	GPQSRDAGRS	PSQPRLSLTQ	900
	AGRPRPTSQG	RSHSSSDPYT	ASSRGMPLTA	LQNQDEDAQG	SYDDDDSTEVE	AQDVRAPAHA	960

ARAKEAAASL PKHQVESPT GAGAGGDHRS QRGHAASPAR PSRPGGPQSR ARVPSRAAPG 1020
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 SLAKEEREPA IALAPRGSL APVKRPLPPP PGSSPRASHV PSRPPPSAA TVSPVAGTHP 1140
 WPRYTTRAPP GHFSTTPMLS LRQRMHARF RNPLSRQPAR PSYRQGYNGR PNVEGKVLPG 1200
 SNGKPNQRI INGPQGTIKWV VDLDRGLVLN AEGRYLQDSH GNPRLIKLGG DGRITVDLEG 1260
 TPVVSFDGLP LFGQGRHGTG LANAQDKPIL SLGGKPLVGL EVIKKTHHP TTTMQPTTTT 1320
 TPLPTTTTTPR PTTATTMQPT TTTTLPPTT PRPTTATRR TTTTRPTTV RTTTRTTTTT 1380
 TPKPTTPIPT CPPGTLEPHD DDGNLIMSSN GIPECYAEED EFSGLETDTA VPTEEAYVIY 1440
 DEDYEFETS RPTTTEPSTT ATTPRVIPEE GAISFPPEE FDLAGRKRFEV APYVYTLNKG 1500
 PSAPCSLTDA LDHFQVDSL EIPNDLKKS DLPPQHAPRN ITVVAVEGCH SFVIVDWDKA 1560
 TPGDLVTGYL VYSASYEDFI RNKFSTQASS VTHLPIENLK PNTRYFVKVQ AQNPHGYGPI 1620
 SPSVSFVTES DNPLLVVREP GGELSGSHSL SNMIPATRTA MDGNM

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 Nucleic Acid Accession #: NM_022743
 Coding sequence: 128..1237

1 11 21 31 41 51
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 AAAGCTGATG CGATGCTCTC AGTGCCGCGT CGCCAAATAC TGTAGTGCTA AGTGTGAGAA 180
 AAAAGCTTGG CCAGACCACA AGCGGGAATG CAAATGCCTT AAAAGCTGCA AACCCAGATA 240
 TCCTCCAGAC TCCGTTGCGA TCTTGGCAG AGTTGTCTTC AAACCTATGG ATGGAGCACC 300
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 TGAAGATAAG AAAGAGGGCC TCAGGCAACT CGTAATGACA TTTCAACATT TCATGAGAGA 420
 AGAAATACAG GATGCTCTC AGCTGCCACC TGCCCTTGAC CTTTTTGAAG CCTTTGCAAA 480
 AGTGATCTGC AACTCTTCA CCATCTGTAA TGCGGAGATG CAGGAAGTTG GTGTTGGCCT 540
 ATATCCCACT ATCTCTTTCG TCAATCACAG CTGTGACCCC AACTGTTTCA TTGTGTTCAA 600
 TGGGCCCCAC CTCTTACTGC GAGCAGTCCG AGACATCGAG GTGGGAGAGG AGCTCACCAT 660
 CTGCTACCTG GATATGCTGA TGACCACTGA GGAGCGCCGG AAGCAGCTGA GGGACCAGTA 720
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 CTGCATCAAC CTCGCCCTGT TGGAGGAAGC CTGTGTCTAT GGTACTCGGA CCATGGAGCC 1020
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 CGGCGTGTGT CTTTGTGTAA TGCCCTATTG AGGTACACCA CTCTATGCTT TGTATAGCTG 1320
 GTGAACCTCT CTTATTGGAA ATTCTGTTCC GTGTTTGTGT AGGTAATAAA AGGCAGACAT 1380
 GGTTTGCAAA CCACAAGAAAT CATTAGTTGT AGAGAAGCAC GATTATAATA AATTCAAAAC 1440
 ATTTGGTTGA GGATGCCAAA AAAAAAAAAA AAAAAA

Seq ID NO: 421 Protein sequence
 Protein Accession #: NP_073580

1 11 21 31 41 51
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 CNSFTICNAE MQEVGVGLYP SISLLNHSCD PNCSIVFNPG HLLLRVRDI EVGEELTICY 180
 LDMLMTSEER RKQLRDQYCF EDCDFRCQTO DKDADMLTGD EQVWKEVQES LKKIEELKAH 240
 WKWEQVLAMC QAIISNSNER LPDINIYQLK VLDCAMDACI NLGLLEALF YGTRTMEPYR 300
 IFPPGSHPRV GVQVMKVGL QLHQGMFPQA MXNLRLAFDI MRVTHGREHS LIEDLILLE 360
 ECDANIRAS

Seq ID NO: 422 DNA sequence
 Nucleic Acid Accession #: NM_003014.2
 Coding sequence: 238..648

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 TTCCTCTCCA TCTAGTGGC GCTGTGCTTG TGGCTGCACC TGGCGCTGGG CGTGCGCGGC 300
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 CAGGAAAGGC CTCCTGATGT TGAAGTAAA CGCCTAAGCC CCGATCGGTG CAAGTGATAA 780
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 CGTTCAAGGA TGATGCTTCT TGAATAATGC TTAGTTGAAA AATGGAGAGA TCAGCTTAGT 1080
 AAAAGATCCA TACAGTGGGA AGAGAGGCTG CAGGAACAGT GGAGAACAGT TCAGGACAAG 1140
 AAGAAAAACG CCGGGCGCAC CAGTCGTAGT AATCCCCCA AACCAGAGG AAAGCCTCCT 1200
 GCTCCCAACG CAGCCAGTCC CAAGAAGAAC ATTAAACTA GGAGTGCCCA GAAGAGAAAC 1260
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 GATGAGGCTG GGCATTGCCT GGGACAGCCT ATGTAAGGCC ATGTGCCCTT TGCCCTAACA 1380

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 AAATGCCATA TTTCACAA CAACACGTAAT TTTTATACAG TATGTTTTAT TACCTTTTGA 1680
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 AGGCATTCAA TAAATGCACA ACGCCCAAAG GAAATAAAAT CCTATCTAAT CCTACTCTCC 2520
 ACTACACAGA GGTATCACT ATTAGTATTT TGGCATATTA TTCTCCAGGT GTTTGCTTAT 2580
 GCACCTATAA AATGATTTGA ACAAATAAAA CTAGGAACCT GTATACATGT GTTTCATAAC 2640
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 TCTCATTTCT AACAGCTGTG TTATATTCCA TAGTATGCAT TACTCAACAA ACTGTTGTGC 2760
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Seq ID NO: 423 Protein sequence
 Protein Accession #: NP_003005.1

1 11 21 31 41 51
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 ESLACDELVE YDRGVCISPE AIVTDLPELV KWIDITPDMM VQERPLDVDC KRLSPDRCKC 180
 KKVKPTLATY LSKNYSYVIH AKIKAVQRSG CNEVTTVVDV KEIFKSSSPI PRTOVPLITN 240
 SSCQCPHILP HQDVLIMCYE WRSRMMLLEN CLVEKWRDQL SKRSIQWEER LQEQRRVTQD 300
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 Coding sequence: 248..1780

1 11 21 31 41 51
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 GCTGTACTCG CTGGCATCAT TTACAGGCCG GTGCCCCCGG GGTGAGCTGG AGACCTCAGA 360
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 GGCAGCGGCT GCGCTCCGAG TGCTGGTGCC TCCCCTGCCC TCACTGAATC CTGGTCCAGC 720
 ACTAGAAGAG GGCCAGGGCC TGACCTTGGC AGCCTCCTGC ACAGCTGAGG GCGAGCCAGC 780
 CCCAGCGCTG ACCTGGGACA CGGAGGTCAA AGGCACAACG TCCAGCCGCT CCTTCAAGCA 840
 CTCCCGCTCT GCTGCGCTCA CCTCAGAGTT CCACCTGGTG CCTAGCCGCA GCATGAATGG 900
 GCAGCCACTG ACTTGTGTGG TGTCCCATCC TGGCCTGCTC CAGGACCAAA GGATCACCCA 960
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 CTCATACAAC TGGACACGGC TGGATGGGCC TCTGCCAGT GGGGTACGAG TGGATGGGGA 1140
 CACTTTGGGC TTTCGCCAC TGACCACTGA GCACAGCGGC ATCTACGTCT GCCATGTGAG 1200
 CAATGAGTTC TCCTCAAGGG ATTTCTAGGT CACTGTGGAT GTTCTTGACC CCCAGGAAGA 1260
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 CCGGAGGCTG CATTCCTATC ACACGGACCC CAGGAGCCAG CCGGAGGAGA GTGTAGGGCT 1500
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 TGAACGTCTG TCTCCAGGCT CTGGGCGGGC CGAGGAGGAG GAAGATCAGG ATGAAGGCAT 1620
 CAAAACAGGC ATGAACCAAT TTGTTACAGG GAATGGGACC CTACGGGCCA AGCCACGGG 1680
 CAATGGCATC TACATCAATG GCGGGGGACA CCTGGTCTGA CCCAGGCCTG CCTCCCTTCC 1740
 CTAGGCCTGG CTCCTTCTGT TGACATGGGA GATTTTAGCT CATCTTGGGG GCCTCCTTAA 1800
 ACACCCCAT TTCTTGGGGA AGATGCTCCC CATCCCACTG ACTGCTTAC CTTTACCTCC 1860
 AACCTTCTGT TTCACTGGGA GGGCTCCACC AATTGAGTCT CTCCCACTAT GCATGCAAGT 1920
 CACTGTGTGT TGTGCTGTGT GCCTGTGTGA GTGTTGACTG ACTGTGTGTG TGTGGAGGGG 1980
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 GTTTGGCGTG TGTGTCTGTG GACCTGTGCT TGAAAGGACA GGTATTTTCT 2160
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 CAGACCCAGG TGTGCGGGCA TAGCTGGAGC TGGAACTGCT CTCGGGTGTG AGGGAACCTG 2280
 TCTCTTACCA CTTCGGAGCC ATGGGGGCAA GTGTGAAGCA GCCAGTCCCT GGGTCAGCCA 2340
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 ACATATTTTC TGTAAATATA CATGCGCCGG GAGCTTCTTG CAGGAATACT GCTCCGAATC 2460
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 TTTTATTTT ATTTTCTTTT AGAGTTTGAG TCCAGCCTGG ACGATATAGC CAGACCCCTG 2580

CTGTAAAAAA ACCAAAACCC AAAAAAAAAA AAAAAAAAAA

Seq ID NO: 425 Protein sequence
Protein Accession #: AAH10423

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DEGEYECRV	TFPAGSFQAR	LRLRLVLPPL	PSLNPGPALE	BQQLTLAAS	CTAEGSPAPS	180
VTWDTEVKGT	TSSRSFKHSR	SAAVTSEFHL	VPSRSMNGQP	LTCVVSHPGL	LQDQRITHIL	240
HVSFLAEASV	RGLEDQNLWH	IGREGAMLKC	LSEGQPPPSY	NWTRLDGPLP	SGVRVDGDTL	300
GFPPLTTEHS	GIYVCHVSNE	FSSRDSQVTV	DVLDPOEDSG	KQVDLVASV	VVVGVIAALL	360
FCLLVVVVVL	MSRYHRRKAQ	QMTQKYEEL	TLTRENSIRR	LHSHHTDPRS	QPEESVGLRA	420
EGHPDLSKDN	SSCSVMSEEP	EGRSYSTLT	VREIETQTEL	LSPGSGRAEB	EEDQDEGIKQ	480
AMNHVQENG	TLRAKPTGNG	IYINGRGHLV				

Seq ID NO: 426 DNA sequence
Nucleic Acid Accession #: NM_003474.2
Coding sequence: 37..3036

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CTTTTTTAAA	AATGAAAGGC	TAGAAGAGCT	CAGCGGCGGC	GCGGGCCGTG	CGCGAGGGCT	180
CCGGAGCTGA	CTCGCCGAGG	CAGGAAATCC	CTCCGCTCGC	GACGCCCGGC	CCCGCTCGGC	240
GCCCCGCTGG	GATGCTGACG	CGCTCGCCGC	CGGGCCCGAG	AGCTGCTGCA	CTGAAGGCCG	300
GCGACGATGG	CAGCGCGCCC	GCTGCCCGTG	TCCCCCGCCC	GCGCCCTCCT	GCTCGCCCTG	360
GCCGGTGCTC	TGCTCGCGCC	CTGCGAGGCC	CGAGGGGTGA	GCTTATGGAA	CGAAGGAAGA	420
GCTGATGAAG	TTGTGAGTGC	CTCTGTTCCG	AGTGGGGACC	TCTGGATCCC	AGTGAAGAGC	480
TTCGACTCCA	AGAATCATCC	AGAAGTGCTG	AATATTCGAC	TACAACGGGA	AAGCAAAGAA	540
CTGATCATAA	ATCTGGAAG	AAATGAAGGT	CTCATTGCCA	GCAGTTTCAC	GGAAACCCAC	600
TATCTGCAAG	ACGGTACTGA	TGCTCTCCCTC	GCTCGAAATT	ACACGGTAAT	TCTGGGTAC	660
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TCTGCTCTCA	GGGGACTTAT	TGTGTTTGAA	AATGAAAGCT	ATGCTTAGA	ACCAATGAAA	780
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CAGACATGGG	CAAGAAGGCA	TAAAAGAGAG	ACCCTCAAGG	CAACTAAGTA	TGTGGAGCTG	960
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AATCATGACA	CAGTGCAGAG	GGGCTGTAGC	TGTCAAATGG	CGGTTGAGAA	AGGAGGCTGC	1440
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GACTTGGAGA	CCAGCCTGGA	GAAAGGAATG	GGGGTGTGCC	TGTTTAACCT	GCCGGAAGTC	1560
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CGTGGCTTCC	AACCTGTGCA	GGCTCACCTC	GGCCACCTTG	GAAAAGGCCT	GATGAGGAAG	2640
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GACATCAGCA	GACCGTCAA	CGGCCTGAAT	GTCCCTCAGC	CCCAGTCAAC	TCAGCGAGTG	2760
CTTCTCTCCC	TCCACCGGGC	CCCACGTGCA	CCTAGCGTCC	CTGCCAGACC	CCTGCCAGCC	2820
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CCTGCAGATC	CTCTGGCCAG	AACAACCTCG	CTCACTCATG	CCTTGGCCAG	GACCCAGGA	2940
CAATGGGAGA	CTGGGCTCCG	CCTGGCACCC	CTCAGACCTG	CTCCACAATA	TCCACACCAA	3000
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GCTGTGCTGT	GCTATGGTGC	TCTGTCTACT	TGCACAGGTA	CTTGTAATAT	ATTAATTTAT	3240
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CCATGGCAGG	AAGGCTTGT	GTGCTTTTAG	TATTTTAGTG	AACTTGAAAT	ATCCTGCTTG	3360
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CCAATACACC	CCAGCTGTGC	TTATGGTACC	AGATGCAGCT	CAAGAGATCC	CAAGTAGAAT	3480
CTCAGTTGAT	TTTCTGGATT	CCCCATCTCA	GGCCAGAGCC	AAGGGCTTTC	AGGTCCAGGC	3540
TGTGTTTGGC	TTTCAGGGAG	GCCCTGTGCC	CCTTGACAAC	TGGCAGGCAG	GCTCCAGGG	3600
ACACCTGGGA	GAAATCTGCC	TTCTGGCCAG	GAAGCTTTGG	TGAGAACCTG	GGTTGCAGAC	3660
AGGAATCTTA	AGGCTGTAGC	ACACAGGAT	AGAGACTGGA	ACACTAGACA	AGCCAGAACT	3720
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GGTGCTTGAT	AGAAATGCCA	AGCACTTCTT	TTTCTCGCTG	TCCTTTCTAG	AGCACTGCCA	3840

5 CCAGTAGGTT ATTTAGCTTG GGAAAGGTGG TGTTCCTGTA AGAAACCTAC TGCCCAAGGCA 3900
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 20 TATATACTAT TAAAAAGGTT TACAGAAATT TATGGTGAT TACGTGGGCA TTGTCTTTT 4980
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Seq ID NO: 427 Protein sequence
 Protein Accession #: NP_003465

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 30 YGHVVRGYSY SAVSLSTCSG LRGLIVFENE SYVLEPMKSA TNRYKLFPK KLKSVRGSCG 180
 SHHNTPNLNA KNVFPFPPST WARRHKRETL KATKYVELVI VADNREFORQ GKDLKVKQR 240
 LLEIANHVDK FYRPLNIRIV LVGVEVWDM DKCSVSQDPF TSLHEFLDWR KMKLLPRKSH 300
 DNAQLVSGVY FQGTITGMAP IMSMCTADQS GGIVMDHSDN PLGAAVTLAH ELGHNFGMNH 360
 35 DTLDRGSCSQ MAVEKGCCIM NASTGYPPFM VFSSCSRKDL ETSLEKMGV CLFNLPEVRE 420
 SFGGQKCGNR FVEEGECCD GEPEECMNR CNATTCTLPK DAVCAHGLCC EDCQLKPAGT 480
 ACRDSSNSCD LPEFCTGASP HCPANVYLHD GHSCQDVG DY CYNGICQTHE QQCVTLWGF 540
 AKPAPGICFE RVNSAGDPYV NCGKVSXSS AKCEMRDAKC GKIQCQGGAS RPIVGTNAVS 600
 IETNIPLOQG GRILCRGTHV YLGDDMPDPG LVLAGTKCAD GKICLNRCQ NISVPGVHEC 660
 40 AMQCCHRGVC NNRKNCHCEA HWAPPFCDFK GFGGSDSGP IRQADNQLT IGLVTLILCL 720
 LAAGFVVYLK RKTLLRLLEF NKKTTEIEKL RVRPSRPPRG FQPCQAHLG LKGLMRKFP 780
 DSYPPKDNPR RLLQCQNVDI SRPLNGLNVP QPQSTQVLP PLHRAPRAPS VPAPPLPAKP 840
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 RSTHTAYIK

Seq ID NO: 428 DNA sequence
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 Coding sequence: 135..1043

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 55 TGGCCACCTT TGACCCGCGC CGGGGGACCG ACGCCACCAA CCCACCCGAG GGTCCCCAAG 240
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 GTTGGTCAA CGCTGGCGAT GTGGGTGTG CGGTGTTTGA ATGTTTCGAG AACAACTCTT 360
 GTGAGATTCC GGGCTTACAT GGGATTGCA TGACTTTCT GCACAACGCT GGAATTTT 420
 ATGCCCAGGG CAAGTCATT ATCAAAGACG CCTGAAATG TAAGGCCAC GCTCTGCGGC 480
 60 ACAGGTTCCG CTCATAAGC CGGAAGTGCC CGGCCATCAG GGAAATGGTG TCCAGTTTGC 540
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 AGTGTGAGCA GAATCGGGGA AGCCTGTGCT CCATCTGTAG CTCTGCAACC TCGGCCATCC 780
 65 AGAAGCCTCC CACGGCGCCC CCGAGCGGCC AGCCCCAGGT GGACAGAAAC AAGCTCTCCA 840
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 TCGGGGGCCT TGGGGCTCAG GGACCTCCG GAAGCAGCGA GTGGGAAGAC GAACAGTCTG 1020
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 70 GTCCATTTTC TTATCTATGG ACATTCCAAA ACATTACCA TTAGAGAGGG GGGATGTCAC 1140
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 TGAGATGGAG ACCCTGGGG CCGTGGGGTC TCAGGGGTGC CTGGTGAATT CTGCACCTTAC 1260
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 CTGGCGATT CAGGAGACCC AGCTGGAAC CTGGCTTCTC CATGTGAGGG GATGGGAAAG 2160
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 GGGAGAGGAA GAAAAGAGAG AGAGAAAAGA GCCTCGTGCC

Seq ID NO: 429 Protein sequence
 Protein Accession #: NP_003705

1 11 21 31 41 51
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 ISRKCPAIRE MVSQLORECY LKHDLCAAAQ ENTRVIVEMI HFKDLLLHEP YVDLVNLLLT 180
 CGEEVKEAIT HSVQVQCQN WGSLSILSF CTSAIQKPPT APPERQPOVD RTKLSRAHHG 240
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Seq ID NO: 430 DNA sequence
 Nucleic Acid Accession #: NM_005940
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 GTCCGCCTTC TACACCTTTC GCTACCCACT GAGTCTCAGC CCAGATGACT GCAGGGGCGT 780
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Seq ID NO: 431 Protein sequence
 Protein Accession #: NP_005931

1 11 21 31 41 51
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 FFPKTHREGD VHFVDYETWT IGDDQGTDL LQVAHEFGHV LGLQHTTAAK ALMSAFYTFR 240
 YPLSLSPDDC RGVQHLYGQP WPTVTSRTPA LGPQAGIDTN EIAPLEPDAP PDACEASFDA 300
 VSTIRGELEF FKAGFVWRLR GGQLQPGYPA LASRHWQGLP SPVDAAFEDA QGHIWFFQGA 360
 QYVWYDGEKP VLGPAPLTEL GLVRFVHAA LVWGPENKI YFFRGRDWR FHPSTRRVDS 420
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Seq ID NO: 432 DNA sequence
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 Coding sequence: 202..1563

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 CCATCTACAT TTTTGGGACT CGGGAATTAT GAGGTAGAGG TGGAGGCGGA GCCGGATGTC 180
 AGAGTCCCTG AAATAGTCAC CATGGGGGAA AATGATCCGC CTGCTGTTGA AGCCCCCTTC 240
 TCATTCCGAT CGCTTTTGG CCTTGATGAT TTGAAATAA GTCCTGTTGC ACCAGATGCA 300

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 TCAGGGAAGT ACAGATGTCG CTCATCCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC 480
 GGAGTCTCGG ATTGCAAGA CGGGGAGGAC GAGTACCGCT GTGTCGGGT GGGTGGTCAG 540
 AATGCCGTGC TCCAGGTGTT CACAGCTGCT TCGTGGAAGA CCATGTGCTC CGATGACTGG 600
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 CTAGTTTCCC TGTGAGACAA TCCAGCCCCA TCCCACTTGG TGGAGAAGAT TGTCTACCAC 1080
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 GCAGTGGCGA AATCCCTGCT CACTGCAGCC TCCGCTTCCC TGGTTCAAGC GATTCTCTTG 1860
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 AAAAA

Seq ID NO: 433 Protein sequence
Protein Accession #: NP_076927

1 11 21 31 41 51
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 MGENDPPAVE APFSFRSLFG LDDLKISPIVA PDADAVAAQI LSLPLKFFP IIVIGIIALI 60
 LALAIGLGH FDCSGKYRCR SSKFCEILIA RCDGVSDCKD GEDEYRCVRV GGQNAVLPVF 120
 TAASWKTMS DWKGHYANV ACAQLGFPSY VSSDNLRVSS LEGQFREEFV SIDHLLPDDK 180
 VTAHHHSYV REGCASGHV TLQCTACGHR RGYSSRIVGG NMSLLSQWPV QASLQFQGVH 240
 LCGGSVITPL WIITAAHCYV DLYLPKSWIT QVGLVSLDN PAPSHLVEKI VYHSKYKPKR 300
 LGNDIALMKL AGPLTFNEMI QVCLPNSEE NFPDGKVCWT SGWGATEDGG DASPLNHAA 360
 VPLISNKICN HRDVYGGIIS PSMCLCAGYLT GGVDSCQGDS GGPLVCQERR LWKLVGATSF 420
 GIGCAEVNKP GYVTRVTSFL DWIHEQMERD LKT

Seq ID NO: 434 DNA sequence
Nucleic Acid Accession #: NM_000493.2
Coding sequence: 97..2139

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 CTGCTAGTAT CTTTGAACCT GTTTCATGGA GTGTTTACG CTGAACGATA CCAATGCCCC 180
 ACAGGCATAA AAGGCCCACT ACCCAACACC AAGACACAGT TCTTCATTCC CTACACCATA 240
 AAGAGTAAAG GTATAGCAGT AAGAGGAGAG CAAGGTAATC CTGGTCCACC AGGCCCTGCT 300
 GGACCTCGAG GGCACCCAGG TCCTTCTGGA CCACCAAGAA AACCAGGCTA CGGAAGTCTC 360
 GGACTCCAAG GAGAGCCAGG GTTGCCAGGA CCACCGGAC CATCAGCTGT AGGGAAACCA 420
 GGTGTGCCAG GACTCCCAGG AAAACCAAGG GAGAGAGGAC CATATGGACC AAAAGGAGAT 480
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 GGTCCACAG GACCATCTGG CCTCTCTGGA GTGGGAAAAA GAGGTGAAAA TGGGGTTCCA 780
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 GGTACTAGAG GCCCTATTGG GCCACCAAGG ATTCCAGGAT TCCCTGGGTC TAAAGGGGAT 1500
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 CCCCCTGGGC CTCCAGGCC ACCAGGTCAA GCAGTCATGC CTGAGGTTT TATAAGGCA 1680
 GGCCAAAGGC CAGTCTTTC TGGGACCCCT CTGTGTAGTG CCAACCAAGG GGTAAACAGGA 1740

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ATGCCTGTGT CTGCTTTTAC TGTATTCTC TCCAAAGCTT ACCCAGCAAT AGGAACTCCC 1800
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TTTACTTGTG AGATACCAGG AATATACTAT TTTTCATACC ACGTGCATGT GAAAGGGACT 1920
CATGTTTGGG TAGGCCTGTA TAAGAATGGC ACCCCTGTAA TGTACACCTA TGATGAATAC 1980
ACCAAGGGCT ACCTGGATCA GGCTTCAGGG AGTGCCATCA TCGATCTCAC AGAAAATGAC 2040
CAGGTGTGGC TCCAGCTTCC CAATGCCGAG TCAAATGGCC TATACTCCTC TGAGTATGTC 2100
CACTCCTCTT TCTCAGGATT CCTAGTGGCT CCAATGTGAG TACACCCAC AGAGCTAATC 2160
TAAATCTTGT GCTAGAAAAA GCATTCTCTA ACTCTACCCC ACCCTACAAA ATGCATATGG 2220
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AACAAACCTT CCCCCTGAAA AGTGAGCAGC AACGTAAAAA CGTATGTGAA GCCTCTCTTG 2340
AATTTCTAGT TAGCAATCTT AAGGCTCTTT AAGGTTTTCT CCAATATTAA AAAATATCAC 2400
CAAGAAAGTC CTGCTATGTT AAAAACAAAC AACAAAAAAC AAAGCAACAA AAAAAAAAT 2460
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AGGAGGTATC ATATAACTTT GTAGAACTTA AATACTTGAA TATTCAAAT TAAAGACAC 2640
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CAATATCTAT TCAATATATC AGGTGCATAT ATACTTGTGA AAGCTCTTAT ATAAAAAAGC 2760
CCCAAAATAT TGAAGTTTCT CTGAAATGCA AGGTGCTTTC ATCAATGAAC CTTTTCAAAA 2820
CTTTTCTATG ATTGCAGAGA AGCTTTTAT ATACCCAGCA TAACTTGGA ACAGGTATCT 2880
GACCTATTCT TATTTAGTTA ACACAGTGT GATTAATTTG ATTTCTTTAA TTCCTTATG 2940
AATCTTATGT GATATGATT TCTGGATTGA CAGAACATTA GCACATGTAC CTTGTGCCCTC 3000
CCATTCAGT GAAGTTATAA TTACTACTGA GGGTTTCAAA ATTCGACTAG AAGTGGAGAT 3060
ATATTATTTA TTTATGCACT GTACTGTATT TTTATATTGC TGTTTAAAA TTTTAAGCTG 3120
TGCTCACTT ATTAAGCAC AAAATGTTT ACCTACTCCT TATTTACGAC ACAATAAAAT 3180
AACATCAATA GATTTTATAG CTGAATTAAT TTGAAAGCAG CAATTGCTG TTCTCAACCA 3240
TTCTTCAAG GCTTTTCATT CGACACAATA AAATAACATC AATAG
  
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Seq ID NO: 435 Protein sequence
Protein Accession #: NP_000484.2

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TPGPPGPAGP RGHPPGSGPP GKPGYGSPLG QGEPGLPGPP GPSAVGKPGV PGLPGKPGER 120
GPYGPKG DVG PAGLPGPRGP PGPPGIPGPA GISVPGKPGQ QGPTGAPGPR GFPGEKGAPG 180
VPMGMGQKGE MGYGAPGRGP ERGLPGPQPG TGPSPGPPGVG KRGENGVPGQ PGIKGDRGFP 240
GEMGPIGPPP PQGPPGERGP EGIGKPGAAG APQPGPIPGT KGLPGAPGIA GPPGPPGFGK 300
PGLPGLKGER GPAGLPGGPG AKGEQGPAGL PGKPLTGP GNMGPQGPKG IPGSHGLPGP 360
KGETGPAGPA GYPGAKGERG SPGSDGKPGY PGKPLDGP GNPGLPGPKG DPGVGGPPGL 420
PGPVGPAGAK GMPGHNGEAG PRGAPGIPGT RGPIGPPGPI GFPGSKGDPG SPGPPGPAGI 480
ATKGLNGPTG PPGPPGPRGH SGEPGLPGPP GPPGPPGQAV MPEGFIKAGQ RPSLSGTPLV 540
SANQGVTKMP VSAFTVILSK AYPAGTPIP FDKILYNRQ HYDPRTGIFT CQIPGIYYFS 600
YHVHVKGTHV WVGLYKNGTP VMTYDEYTK GYLDQASGSA IIDLTENDQV WLQLPNAESN 660
GLYSSEYVHS SFGSFLVAPM
  
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Seq ID NO: 436 DNA sequence
Nucleic Acid Accession #: XM_062811
Coding sequence: 1..888

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1 11 21 31 41 51
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TGGCTGGACG CGCAGGGCGT CTGGCGCATC GGCTTCCAGT GTCCCGAGCG CTTCGACGGC 180
GGCGACGCCA CCATCTGCTG CGGCAGCTGC GCGTTGCGCT ACTGCTGCTC CAGCGCGCGAG 240
GCGGCGCTGG ACCAGGGCGG CTGCGACAAT GACCGCCAGC AGGGCGCTGG CGAGCCTGGC 300
CGGCGCGACA AAGACGGCCC CGACGGCTCG GCAGTGCCCA TCTACGTGCC GTTCCTCATT 360
GTTGGCTCCG TGTTTGTGCG CTTTATCATC TTGGGGTCCC TGGTGGCAGC CTGTTGCTGC 420
AGATGTCTCC GGCCTAAGCA GGATCCCGAG CAGAGCCGAG CCCAGGGGGG TAACCGCTTG 480
ATGGAGACCA TCCCATGAT CCCCAGTGCC AGCACCTCCC GGGGGTCTGC CTCACGCCAG 540
TCCAGCACAG CTGCCAGTTC CAGCTCCAGC GCCAACTCAG GGGCCCGGGC GCGCCCAACA 600
AGGTACAGA CCAACTGTTG CTTGCCGGA GGGACCATGA ACAACGTGTA TGTCAACATG 660
CCCACGAATT TCTCTGTGCT GAACTGTCAG CAGGCCACCC AGATTGTGCC ACATCAAGGG 720
CAGTATCTGC ATCCCCCATA CGTGGGGTAC ACGGTGCAGC ACGACTCTGT GCCCATGACA 780
GCTGTGCCAC CTTTCATGGA CGGCCTGCAG CTTGGCTACA GGCAGATTCA GTCCCCCTTC 840
CCTCACACCA ACAGTGAACA GAAGATGTAC CCAGCGGTGA CTGTATAA
  
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Seq ID NO: 437 Protein sequence
Protein Accession #: XP_062811

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1 11 21 31 41 51
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MWGARRSSVS SSWNAASLLQ LLLAALLAAG ARASGEYCHG WLDAQGVWRI GFQCPERFDG 60
GDATICCGSC ALRYCCSSAE ARLDQGGCDN DRQQGAGEPG RADKDGPDGS AVPIYVFLI 120
VGSVFVAFII LGSLVAACCC RCLRPKQDPQ QSRAPGNGRL METIPMIPSA STSRGSSSRQ 180
SSTAASSSSS ANSGARAPPT RSQTNCLPE GTMNNVYVNM PTNPSVLNQC QATQIVPHQG 240
QYLHPPVVG TVQHDVSPMT AVPPFMDGLQ PGYRQIQSPF PHTNSEQKMY PAVTV
  
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Seq ID NO: 438 DNA sequence
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Coding sequence: 1..681

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1 11 21 31 41 51
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AAGGAGGTGT GGGGAGATGA GCAGGCCGAC TTTGTCTGCA ACACCTGCA GCCAGGCTGC 180
  
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AAGAACGTGT GCTACGATCA CTACTTCCCC ATCTCCACA TCCGGCTATG GGCCCTGCAG 240
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 GAGAAGAAGA GGAAGTTTCAT CAAGGGGGAG ATAAAGAGTG AATTTAAGGA CATCGAGGAG 360
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 TTCTTCCGGG TCATCTTCGA AGCCGCCTTC ATGTACGTCT TCTATGTCAT GTACGACGGC 480
 TTCTCCATGC AGCGGCTGGT GAAGTGCAAC GCCTGGCCTT GTCCCAACAC TGTGGACTGC 540
 TTTGTGTCCC GGCCACGGA GAAGACTGTC TTCACAGTGT TCATGATTGC AGTGTCTGGA 600
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 AAGTCAAAAA AGCCAGTTTA A

Seq ID NO: 439 Protein sequence
 Protein Accession #: NP_003995.1

1 11 21 31 41 51
 MDWGLTQIL GGVNKHSTSI GKILVTLFI FRIMILVVAA KEVWGDEQAD FVCNTLQPGC 60
 KNVCYDHYFP ISHIRLWAL LIFVSSPAL VAMHVAYRRH EKRRKFIKGE IKSEFKDIEE 120
 IKTKVRIEG SLWWYTTSSI FFRVIFEAAF MYVFVYMDG FSMQRLVKCN AWPCPNTVDC 180
 FVSRPTEKT VTFVFMIAVSG ICILNLNTEL CYLLIRYCSG KSKKPV

Seq ID NO: 440 DNA sequence
 Nucleic Acid Accession #: XM_061091.1
 Coding sequence: 1..2481

1 11 21 31 41 51
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 CAGATGCATG GTGAGAAGT AGATCTCTGG AGCCTTGGTG TTCTTTGCTA TGAATTTTAA 240
 GTTGGGAAGC CTCCTTTTGA GGCAAACGAA GTCCATGTAA GCAAAGAAAC CATCGGAAG 300
 ATTTCACTG CCAGCAAAAT GATGTGGTGC TCGGCTGCAG TGGACATCAT GTTCTGTGTA 360
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 GTCTGTGACG GTCTGGACAT CAGCCCCGAG AGGGTCAGAG TGGGAGCAIT CCAGTTCAGT 480
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Seq ID NO: 441 Protein sequence
 Protein Accession #: XP_061091.1

1 11 21 31 41 51
 MPNTSGTTRI EIWLLQEPPE HRALVAALLP VSPSPALALA PGYPPVPAAD DRFTLPMIGG 60
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 DGSNSVKGGS FERSKHFAIT VCDGLDISPE RVRVGAFFQS STPHLEFPLD SFSTQEVKA 180
 RIKRMVFKGG RTETELALKY LLHRGLPGGR NASVPQILII VTDGKSQGDV ALPSKQLKER 240
 GVTVFAVGVR FPRWEELHAL ASEPRGQHLV LAEQVEDATN GLFSTLSSA ICSSATPAGS 300
 PELVFMERLM GISLIGPCDS QPCQNGGTCV PEGLDGVQCL CPLAFGGEAN CALKLSLECR 360
 VDLLFLDLSS AGTTLDFGLR AKVFKRFVR AVLSSEDSRAR VGVATYSREL LVAVPVGEYQ 420
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 AGPARHARAR ELLLLGVSGE AVRAELEBIT GSPKHMVYVS DPQDLFNQIP ELQGLKCSRQ 540
 RFGCRQTALD LVFMMLDSAS VGPFNFQMQ SFVRSALQF EVNPDVTQVG LVVYGSQVQT 600
 AFGLDTKPTR AAMLRAISQA PYLGGVGSAG TALLHIYDKV MTVQGRARPG VPKAVVVLTG 660
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780

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	GGAGGATGCC	ACCAACGGCC	TCTTCAGCAC	CCTCAGCAGC	TGGGCCATCT	GCTCCAGCGC	780
5	CACGCCAGAC	TGCAGGGTCG	AGGCTCACCC	CTGTGAGCAC	AGGACGCTGG	AGATGGTCCG	840
	GGAGTTGCGT	GGCAATGCC	CATGCTGGAG	AGGATCGCGG	CGGACCCCTG	CGGTGCTGGC	900
	TGCACACTGT	CCCTTCTACA	GCTGGAAGAG	AGTGTTCCTA	ACCCACCCTG	CCACCTGCTA	960
	CAGGACCACC	TGCCCAGGCC	CCTGTGACTC	GCAGCCCTGC	CAGAAATGGAG	GCACATGTGT	1020
	TCCGAAGGA	TGGACGGCT	ACCAGTGCCT	CTGCCCCTG	GCCTTTGGAG	GGGAGGCTAA	1080
10	CTGTGCCCTG	AAGCTGAGCC	TGGAATGCAG	GGTCGACCTC	CTCTTCTCTG	TGGACAGCTC	1140
	TGCGGGCACC	ACTCTGGACG	GCTTCCTGCG	GGCCAAAGTC	TTCGTGAAGC	GGTTTGTGCG	1200
	GGCCGTGCTG	AGCGAGGACT	CTCGGGCCCG	AGTGGGTGTG	GCCACATACA	GCAGGGAGCT	1260
	GCTGTGGCG	GTGCCTGTGG	GGGAGTACCA	GGATGTGCCT	GACCTGGTCT	GGAGCCTCGA	1320
	TGGCATTCCC	TTCCGTGGTG	GCCCCACCT	GACGGGCAGT	GCCTTGCCTG	AGGCGGCAGA	1380
15	GCGTGGCTTC	GGGAGCGCCA	CCAGGACAGG	CCAGGACCGG	CCACGTAGAG	TGGTGGTTTT	1440
	GCTCACTGAG	TCACACTCCG	AGGATGAGGT	TGCGGGCCCA	GCGCGTCACG	CAAGGGCGCG	1500
	AGAGCTGCTC	CTGCTGGGTG	TAGGCAGTGA	GGCCGTGCGG	GCAGAGCTGG	AGGAGATCAC	1560
	AGGCAGCCCA	AAGCATGTGA	TGGTCTACTC	GGATCCTCAG	GATCTGTTC	ACCAAATCCC	1620
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20	CCTCGTCTTC	ATGTTCTTTC	CCTCTGCCTC	AGTAGGGCCC	GAGAATTTTG	CTCAGATGCA	1740
	GAGCTTTGTG	AGAACTGTGT	CCCTCCAGTT	TGAGGTGAAC	CCTGACGTGA	CACAGGTCCG	1800
	CCTGTGTGTG	TATGGCAGCG	AGGTGCAGAC	TGCCTTCGGG	CTGGACACCA	AACCCACCCG	1860
	GGCTGCGATG	CTGCGGGCCA	TTAGCCAGGC	CCCCTACCTA	GGTGGGGTGG	GCTCAGCCGG	1920
	CACCCGCCCTG	CTGCACATCT	ATGACAAAGT	GATGACCGTC	CAGAGGGGTG	CCCGGCCCTGG	1980
25	TGTCCCCAAA	GCTGTGGTGG	TGCTCACAGG	CGGGAGAGGC	GCAGAGGATG	CAGCCGTTCC	2040
	TGCCCAGAA	CTGAGGAACA	ATGGCATCTC	TGTCTTGGTC	GTGGGCGTGG	GGCCTGTCTC	2100
	AAGTGAGGGT	CTGCGGAGGC	TTGACAGTCC	CCGGGATTCC	CTGATCCACG	TGGCAGCTTA	2160
	CGCCGACCTG	CGGTACCAAC	AGGACGTGCT	CATTGAGTGG	CTGTGTGGAG	AAGCCAAGCA	2220
	GCCAGTCAAC	CTCTGCAAA	CCAGCCCGTG	CATGAATGAG	GGCAGCTGCG	TCCTGCAGAA	2280
30	TGGGAGCTAC	CGCTGCAAGT	GTGCGGATGG	CTGGGAGGGC	CCCCACTGCG	AGAACCATT	2340
	CTTGAGACGC	CCCTGAGGCA	CATGGCTCCC	GTGCAGGAGG	GCAGCAGCCG	TACCCCTCCC	2400
	AGCAACTACA	GAGAAAGGCT	GGGCACTGAA	ATGGTGCCTA	CCTTCTGGAA	TGCTGTGTCC	2460
	CCAGTCTCCT	AGAAATGTCT	CTTCCGCGCG	TGGCCAGGAC	CACATTTCTC	ACTGAGGGAG	2520
	GAGGATGTCC	CAACTGCAGC	CATGCTGCTT	AGAGACAAGA	AAGCAGCTGA	TGTACCCAC	2580
35	AAACGATGTT	GTTGAAAAGT	TTTGTATGTT	AAGTAAATAC	CCACTTTCTG	TACCTGCTGT	2640
	GCCTTGTGTA	GGCTATGTCA	TCTGCCACCT	TTCCTTGTAG	GATAAACCAAG	GGGTCTGTAA	2700
	GACTTAAATT	TAGCGGCCTG	ACGTTCTCTT	GCACACAATC	AATGCTCGCC	AGAATGTTGT	2760
	TGACACAGTA	ATGCCAGCA	GAGGCCTTTA	CTAGAGCATC	CTTTGGACCG		

Seq ID NO: 445 Protein sequence
Protein Accession #: Eos sequence

	1	11	21	31	41	51	
45	MPPFLLEAV	CVFLFSRVPP	SLPLQEVHVS	KETIGKISAA	SKMMWCSAAV	DIMFLLDGSN	60
	SVGKGSFERS	KHFAITVCDG	LDISPERVRV	GAQFSSSTPH	LEFPLDSFST	QOEVKARIKR	120
	MVFKGGRTET	ELALKYLLHR	GLPGGRNASV	PQILIIIVTDG	KSQGDVALPS	KQLKERGVTV	180
	FAVGVRFPWR	EELHALASEP	RQHVLLAEQ	VEDATNGLFS	TLSSSAICSS	ATPDCRVEAH	240
	PCEHRTLEMV	REFAPNAPCW	RGSRRTLAVL	AAHCPFYSWK	RVFLTHPATC	YRTTCPPGCD	300
50	SQPCQNGGTC	VEEGLDGYQC	LCPLAFGGEA	NCALKLSLEC	RVDLLFLDLS	SAGTTLDGFL	360
	RAKVVFVKRFV	RAVLSEDSRA	RVGVATYSRE	LLVAVPVGEY	QDVPLVWSL	DGIPFRGGPT	420
	LTGSALRQAA	ERGFSGSATR	GQDRPRRVVV	LLTESHSEDE	VAGPARHARA	RELLLLGVGS	480
	BAVRAELEEI	TGSPKHVMVY	SDPQDLFNQI	PELQKLCISR	QRPGCRTQAL	DLVFMLDTS	540
	SVGPENFAQM	QSFVRSALQ	FEVNPVDTQV	GLVVYGSQVQ	TAFGLDTPKT	RAAMLRAISQ	600
55	APYLGGVGS	GTALLHIYDK	VMTVQRGARF	GVPKAVVVLT	GGRGAEDAAV	PAQKLNNNGI	660
	SVLVVGVGPF	LSEGLRRLAG	PRDSLHVAA	YADLRVHQDV	LIEWLCGEAK	QPVNLCKPSP	720
	CMNEGSCVLQ	NGSYRCKCRD	GWEGPHCENR	FLRRP			

Seq ID NO: 446 DNA sequence
Nucleic Acid Accession #: NM_031942.1
Coding sequence: 145..1260

	1	11	21	31	41	51	
65	CCCGAGCCCC	GCCCCCTCCG	GCCCCGGTCG	GCGCGCCCAG	CCTGCCAGCC	GCGCTGCTGC	60
	TGCTCCTCCT	GCTGTGGGAC	CGCTGACCGC	GCGGCTGCTC	CGCTCTCCCC	GCTCCAAGCG	120
	CGGATCTGGG	CACCCGCCAC	CAGCATGGAC	GCTCGCCGCG	TGCCGCAGAA	AGATCTCAGA	180
	GTAAAGAAGA	ACTTAAAGAA	ATTGAGATAT	GTGAAGTTGA	TTTCCATGGA	AACCTCGTCA	240
	TCCTCTGATG	ACAGTTGTGA	CAGCTTTGCT	TCTGATAATT	TTGCAAAAC	GAGGCTGCAG	300
70	TCAGTTCCGG	AAGGCTGTAG	GACCCGCAGC	CAGTGCAGGC	ACTCTGGACC	TCTCAGGGTG	360
	GCGATGAAGT	TTCCAGCGCG	GAGTACCAGG	GGAGCAACCA	ACAAAAAAGC	AGAGTCCCGC	420
	CAGCCCTCAG	AGAATTTCTG	GACTGATTCC	AACCTCCGAT	CAGAAGATGA	AAGTGGAATG	480
	AATTTTCTGG	AGAAAAGGGC	TTTAAATATA	AAGCAAAACA	AAGCAATGCT	TGCAAAACTC	540
	ATGTCGTAAT	TAGAAAGCTT	CCCTGGCTCG	TTCCGTGGAA	GACATCCCTC	CCCAGGCTCC	600
75	GACTCACAAT	CAAGGAGACC	GCGAAGGCGT	ACATTTCCCG	GTGTTGCTTC	CAGGAGAAAC	660
	CCTGAACGGA	GAGCTTCGTC	TCTTACCAGG	TCAAGGTCCC	GGATCCTCGG	GTCCCTTGAC	720
	GCTCTACCCA	TGGAGGAGGA	GGAGGAAGAG	GATAAGTACA	TGTTGGTGAG	AAAGAGGAAG	780
	ACCGTGGATG	GCTACATGAA	TGAAGATGAC	CTGCCACAG	GCCGTCGCTC	CAGATCATCC	840
	GTGACCCCTC	CGCATATAAT	TCGCCCAGTG	GAAGAAATTA	CAGAGGAGGA	GTTGGAGAAC	900
80	GTCTGCAGCA	ATTCTCGAGA	GAAGATATAT	AACCGTTCAC	TGGGCTCTAC	TTGTCTATCA	960
	TGCCGTCAGA	AGACTATTGA	TACCAAAACA	AACCTGCAG	ACCCAGACTG	CTGGGGCGTT	1020
	CGAGGCCAGT	CTGTGGGCC	CTGCCCTTCA	AACCGTTATG	GTGAAGAGGT	CAGGGATGCT	1080
	CTGTGGATC	GCAACTTGCA	TTGCCCGCCT	TGTCGAGGAA	TCTGCAACTG	CAGTTCTGTC	1140
	CGGCAGCGAG	ATGGACGGTG	TGCGACTGGG	GTCCTTGTGT	ATTTAGCCAA	ATATCATGGC	1200
85	TTTGGGAATG	TGCATGCCTA	CTTGAAGAGC	CTGAAGCAGG	AATTTGAAAT	GCAAGCATAA	1260
	TATCTGGAAA	ATTGCTCTCC	TGCTCTCTAC	TCTCAAAATC	TTTCTGTGTA	AAGTTTCCAA	1320
	TTTTTTCAC	GAAACCTGAG	TTAAAATCT	TGATGATCAG	CCTGTTTCAT	AAGAACTCC	1380
	AATCAAGTTA	ATCTTAGCAG	ACATGTGTTT	CTGGAGCATC	ACAGAAGGTA	TATTGCTAGT	1440

TACACTTTGC CCTCTGCGAG TTCTCTCTCT GCTCCCAACC CCCATCTCAT AGCATCCCCC 1500
TCTATTTCCA ATGCTCCTCT CCAACCGCTT AGTTTCTGAA TTCTTTTAA ATTACAGTTT 1560
TATGAAAGCA TATTTTATTT ACTTGGTGTG GAAATAGCCC TCATAAAACC TAAGCACTTG 1620
GAAACACAAT AATAGTATTA ACTAAGTAGA TCTATTGAAT TTCAGAGAAG AGCCTTCTAA 1680
5 CTTGTTTACA CAAAACGAG TATGATTAG CACTCATACT AGTTGAAATT TTTAATAGAA 1740
TCAAGGCACA AAAGTCTTAA AACCATGTGG AAAAATTAGG TAATTATTGC AGATTGATGT 1800
CTCTCAATCC CATGTATTGC GCTTATGTTA CAAGTTGTTG TCACAGTTGA GACTTAATTT 1860
10 CTCTTAATTT CTCTGCCCCG AAGGGTAAGT GGTGCGTCCA GCTTACACGA TCATAATTCA 1920
AAGGTGTGGT GGCATGTAA TACTTAATTA AAATAATGAT GGAAGAGCTA TCTGGAGATT 1980
ATGAGTAAGC TGATTTGAAT TTTCAGTATA AAACCTTAGT ATAATTGTAG TTTGCAAAGT 2040
TTATTTCAGT TCACATGTAA GGTATTGCAA ATAAATTCCT GGACAATTTT GTATGGAAAC 2100
TTGATATTAA AAACAGTCTC GTGGTTCTTT GCAGTTTCTT GTAAATTTAT AAACCAGGCA 2160
CAAGGTTCAA GTTTAGATT TAAGCACTTT TATAACAATG ATAAGTGCCT TTTTGGAGAT 2220
15 GTAACCTTTA GCAGTTTGTG AACCTGACAT CTCTGCCAGT CTAGTTTCTG GGCAGGTTTC 2280
CTGTGTCACT ATTCCTCCCTC CTCTTTGCAT TAATCAAGGT ATTTGGTAGA GGTGGAATCT 2340
AAGTGTGTGT ATGTCCAAAT TACTTGCTA TGTAACCAT TGCTGTGCCA TTCAATGTTT 2400
GATGCATAAT TGGACCTTGA ATCGATAAGT GTAAATACAG CTTTGTATCT GTAATGCTTT 2460
TATACAAAAG TTTATTTTAA TAATAAAATG TTTGTTCTAA AAAAAAAAAA

Seq ID NO: 447 Protein sequence
Protein Accession #: NP_114148.1

1 11 21 31 41 51
MDARRVPQKD LRVKKNLKPF RYVKLISMET SSSDDSDSCDS FASDNFANTR LQSVREGCRT 60
25 RSQCRHSGPL RVAMKFPARS TRGATNKAE SRQPSSENSVT DSNDSSEDES GNMFLKRAL 120
NKKQNKAMLA KLMSELESFP GSFRGRHPLP GSDSQSRRLR RRTFPGVASR RNPERRARPL 180
TRSRSRILGS LDALPMEEEE EEDKMYLVRK RKTVDGYMNE DDLPRSRRLR SSVTLPHIIR 240
PVEITEEBEL ENVCSNSREK IYNRSLGSTC HQCRQKTIDT KTNCRNPDCW GVRGQFCGFC 300
30 LRRRYGEEVR DALLDPNWHC PPCRGICNCS FCRQRDGRCA TGVLVYLAKY HGFNGVHAYL 360
KSLKQEFEMQ A

Seq ID NO: 448 DNA sequence
Nucleic Acid Accession #: NM_019894
Coding sequence: 1..1314

1 11 21 31 41 51
ATGTTACAGG ATCCTGACAG TGATCAACCT CTGAACAGCC TCGATGTCAA ACCCCTGCGC 60
40 AAACCCCGTA TCCCATGGA GACCTTCAGA AAGGTGGGGA TCCCCATCAT CATAGCACTA 120
CTGAGCCTGG CGAGTATCAT CATTTGTGTT GTCCCTCATCA AGGTGATTCT GGATAAATAC 180
TACTTCTCTC GCGGGCAGCC TCTCCACTTC ATCCCGAGGA AGCAGCTGTG TGACGGAGAG 240
CTGGACTGTG CCTTGGGGGA GGACGAGGAG CACTGTGTCA AGAGCTTCCC CGAAGGGCCT 300
45 GCAGTGGCAG TCCGCTCTCT CAAGGACCGA TCCACACTGC AGGTGCTGGA CTCGGCCACA 360
GGGAACCTGGT TCTCTGCTGT TTTGACAAC TCCACAGAAG CTCTCGCTGA GACAGCCTGT 420
AGGCAGATGG GCTACAGCAG CAAACCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCAG 480
GATCTGGATG TTGTTGAAAT CACAGAAAAC AGCCAGGAGC TTCGCATGCG GAACTCAAGT 540
GGGCCCTGTG TCTCAGGCTC CCTGGTCTCC CTGCACTGTC TTGCCTGTGG GAAGAGCCTG 600
50 AAGACCCCCC GTGTGTGGG TGGGGAGGAG GCCTCTGTGG ATTCTTGGCC TTGGCAGGTC 660
AGCATCCAGT ACGACAAACA GCACGCTCTGT GGAGGGAGCA TCCTGGACCC CCACTGGGTC 720
CTCACGGCAG CCACTGTGCT CAGGAAACAT ACCGATGTGT TCAACTGGAA GGTGCGGGCA 780
GGCTCAGACA AACTGGGGCA CTTCCTCATCC CTGGCTGTGG CCAAGATCAT CATCATTTGA 840
TTCAACCCCA TGTAACCCAA AGACAATGAC ATCGCCCTCA TGAAGCTGCA GTTCCCACCT 900
55 ACTTTCTCAG GCACAGTCAG GCCCATCTGT CTGCCCTTCT TTGATGAGGA GCTCACTCCA 960
GCCACCCCAC TCTGGATCAT TGGATGGGGC TTACGAAGC AGAATGGAGG GAAGATGTCT 1020
GACATACTGC TGCAGGCGTC AGTCCAGGTC ATTGACAGCA CACGGTGCAT TGCAGACGAT 1080
GCGTACCAGG GGGAAAGTCA CGAGAAGATG ATGTGTGCAG GCATCCCGGA AGGGGGTGTG 1140
GACACCTGCC AGGGTGACAG TGGTGGGGCC CTGATGTACC AATCTGACCA GTGGCATGTG 1200
60 GTGGGCATCG TTAGCTGGGG CTATGGCTGC GGGGGCCCGA GCACCCACAG AGTATACACC 1260
AAGGTCTCAG CCTATCTCAA CTGGATCTAC AATGTCTGGA AGGCTGAGCT GTAA

Seq ID NO: 449 Protein sequence
Protein Accession #: NP_063947.1

1 11 21 31 41 51
MLQDPDSQDP LNSLDVKPLR KPRIPMETFR KVGIPIIIAL LSLASIIIV VLIKVILDKY 60
65 YFLCGQPLHF IPRKQLCDGE LDCPLGEDEE HCVKSFPEGP AVAVRLSKDR STLQVLDSAT 120
GNWFSACFDN FTEALAEATC RQMGYSKPT FRAVEIGPDQ DLDVVEITEN SQELMRNNS 180
70 GPCLSGSLVS LHCLACGKSL KTPRVVGEE ASVDSWFWQV SIQYDKQHVC GGSILDPHV 240
LTAAHCFRKH TDVFNWVKRA GSKLGSFPP LAVAKIIIE FNPMPKDN 300
TFSGTVRPIC LPFFDEELTP ATPLWIIIGW FTKQNGGKMS DILLQASVQV IDSTRCNADD 360
AYQGEVTEKM MCAGIPBGGV DTCQDSGGP LMYQSDQWHV VGLVSWGYGC GGPSTPGVYT 420

Seq ID NO: 450 DNA sequence
Nucleic Acid Accession #: XM_051860.2
Coding sequence: 52..3042

1 11 21 31 41 51
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80 GTTAACCTCA GCACCGAGGT TGTCTACAAA AAAGGCCAGG ATTATAGGTT TGCTTGCTAC 120
GACCGGGGCA GAGCCTGCCG GAGCTACCGT GTACGGTTCC TCTGTGGGAA GCCTGTGAGG 180
85 CCCAACTCA CAGTCAACAT TGACACCAAT GTGAACAGCA CCATTCTGAA CTGGAGGAT 240
AATGTACAGT CATGGAAC TGGAGATACC CTGGTCAATT CCAGTACTGA TTAATCCATG 300
TACCAGGCAG AAGAGTTCCA GGTGCTTCCC TGCAGATCCT GCGCCCCCAA CCAGGTCAAA 360

	GTGGCAGGGA	AACCAATGTA	CCTGCACATC	GGGGAGGAGA	TAGACGGCGT	GGACATGCGG	420
	GCGGAGGTTG	GGCTTCTGAG	CCGGAACATC	ATAGTGATGG	GGGAGATGGA	GGACAAATGC	480
	TACCCCTACA	GAACACACAT	CTGCAATTTT	TTTGACTTCG	ATACCTTTGG	GGGCCACATC	540
5	AAGTTTGTCT	TGGGATTAA	GGCAGCACAC	TTGGAGGGCA	CGGAGCTGAA	GCATATGGGA	600
	CAGCAGCTGG	TGGGTCACTA	CCCGATTAC	TTCCACTTGG	CCGGTGATGT	AGACGAAAGG	660
	GGAGGTTATG	ACCCACCCAC	ATACATCAGG	GACCTCTCCA	TCCATCATAC	ATTCTCTCGC	720
	TGCGTCACAG	TCCATGGCTC	CAATGGCTTG	TTGATCAAGG	ACGTTGTGGG	CTATAACTCT	780
	TTGGGCCACT	GCTTCTTAC	GGAGATGGG	CCGGAGGAAC	GCAACACTTT	TGACCACTGT	840
10	CTTGGCTCC	TTGTCAAGTC	TGGAACCTCT	CTCCCTCGG	ACCGTGACAG	CAAGATGTGC	900
	AAGATGATCA	CAGGAGACTC	CTACCCAGGG	TACATCCCCA	AGCCCAGGCA	AGACTGCAAT	960
	GCTGTGTCCA	CCTTCTGGAT	GGCCAATCCC	AACAACAACC	TACATCAACTG	TGCCGCTGCA	1020
	GGATCTGAGG	AAACTGGATT	TTGGTTTATT	TTTACCACAG	TACCAACGGG	CCCTCCGTG	1080
	GGATGTACT	CCCCAGTTA	TTCAGAGCAC	ATTCCTCTGG	GAAAATTTCTA	TAACAACCGA	1140
15	GCACATTCCA	ACTACCGGGC	TGGCATGATC	ATAGACAACG	GAGTCAAAAC	CACCGAGGCC	1200
	TCTGCCAAGG	ACAAGCGGCC	GTTCCTCTCA	ATCATCTCTG	CCAGATACAG	CCCTCACCAG	1260
	GACGCCGACC	CGCTGAAGCC	CCGGAGCCG	GCCATCATCA	GACACTTCAT	TGCCTACAAG	1320
	AACCGAGGACC	ACGGGGCCTG	GCTGCGCGGC	GGGATGTGT	GGCTGGACAG	CTGCCGGTTT	1380
	GCTGACAATG	GCATTGGCCT	GACCTTGGCC	AGTGGTGGAA	CCTTCCCGTA	TGACGACGGC	1440
20	TCCAAGCAAG	AGATAAAGAA	CAGCTTGTTC	GTGGCGAGA	GTGGCAACGT	GGGGACGGAA	1500
	ATGATGGACA	ATAGGATCTG	GGGCCCTGGC	GGCTTGGACC	ATAGCGGAAG	GACCTTCCCT	1560
	ATAGGCCAGA	ATTTTCCAAT	TAGAGGAATT	CAGTTATATG	ATGGCCCCAT	CAACATCCAA	1620
	AACTGCACCT	TCCGAAAGTT	TGTGGCCCTG	GAGGGCCGCG	ACACCAGCGC	CCTGGCCTTC	1680
	CGCCTGAATA	ATGCTTGGCA	GAGCTGCCCC	CATAACAACG	TGACCGGCAT	TGCCTTTGAG	1740
25	GACGTTCCGA	TACTTCCAG	AGTGTCTTTC	GGAGAGCCTG	AGCCCTGGTT	CAACCAAGTG	1800
	GACATGGATG	GGGATAAGAC	ATCTGTGTTC	CATGACGTG	ACGGCTCCGT	GTCCGAGTAC	1860
	CCTGGCTCCT	ACCTCACGAA	GAATGACAAC	TGGCTGGTCC	GGCACCAGCA	CTGCATCAAT	1920
	GTTCCTGACT	GGAGAGGGGC	CATTTCAGT	GGGTGCTATG	CACAGATGTA	GATTCAAGCC	1980
	TACAAGACCA	GTAACCTGCG	AATGAAGATC	ATCAAGAAATG	ACTTCCCCAG	CCACCTCTT	2040
30	TACCTGGAGG	GGCGCTCAC	CAGGAGCACC	CATTACCAGC	AATACCAACC	TTTGTTCACC	2100
	CTGCAGAAGG	GCTACACCAT	CCACTGGGAC	CAGACGGCCC	CCGCCGAAC	CGCCATCTGG	2160
	CTCATCAACT	TCAACAAGGG	CGACTGGATC	CGAGTGGGGC	TCTGTACCC	CGGAGGCACC	2220
	ACATTCTCCA	TCTCTCGGGA	TGTTCACAAT	CGCCTGCTGA	AGCAACACGTC	CAAGACGGGC	2280
	GTCTTCTGTA	GGACCTTGCA	GATGGACAAA	GTGGAGCAGA	GCTACCTTGG	CAGGAGCCAC	2340
35	TACTACTGGG	ACGAGGACTC	AGGGCTGTTG	TTCTTGAAGC	TGAAAGCTCA	GAACGAGAGA	2400
	GAGAAGTTTG	CTTCTGCTC	CATGAAAGGC	TGTGAGAGGA	TAAAGATTAA	AGCTCTGATT	2460
	CCAAAGAACG	CAGGGCTCAG	TGACTGCACA	GCCACAGCTT	ACCCCAAGTT	CACCGAGAGG	2520
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	CATTTCTTGG	AGGTGAAGAT	GGAGAGTTCC	AAGCAGCACT	TCTTCCACCT	CTGGAACGAC	2640
40	TTGCTTACA	TTGAAGTGGG	TGGGAAGAAG	TACCCAGATT	CGGAGGATGG	CATCCAGGTG	2700
	GTGGTGATTG	ACGGGAACCA	AGGGCCGCTG	GTGAGCCACA	CGAGCTTCAG	GAACTCCATT	2760
	CTGCAAGGCA	TACCATGGCA	GCTTTTCAAC	TATGTGGCGA	CCATCCCTGA	CAATTCCATA	2820
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	AAGCTTGGGG	CAGACAGGGG	TCTCAAGTTG	AAAGAGCAAA	TGGCATTTCG	TGGCTTCAAA	2940
45	GGCAGCTTCC	GGCCCATCTG	GGTGACACTG	GACACTGAGG	ATCACAAGGC	CAAAATCTTC	3000
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	GCCACCTCGT	GGTAGACTAT	GACGGTGACT	CTTGGCAGCA	GACCAGTGGG	GGATGGCTGG	3120
	GTCCCCCAGC	CCCTGCCAGC	AGCTGCCTGG	GAAGGCCGTG	TTTCAGCCCT	GATGGGCCAA	3180
	GGGAAGGCTA	TCCAGTACCC	TGGTCTGCTC	ACCTGCCCTT	ACTCAAGTGT	CTACCTGGAG	3240
50	CCCCTGGGGC	GGTGTGGGCC	AATGTGGGAA	ACATTCACTT	TCCTGCAGCC	TCTTGGGTGC	3300
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65	ATTCACTCCC	CAGGCAGCCC	TGCCCTCTGAC	TCCAAGAGGG	TGAAGTCCAC	AGAAGTGAGC	4200
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	AGACCCTAGA	TGTGCTCGTA	CTCCCTCGGC	CTGGGATTTC	AGAGCTGGAA	ATATAGAAAA	4320
	TATCTAGCCC	AAAGCCTTCA	TTTTAACAGA	TGGGGAAGT	GAGCCCCCAA	GATGGGAAGG	4380
	AACCAACAG	CTAAGGGGAG	GCCTGGGGAG	CCCCACCCTA	GCCCTTGCTG	CCACACCACA	4440
70	TTGCCCTCAAC	AACCGGCCCC	AGAGTGCCCA	GGCACTCCTG	AGGTAGCTTC	TGGAAATGGG	4500
	GACAAGTCCC	CTCGAAGGAA	AGGAATGAC	TAGAGTAGAA	TGACAGCTAG	CAGATCTCTT	4560
	CCCTCCTGCT	CCCAGCGCAC	ACAAACCCGC	CCTCCCTTTG	GTGTTGGCGG	TCCCTGTGGC	4620
	CTTCACTTTG	TCTACTACCT	GTCAGCCGAG	CCTGGGTGCA	CAGTAGCTGC	AACTCCCAT	4680
	TGGTGCTACC	TGGCTCTCCT	GTCCTCTGAG	CTCTACAGGT	GAGGCCAGC	AGAGGGAGTA	4740
75	GGCTCGCCCA	TGTTTCTGTC	GAGCCAATTT	GGCTGATCTT	GGGTGTCTGA	ACAGCTATTG	4800
	GGTCCACCCC	AGTCCCTTTT	AGCTGCTGCT	TAATGCCCTG	CTCTCTCCCT	GGCCCACTT	4860
	ATAGAGAGCC	CAAGAGCTCT	CTGTAAGAGG	GAGAACTCTA	TCTGTGGTTT	ATAATCTTGC	4920
	ACGAGGCACC	AGAGTCTCCC	TGGGTCTTGT	GATGAACCTA	ATTTATCCCC	TTTCTGCCC	4980
	CAACCACAAA	CTCTTCTCCT	CAAGAGGGC	CTGCCTGGCT	CCCTCCACCC	AACTGCACCC	5040
80	ATGAGACTCG	GTCCAAGAGT	CCATTCCCCA	GGTGGGAGCC	AACTGTCAAG	GAGGTCTTTT	5100
	CCACCAACCA	TCTTTTCACT	GCTGGGAGGT	GACCATAGGG	CTCTGCTTTT	AAAGATATGG	5160
	CTGCTTCAAA	GGCCAGAGTC	ACAGGAAGGA	CTTCTTCCAG	GGAGATTAGT	GGTGTGGAG	5220
	AGGAGAGTTA	AAATGACCTC	ATGCTCTTCT	TGTCACCGGT	TTTGTGAGT	TTTCACTCTT	5280
	CTAATGCAAG	GGTCTCACAC	TGTGAACCAC	TTAGGATGTG	ATCACTTTCA	GGTGGCCAGG	5340
85	AATGTGAAT	GTCTTTGGCT	CAGTTCAATT	AAAAAAGATA	TCTATTTGAA	AGTTCTCAGA	5400
	GTGTACATA	TGTTTACAG	TACAGGATCT	GTACATAAAA	GTTTCTTTCC	TAAACCATTG	5460
	ACCAAGAGCC	AATATCTAGG	CATTTTCTTG	GTAGCACAAA	TTTTCTTATT	GCTTAGAAAA	5520
	TTGTCTCTCT	TGTTATTCTT	GTTTGTAAAG	CTTAGGTGAG	TTAGTCTTTT	AAGGAAAGCA	5580

ACGCTCCTCT GAAATGCTTG TCTTTTCT GTTGCCGAAA TAGCTGGTCC TTTTCGGGA 5640
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 TATATTTTCT ATTTATTTAT TATATGTGCA CTTCAAGAAG TCACTGTCTAG AGAAATAAAG 5760
 AATTGTCTTA AATGTCAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAA

Seq ID NO: 451 Protein sequence
 Protein Accession #: XP_051860.2

1 11 21 31 41 51
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 DMRAEVGLLS RNIIVMGEME DKCYPYRNHI CNFFDFDTFG GHKIFALGFK AHLEGTTELK 180
 HMQQLVGVQY PIHFHLAGDV DERGGYDPPY YIRDLISHT FSRCVTVHGS NGLLIKDVVG 240
 YNSLGHCFET EDGPERNTF DHCLGLLVKS GTLLPSDRDS KMCKMITGDS YPGYIPKPRQ 300
 DCNAVSTFWM ANPNNNLINC AAAGSEETGF WFIHHVPTG PSVGMYSPTY SEHILPKFQY 360
 NNRAHSNYRA GMIIDNGVKT TEASAKDKRP FLSIISARYS PHQDADPLKP REPATIRHFI 420
 AYKNQDGHAW LRGGDVWLDS CRFADNGIGL TLASGGTFPY DDGSKQEIKN SLFVGESGNV 480
 GTEMMDNRW GPGLLDHSGR TLPIGQNFPI RGIQLYDGP NIQNTCTFRKF VALEGRHTSA 540
 LAFRLNNANW SCPHNNVFTL AFEDVPITSR VFFGEPGPWF NQLDMDGDKT SVFHDVDGSV 600
 SEYPGSYLTK NDNWLVRHDP CINVPDWRGA ICSGCYAQMY IQAYKTSNLR MKIINKDFPS 660
 HPLYLEGALT RSTHYQQYQP VVTLOKGYTI HWDQTAPEL AIWLINFNKG DWIRVGLCYP 720
 RGTTFSLSD VHNRLKQTS KTGVPVRTLQ MDKVEQSYPG RSHYYWDEDS GLLFLKLKAQ 780
 NEREKFAFCS MKGCERIKK ALIPKNAGVS DCTATAYPKF TERAVVDVPM PKKLFQSGLK 840
 TKDHLFLEVM ESKKHVFTL WNDFAFIEVD GKYPSESDG IQVVDVGNQ GRVVSHTSFR 900
 NSILQGIPIW LFNYVATIPD NSIVLMASKG RYVSRGPWTR VLEKLGADRG LKLKEQMAFV 960
 GFKGSFRPIW VTLDTEHDKA KIFQVPIPV VKKKKL

Seq ID NO: 452 DNA sequence
 Nucleic Acid Accession #: Bos sequence
 Coding sequence: 261..2861

1 11 21 31 41 51
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 TTGGAATAAT TTTGCTGTTA TTATAGTAAA CATACAAAGG ATGTCAAAAA AAAAAAATAA 4680
 AAAAAAATAA AAAAAAATAA AA

Seq ID NO: 453 Protein sequence
 Protein Accession #: Eos sequence

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 TIILYGRADE GIQPPDPYYGL KYIGVGKGGG LELHGQKKLS WTFLNKLHPH GGMAEGGYFF 180
 ERSWGHRRGVI VHVIDPKSST VIHSDFRFDY RSKKESERLV QYLNAVDPGR ILSVAVNDEG 240
 SRNLDDMARK AMTKLGSKEF LHLGFRHPWS FLTUVKGNPSS SVEDHIEYHG HRGSAAARVF 300
 KLFQTEHGEY FNVLSSEWV QDVEWTEWFD HDKVSQTKGG EKISDLWKAH PGKICNRPID 360
 IQATTMDGVN LSTEVVYKKG QDYRFACYDR GRACRSYRVR FLCGKPVPRK LTVTIDTNNV 420
 STILNLEDNV QSWKPGDITLV IASTDYSMYQ ABEFQVLPGR SCAPNQVKVA GKPMYLIHGE 480
 EIDGVDMRAE VGLLSRNIV MGEMEDKCPY YRNHICNFFD PDTFGGHKIF ALGFKAHLE 540
 GTELKHMGGQ LVGQYPIHFP LAGDVDERGG YDPPTYIRDL SIHHTFSRCV TVHGSNGLLI 600
 KDVVGYNSLG HCFFTEDGPE ERNTFDHCLG LLVKSGLTLLP SDRDSKMKCM ITEDSYPGYI 660
 PKPRQCDNAV STFWMANPNN NLINCAAAGS EBTGFWFIFH HPPTGPSVGM YSPGYSEHIP 720
 LGKFVNNRAH SNYRAGMID NGVKTTEASA KDKRPFLSII SARYSFHQDA DPLKPREPAI 780
 IRRFIAYKQV DHGAWLRGGD VWLDSCHFRRG EAQEGFLLTG MKAGGILLGG DEAAAGMAQG 840
 FSPPCRCLLK LVTGSGPFAH VSLAHS

Seq ID NO: 454 DNA sequence
 Nucleic Acid Accession #: NM_013282.2
 Coding sequence: 85..2466

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 CAGGAGCTGT TCCACGTGGA GCCAGGCCTG CAGAGGCTGT TCTACAGGGG CAAACAGATG 240
 GAGGACGGCC ATACCTCTCT CGACTACGAG GTCCGCCTGA ATGACACCAT CCAGCTCCTG 300
 GTCCGCCAGA GCTCTGTGCT CCCCACAGC ACCAAGGAGC GGGACTCCGA GCTCTCCGAC 360
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 AAGTGGCAGG ACCTGGAGGT GGGCCAGGTG GTCATGCTCA ACTACAACCC CGACAACCCC 780
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 GCGGGAGAGC GGCTGAGAGA GAGCAAGAAG AAGGCGAAGA TGCCCTCGGC CACATCGTCC 1260
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 GTCCCGTCCA ACCACTACGG ACCATCCCG GGGATCCCCG TGGGCACCAT GTGGCGGTTT 1380
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 AGCAACGACG GAGCGTACTC CTAGTCTCTG GCGGGGGGCT ATGAGGATGA CGTGGACCAT 1500
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 TTTCTCGTGT GCGCTTACCT TCTGCGGAGG GACGATGATG AGCCTGGCCC TTGGACGAAG 1860
 GAGGGGAAGG ACCGGATCAA GAAGCTGGGG CTGACCATGC AGTATCCAGA AGGCTACCTG 1920

5	GAAGCCCTGG	CCAACCCGAGA	GCGAGAGAAG	GAGAACAGCA	AGAGGGAGGA	GGAGGAGCAG	1980
	CAGGAGGGGG	GTTTCGCGTC	CCCCAGGACG	GGCAAGGGCA	AGTGGAAGCG	GAAGTCGGCA	2040
	GGAGGTGGCC	CGAGCAGGGC	CGGGTCCCGC	CGCCGGACAT	CCAAGAAAAC	CAAGGTGGAG	2100
	CCCTACAGTC	TCACGGCCCA	GCAGAGCAGC	CTCATCAGAG	AGGACAAGAG	CAACGCCAAG	2160
	CTGTGGAAATG	AGGTCTTGCG	GTCACTCAAG	GACCGGCCGG	CGAGCGGCAG	CCCGTTCAG	2220
	TTGTTCTCTGA	GTAAAGTGGA	GGAGACGTTC	CAGTGTATCT	GCTGTCAGGA	GCTGGTGTTC	2280
	CGGCCCATCA	CGACCGTGTG	CCAGCACAAAC	GTGTGCAAGG	ACTGCCTGGA	CAGATCCTTT	2340
	CGGGCACAGG	TGTTTCACTG	CCCTGCCTGC	CGCTACGACC	TGGGCGCGAG	CTATGCCATG	2400
10	CAGGTGAACC	AGCCTCTGCA	GACCGTCTCT	AACCAGCTCT	TCCCCGGCTA	CGGCAATGGC	2460
	CGGTGATCTC	CAAGCACTTC	TCGACAGGCG	TTTGTCTGAA	AACGTGTGCG	AGGGCTCGTT	2520
	CATCGGCACT	GATTTTGTTC	TTAGTGGGCT	TAACTTAAAC	AGGTAGTGT	TCCTCCGTTC	2580
	CCTAAAAAGG	TTTGTCTTCC	TTTTTTTTTA	TTTTTATTTT	TCAATCTAT	ACATTTTCAG	2640
	GAATTTATGT	ATTCTGGCTA	AAAGTTGGAC	TTCTCAGTAT	TGTGTTTAGT	TCCTTGAAAA	2700
15	CATAAAGCC	TGCAATTTCT	CGACAAAACA	ACACAAGATT	TTTTAAAGAT	GGAATCAGAA	2760
	ACTACGTGGT	GTGGAGGCTG	TTGATGTTTC	TGGTGTCAAG	TTCTCAGAAG	TGCTGCCAC	2820
	CAACTCTTTA	AGAAGGCGAC	AGGATCAGTC	CTTCTCTAGG	GTTCTGGCCC	CCAAGGTCAG	2880
	AGCAAGCATC	TTCCTGACAG	CATTTTGTCA	TCTAAAGTCC	AGTGACATGG	TTCCTCCGTG	2940
	TGGCCCGTGG	CAGCCCGTGG	CATGGCGTGG	CTCAGCTGTC	TGTTGAAGTT	GTTGCAAGGA	3000
20	AAAGAGGAAA	CATCTCGGCG	CTAGTTCAAA	CCTTTGCCTC	AAAGCCATCC	CCCACCAGAC	3060
	TGCTTAGCGT	CTGAGATCCG	CGTGAAGAGT	CCTCTGCCCA	CGAGAGCAGG	GAGTTGGGGC	3120
	CACGCAGAAA	TGGCCTCAAG	GGGACTCTGC	TCCACGTGGG	GCCAGGCGTG	TGACTGACGC	3180
	TGTCCGACGA	AGGCGGCCAC	GGACGACGCG	CAGCACACGA	AGTCACGTGC	AAGTGCCTTT	3240
	GATTCGTTCC	TTCTTTCTAA	AGACGACAGT	CTTGTGTGTT	AGCACTGAAT	TATTGAAAAT	3300
25	GTCAACCAGA	TTCTAGAAAC	TGCGGTCAAT	CAGTTCTTCC	TGACACCCGA	TGGGTGCTTG	3360
	GGAAACCGTT	GAGCCTTATA	GATCATTTAC	ATTCAATTTT	TTTAACTCAG	CAAGTGAGAA	3420
	CTTACAAGAG	GGTTTTTTT	TAATTTTTTT	TTCTCTTAAT	GAACACATTT	TCTAAATGAA	3480
	TTTTTTTTGT	AGTTACTGTA	TATGTACCAA	GAAAGATATA	ACGTTAGGGT	TTGGTTGTGT	3540
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30	TTGCAGCCTA	TACCTCAATA	AAACAGGGAT	ATTTTAAATC	ACATACCTGC	AGACAAACTG	3660
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	TTAGATTCTC	AGAATTAATG	TTTTTCACAG	ATTGAAAAAA	AAAAAAA		

Seq ID NO: 455 Protein sequence
Protein Accession #: NP_037414.2

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40	YEVRLNDTIQ	LLVRQSLVLP	HSTKERDSEL	SDTDSGCCLG	QSEDKSSTH	GEAAAEETDSR	120
	PADEMDMDET	ELGLYKVNEY	VDARDTNMGA	WFEAQVVRVT	RKAPSRDEPC	SSTRPALEE	180
	DVIYHVKYDD	YPENGVVQMN	SRDVRARART	IIKWQDLEVG	QVVMNLNYPD	NPKERGFWD	240
	AEISRKRETR	TARELYANVV	LGDDSLNDCR	IIFVDEVFKI	ERPGEGBPMV	DNPMRRKSGP	300
45	SKKHCKDDVN	RLCRVCACHL	CGGRQDPDKQ	LMCDECDMAF	HIYCLDPPLS	SVPSEDEWYC	360
	PBCRNDADEV	VLAGERLRES	KKAKAMASAT	SSSQRDWKG	MACVGRTEKC	TIVPSNHYGP	420
	IPGIPVGTMW	RFRVQVSESG	VHRPHVAGIH	GRSNDGAYSL	VLAGGYEDDV	DHGNFFTYTG	480
	SGGRDLSGNK	RTAEQSCDQK	LTNTNRLAL	NCFAPINDQE	GAEAKDWRSG	KPVRVVRNVK	540
	GGKNSKYAPA	EGNRYDGIYK	VVKYWPEKKG	SGFLVWRYLL	RRDDDEPGPW	TKEGKDRIKK	600
50	LGLTMQYPEG	YLEALANRER	EKENSKREEE	EQQEGGFASP	RTGKGKWKRK	SAGGSPSRAG	660
	SPRRTSKTKK	VEPYSLTAQQ	SSLIREDKSN	AKLWNEVLAS	LKDRPASGSP	FQLFLSKVEE	720
	TFQCICCCQL	VFRPITTVQC	HNVCCKDLDR	SFRAQVFSFP	ACRYDLGRSY	AMQVNQPLQT	

Seq ID NO: 456 DNA sequence
Nucleic Acid Accession #: NM_001200.1
Coding sequence: 325..1514

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	TGCCCGACAC	TAGACGCTGT	TCCCGACGCT	GAAAAGAGAG	ACTGCGCGGC	CGGCACCCGG	180
	GAGAGGAGAG	AGGCAAGAAA	AAGGAACGGA	CATTGCGTCC	TTGCGCCAGG	TCCTTTGACC	240
	AGAGTTTTTC	CATGTGGACG	CTCTTTCAAT	GGACGTGTCC	CCGCGTGCTT	CTTAGACGGA	300
65	CTGCGGTCTC	CTAAAGGTGC	ACCATGGTGG	CCGGGACCCG	CTGCTTCTTA	GCGTTGCTGC	360
	TTCCCCAGGT	CCTCCTGGGC	GGCGCGGCTG	GCCTCGTTCC	GGAGCTGGGC	CGCAGGAAGT	420
	TCGCGGCGCG	TGCTCGGGC	CGCCCCCTCAT	CCCAGCCCTC	TGACGAGGTC	CTGAGCGAGT	480
	TCGAGTTGCG	GCTGCTCAGC	ATGTTGCGCC	TGAAACAGAG	ACCCACCCCC	AGCAGGGACG	540
	CCGTGGTGCC	CCCCTACATG	CTAGACCTGT	ATCGCAGGCA	CTCAGGTCAG	CCGGGCTCAC	600
70	CCGCCCCAGA	CCACCGTTG	GAGAGGGCAG	CCAGCCGAGC	CAACACTGTG	CGCAGCTTCC	660
	ACCATGAAGA	ATCTTTGGA	GAACCTACAG	AAACGAGTGG	GAAAACAACC	CGGAGATTCT	720
	TCCTTAATTT	AAGTTCTATC	CCCACGGAGG	AGTTTATCAC	CTCAGCAGAG	CTTCAGGTTT	780
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	TTTATGAAAT	CATAAAACCT	GCAACAGCCA	ACTCGAAATT	CCCCGTGACC	AGACTTTTGG	900
75	ACACCAAGTT	GGTGAATCAG	AATGCAAGCA	GGTGGGAAAG	TTTTGATGTC	ACCCCGCTG	960
	TGATGCGGTG	GACTGCACAG	GGACACGCCA	ACCATGGATT	CGTGGTGGAA	GTGGCCCACT	1020
	TGGAGGAGAA	ACAAGGTGTC	TCCAAGAGAC	ATGTTAGGAT	AAGCAGGTCT	TTGCACCAAG	1080
	ATGAACACAG	CTGGTCACAG	ATAAGGCCAT	TGCTAGTAAC	TTTTGGCCAT	TGTGGAAGAA	1140
	GGCATCCTCT	CCACAAAAGA	GAAAACGCTC	AAGCCAAAAC	CAACACGCGG	AAACGCCCTA	1200
80	AGTCCAGCTG	TAAAGACAC	CCTTTGTACG	TGGACTTCAG	TGACGTGGGG	TGGAATGACT	1260
	GGATTGTGGC	TCCCCGGGGG	TATCACGCCCT	TTTACTGCCA	CGGAGAATGC	CCTTTTCCTC	1320
	TGGCTGATCA	TCTGAACTCC	ACTAATCATG	CCATTGTTCA	GACGTGTGTC	AACTCTGTGA	1380
	ACTCTAAGAT	TCTAAGGCA	TGCTGTGTCC	CGACAGAACT	CAGTGCTATC	TCGATGCTGT	1440
	ACCTTGACGA	GAATGAAAAG	GTTGTATTAA	AGAACTATCA	GGACATGGTT	GTGGAGGGIT	1500
85	GTGGGTGTCG	CTAGTACAGC	AAAATTAAT	ACATAAATAT	ATATATA		

Seq ID NO: 457 Protein sequence
Protein Accession #: NP_001191.1

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	FGLKQRPTPS	RDVAVPPYML	DLYRRHSGQP	GSPAPDHRLE	RAASRANTVR	SFHHESLEE	120
	LPETSGKTTR	RFFFLNLSIP	TEEFITSDEL	QVFRQMQDA	LGNNSSFHHR	INIYEIIPKA	180
	TANSKFPVTR	LLDT					

10 Seq ID NO: 458 DNA sequence
Nucleic Acid Accession #: NM_001999.2
Coding sequence: 1..8736

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	CAGCCGCCCG	CGCAACAGGT	TCGGTCCGCT	ACAGCAGGCT	CTGAAGCGCG	GTTTCTAGCG	180
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20	GACGTGCTCC	GAGGGCCCAA	CGTGTGCGGC	TCCAGATTCC	ACTCCTACTG	CTGCCCTGGA	300
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Seq ID NO: 461 Protein sequence
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Seq ID NO: 462 DNA sequence
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5	AGCTCAGCGT	TACTAGAGAC	ATTAGAAAAC	ATCAGCACCTC	TGGTGCCTCC	GACAGCTCTT		1260
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10	GTCAATGGAC	CTGTGATATC	CACGGTTATT	CAAAACTATT	CCATAAATGA	AGTTTTTCTA		1560
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15	ATTTTATGCC	TGATCATCGA	GGCTTTGTTT	TGGAAGCAGA	TTAAAAAAG	CCAAACCTCT		1860
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25	GGGCTCACCT	GGGGCTTTGG	AATAGGAACA	ATAGTGGACA	GCCAGAATCT	GGCTTGGCAT		2460
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	CAAAACAGAA	AGCAAAACTC	ATCAGATTTA	TCGTGCCAAAC	CCAAATTTCT	AAAGCCTTTC		2640
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Seq ID NO: 463 Protein sequence
Protein Accession #: Eos sequence

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40	IBIQLKKAYE	RQGFESVQV	TQFRNGSIVA	GVEVVGSSSA	SELLSAIEHV	AEKAKTALHK	240
	LFPLEDGSFR	VFGKAQCNDI	VFGFGSKDDE	YTLPCSSGYR	GNITAKCESS	GWQVIRETCV	300
	LSLLEELNKN	FSMIVGNATE	AAVSSFVQNL	SVIIRQNPST	TVGNLASVVS	ILSNISLSL	360
	ASHFRVSNST	MEDVISIADN	ILNSASVTNW	TVLLREEKYA	SSRLLETLEN	ISTLVPTAL	420
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45	SMASLTGLNI	LPVSKNGNAG	VNGPVISTVI	QNYISINEVFL	FFSKIESNLS	QPHCVFWDPS	540
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	ILCLIIIEALF	WKQIKKSQTS	HTRRICMVNI	ALSLLIADVN	FIVGATVDTT	VNPSGVCTAA	660
	VFFTHFFYLS	LEFFMMLMGI	LLAYRIILVF	HHMAQHLMM	VGFCLGYGCP	LIISVITIAV	720
	TQPSNTYKRR	DVCWLWNSNG	SKPLLAFFVP	ALAIIVAVNFV	VVLLVLTKLV	RPTVGERLSR	780
50	DDKATIIIRVG	KSLILLTPLL	GLTWGFGIGT	IVDSQNLAWH	VIFALLNAFQ	GFFILCFGIL	840
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Seq ID NO: 464 DNA sequence
Nucleic Acid Accession #: AB035089.1
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	CGTTAAAAAT	AAAGGAAAAA	CTTTAAATGT	CAAAATCTCA	CAACCCAGAT	ATATCATTTT	4260
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	TGATGCTTTT	CCAGGAGTTC	CAGATCAGAT	CGAGTTCACC	ATGAATTTCAC	TCAGTGAAGC	4380
45	CAACACCAAG	TTTATGTTCTG	ATCTGTTCCA	ACAGTTTACA	AAATCAAAAG	AGAACAACAT	4440
	CTTCTATTCC	CCTATCAGCA	TCACATCAGC	ATTAGGGATG	GTCTCTTAG	GAGCCAAAGA	4500
	CAACACTGCA	CAACAAATTA	GCAAGGTAGC	TATCAGCATC	ATTACGTTGT	CCTGTTGCAG	4560
	TTTTTCTCTG	GTTCCTGTCG	CTAGCACGCA	GATGGTAATA	GATGTGGTGG	TCTGATGGGT	4620
50	AGCACAGGGG	GCTGTGACGG	AAITCCCAT	ACTGTGAGAC	CAGTGACTTA	AACAGATCTT	4680
	TTGAGTAAAG	TTTTCTTTGTC	CCGCTTCATG	TCTCTTCCAG	GTCTTCTACT	TTGATCAAGT	4740
	CACAGAGAAC	ACCACAGAAA	AAGCTGCAAC	ATATCATGTG	AGTCACAGAG	CACCTCTGATT	4800
	CAGCTTTAGA	TCCTTGAAAC	GGTCATAGTT	TAAACCTGGA	ACTTCACAAA	AACTAAGAAA	4860
	AGGCCAGTTT	TAGGGAATAAT	CTTGGACACA	AAGATTGAGA	CATACAGAGT	GGGTTGGCAT	4920
55	TTTATGGCAC	ATAATTATTA	TTCTCTATT	CTGCGTTACT	AAAAGACAGT	CAGCACTGTA	4980
	CCTCAGAGCA	TAGGTCCTGGA	TCAGGATAGG	CTGGGTTTCA	ACTCCAGCTT	TGCTCTTCAC	5040
	AAATGATGAA	TAAAGACAGG	ACACAACCTG	TCGGAGTCCC	AGTGACCTCA	TCCCAGAAAA	5100
	CTAAGGGTAA	GAAAAATCT	GACTCAATAC	ATGCAAAATG	ATGCAAAATG	TTACAACAGT	5160
	GCCTTGCCCA	TAAAGTTCAT	AATAAATGTT	ATTATTATTA	TAAAGTAGCT	ATAATTATAC	5220
60	TAATCATAAAT	AATGTGAAAA	TAATTTAATT	TTTATTGAGT	CATTAATGAG	ATTACAGGGA	5280
	ATAAGCACAA	GTCCAAGTAT	ATTTTGGAAA	ATGATTGCTA	TGGAATATAT	TGGTTTAGAG	5340
	CCTTAATAGT	GCAAAATGCT	TTGCTGGAAG	GTAGAAAGTT	CTAGATTATA	ACAGGCTTAG	5400
	GTTCAAAAC	TGGCACTTCT	AATTTATGTC	TCTATAAACA	GGGTTTTTTT	CCCCATTTCT	5460
	TGAGCTTTCT	TGTTGTTTATC	TGAATTGAAC	TAAAGACTTA	GAGTTACCCA	TGTAAAGTCC	5520
65	TTAGCCATGG	ACCTGGCATA	CACCTTCTT	ACGTGCAGAG	AATGACCATC	ATGAGGAAAG	5580
	AGCCACAGAT	CAGTCAATGT	GTCTTACAAG	ATAATAGCAC	CAACAGGTAT	AACAGGGCTT	5640
	CCTGGCATAA	TCTATTTTAA	ATATCCAACC	TTCAACATAC	TCGTATCCTT	GATGACTGTT	5700
	AGAAAGTAAA	TATGGTCCCT	GCCCATAGAG	AGCTGAGAGT	TTAACTGGGA	AGCTAAACCT	5760
	AACCTTTTAA	ACCAACAAGG	AGAAAACTTA	CTGGTAGACA	CGCTGTCATC	TTTAGTTTCA	5820
70	AAGAGAAAAA	ATTGCAGTAC	GTTAGAGCAA	GAAGAATTTT	CTGGAAGAAAG	TCAAATATAA	5880
	GGTGGATTTT	GAAGGGTATT	TGAGGTGAAA	TACACCAATT	ATCAGGGAAAT	AACATCAAG	5940
	GTCTCTAATG	AGACTACAGG	CATTTAGGGA	CTGATCTAAC	AGACTTAGCA	TGGGTTTAGT	6000
	ATTACATTG	ATACAGCAAT	TGAATGATCT	CCTTTTTTGA	TGTTTGAAGG	TTGATAGGTC	6060
	AGGAAATGTT	CATCACCAGT	TTCAAAAGCT	TCTGACTGAA	TTCAACAAAT	CCACTGATGC	6120
75	ATATGAGCTG	AAGATCGCCA	ACAAGCTCTT	CGGAGAAAAA	ACGTATCAAT	TTTTACAGGT	6180
	AAATTCACCT	GGCTACACCA	CATTTTCAAT	GCATCCTGAT	GTCTGTGTCT	CTGAGTGGCC	6240
	AAATGGAAGA	AAGCAAGGCA	GATGAGCCTG	CGCGACCCAG	GTGGAGAGCA	TTTACTCAGA	6300
	GTGCATTAGC	TCCATTTCCT	CAACTCTCCC	CCACTGGAGT	GTCCAGAGCC	CCAACGATAC	6360
	ATCACTGAAG	TGTGGATTTA	GGGATAATCT	TGTGATAAAA	GAGGAGGTTG	TGTAATAGAG	6420
80	TGAGTAAGAG	TAATAAGTAA	TAAAGATACA	TCGATAAACT	GGCAGTGACT	CAGTCACATA	6480
	CGATACATCT	TGGTGGGAAA	TGTATGACTA	ATGGGATATT	ATTGGAATGG	GCAGGCTTGG	6540
	GTGAGTTCTCT	GAGAATAGTT	GAGGAAGTAC	CAGGAAATAT	TGAATGCACA	GGATGAAAGA	6600
	CAAAAAACAA	GATCAGAAAC	ATCATGGTTA	AAATTACTGG	AGAGAAGTCT	GAGAAGCAAT	6660
	GAATCTCCCT	CAGGGAAGCC	TGCTCTGAGC	TTTGCAAAAC	ACAGCCTCTT	CTGCTTCTGC	6720
85	CTTTTGCCAA	GATGATATTG	ACCTTCAGTG	ACCTCTTTCT	TGTGCCAGCC	CACATTTCCC	6780
	TTTTGCAATTG	CCTACATGAC	ACCTGTATAA	AAATATCCAT	GGACAGGAGA	TACTGCATCT	6840
	ATTACAGGTC	TGGATTTCAG	TTACTGTTGT	TACAATAAAG	TAAGTTTGGT	AATATATAGT	6900
	TACATAAAT	ACTCCTAAT	CCTACTTCTT	CCTTCATATC	TCAAAGGAAT	ATTTAGATGC	6960

	CATCAAGAAA	TTTTACCAGA	CCAGTGTGGA	ATCTACTGAT	TTTGCAAATG	CTCCAGAAGA	7020
	AAGTCGAAAG	AAGATTAACT	CCTGGGTGGA	AAGTCAAACG	AATGGTAGGA	GAGCCACCCA	7080
	TTATAGAAAC	ACCTTTGAGA	AACCTATGCC	AGTGAGCCTT	GTGCTTGACA	CTGCATGGGG	7140
5	GAACAGGTGT	GGGGATTGAG	ATGGGTTTGC	AGGGAGGGCT	GAAGAGGGCA	CTCCAGATGA	7200
	AGGATTTGTC	CAAATGAATA	TGAAGAGAGC	CTAGGGGAGC	CAAGGAGGAA	ATCACAGGAA	7260
	GCCAAATTAGA	TGGAACACA	TCTGGAGAAT	TATTTGCTTA	TGGCCCTGCA	TGACAATAGC	7320
	TTTGTGGATC	CCCTGTCTCC	GCTCAGACCT	ATTTTGAGAT	CATATCCTTT	ACTTTAAATC	7380
	AGACTCAAA	TTTTATGATG	AATATTTAAT	AGAAAACATT	AGAAAGCGTC	TCTCGTCTCC	7440
10	TTTACTAATT	GGGAAACAAG	CAGCTCTCTG	GTAAATCACC	CTTTTGTCTC	TGAGCTGGAG	7500
	CTGCCCTGGAT	CACATCTGTA	GCCAAATGTGT	TCTGCAGGGA	TTATCACAGC	TCTCTTCCCC	7560
	ATCAAGGGCA	AAGAGCTTGA	CAAAGTCTCC	ATTCTACAGA	CATCTTCTTT	ACCTCCCACC	7620
	TCTCATTACA	GGCCAAACTT	ACAGCAACTC	AACATGAGAG	TGAATAGGAA	GATACCCCCG	7680
	GAAGTAGTGT	CTGACAGCAC	AGGACATGCG	TTTCATATTA	CAGAGCTCAA	GTCACTCATC	7740
15	CTAAATGCA	ATCAGGGCCT	CCTTCTCTG	AATGGGGACC	CCGTAGTTAA	AAAAAATAA	7800
	AAGTAGGAAG	AGGAGGGAGG	GAGAAAGGAA	AGACACATGT	TGGAAGAGTA	GACAAAATCA	7860
	GTTTATCAGT	ATTCCAATC	AGATGATTGG	AGACATTCAT	ACACAGAGAA	CGTGAACCTC	7920
	TTCTCTATCA	CAAGAAGTGA	TGCTCTCCATC	AAGGGTAACT	TTATACGACT	GGAGCCTTGA	7980
	AGAAAGCTGC	ATCTGGTGAA	CCAATGGTCA	GTGAGTCTAA	CAATTCAAAG	ATCAAAGTCA	8040
20	GTGAGTCTCA	AGCAGGGATT	TGGGTCAATA	ATTAACGATC	AGTCACGAAC	ATTTGCAAG	8100
	CATCTTCCAG	ACAAGCCATT	TGTAGCTTGT	GTAAAAGACT	CTTTTATTCT	TCCCTTGCA	8160
	GAAAAAATTA	AAAACCTATT	TCCGTATGGG	ACTATTGGCA	ATGATACGAC	ACTGGTTCTT	8220
	GTGAACGCAA	TCTATTTCAA	AGGGCAGTGG	GAGAAATAAT	TTAAAAAGA	AAACACTAAA	8280
	GAGGAAAAAT	TTTGGCCAAA	CAAGGTATTG	TCTATATTTT	ATTTATATAG	TGTAATATGT	8340
25	TAATACATGG	AATGTTAAAC	ATTTCTGATG	GAATGTAACA	GATAAGTAA	AAAAATAAAA	8400
	TGTTTCATGT	CTGTTATTTT	GTGTTTTCAC	TCTTATAACT	TTATTAGATT	AGGAATACCT	8460
	GAAAAACTAT	TGTTTCTAAC	TCATGGAATT	CCTGGGTTAT	TTCTTAGAAG	AAGAAGGATG	8520
	TGTTGCTATC	TCAATAATAT	TATCTTTTTT	GTCTTGTGTT	TCACGTGTTA	TTTGTGGAC	8580
	ACATTGATTT	ATTGCAAGAT	ACATACAAAT	CTGTACAGAT	GATGAGGCAA	TACAATTCCT	8640
30	TTAATTTTGC	CTTGTCTGAG	GATGTACAGG	CCAAGGTCTC	GGAAATACCA	TACAAAGGCA	8700
	AAGATCTAAG	CATGATTGTG	CTGCTGCCAA	ATGAAATCGA	TGGTCTGCAG	AAGGTAAGAA	8760
	CTTGCACTCA	CAACTCTTCC	TTCTACTGCC	GGACATTTTT	CCAAAGATAC	CAAGTTTAAA	8820
	CAGAGTAAAA	GCTTATGACC	GAGTTGCCCC	AAAATGATGA	AAAATCTAA	ATGAGGAATG	8880
	ATGACTCACC	TTTCATATTAC	AAATATTGGA	GCATAGGGCC	TGACACAAAC	TGAAAGCTTA	8940
35	GTFTTTGTTT	CTTTGTTTGT	TTTTATTATT	ATTATTATAA	TACTTTAAGC	TTTAGGGTAC	9000
	ATGTGCACAA	TGTGCAGGTT	AGTTACATAT	GTATACATGT	GCCATGCTGG	TGTGCTGCAC	9060
	CCATTAAACTC	ATCATTTAGC	GTTAGGTATA	TCTCCTAATG	CTATCCCTCC	CCCCCTCCCC	9120
	CACCCACAAA	CAGTCCCTCAG	AGTGTGATGT	TACCTTCTCG	TGTCCAAGTG	TTCTCATTGT	9180
	TCRAATCCCA	TCTATGATTT	AAATCCATCT	ATGGCTTAGT	TAATGATTAA	TTTATTAGAG	9240
40	TTACATGCAT	TGGATATCAA	TTTGATGATA	TTATTATGCA	GCAATTTAAA	CTTGACTGGG	9300
	AGAAATATAT	ACCAATGTGA	GGAAAGTTTA	CAAATAGGCC	GAGTAGAAAA	GGGAATACAA	9360
	ATTTAGGAAT	TAGGAGAAAT	ACAATTTAAT	AATTGCAATG	TGTACTAAAT	AATGTATACA	9420
	GAAAAATATG	ATGAGCCTAT	TAAAAATTGA	CACATGTAGT	AGGCTGTTGG	CACAAGAAAT	9480
	AGTGATACAT	ACAGTTTCAT	GTGTACAAAA	TAATGTAATC	ATATTTTACA	TGTGTATCAT	9540
45	ACAGTTGTAT	ACATACATAT	GTACACATAT	ACATATACGT	AAAAACATGA	TTCTGTTTTT	9600
	ACATACATGT	ATATACATAT	ACACATATAA	CCCAATGTAT	TTATATATTTC	AGGACTCATA	9660
	TTTTACCTAT	TAGAAATAATA	ATGCTATTAT	AAGTGAACCT	TCTGTATTTC	ACATTTTATTG	9720
	CCAAAAAATC	GAATCTCCAC	ATAGTCAATT	CATTGTTAAG	GTGTATTAGA	GATCGACAGT	9780
	TAGTCATATC	AGTTTCTTTT	TTCCATTGTT	ATAGCTTGAA	GAGAAACTCA	CTGCTGAGAA	9840
50	ATTGATGGAA	TGAGCAAGTT	TGAGAATAT	GAGAGAGACA	TGTGTGATG	TACACTTACC	9900
	TCGGTTCAAA	ATGGAAGGAT	GCTATGACCT	CAAGGACACG	TTGAGAACCA	TGGGAATGGT	9960
	GAATATCTTC	AATGGGGATG	CAGACCTCTC	AGGCATGACC	TGGAGCCACG	GTCTCTCAGT	10020
	ATCTAAAGAT	CTACACAAGG	CCTTTGTGGA	GGTCACTGAG	GAGGGAGTGG	AAGCTGCAGC	10080
	TGCCACCGCT	GTAGTAGTAG	TCGAATTATC	ATCTCCTTCA	ACTAATGAAG	AGTTCTGTTG	10140
55	TAATCACCCT	TTCTTATTCT	TCATAAGGCA	AAATAAGACC	AACAGCATCC	TCTTCTATGG	10200
	CAGATTCTCA	TCCCCATAGA	TGCAATTAGT	CTGTCACTCC	ATTAGAAAA	TGTTCCACCTA	10260
	GAGGTGTTCT	GGTAAACTGA	TTGCTGGCAA	CAACAGATTTC	TCTTGGCTCA	TATTTCTTTT	10320
	CTATCTCATG	TTGATGATGA	TAGTCATCAT	CAAGAATTTA	ATGATTAAAA	TAGCATGCCT	10380
60	TTCTCTCTTT	CTCTTAATAA	GCCACATAT	AAATGTACTT	TTCTTCCAG	AAAAATTTCC	10440
	CTTGAGGAAA	AATGTCCAAG	ATAAGATGAA	TCATTTAATA	CCGTGTCTTC	TAAATTTGAA	10500
	ATATAATTCT	GTCTTCTGACC	TGTTTAAAAA	GAACCAAACC	AAATCATACT	TTCTCTTCAA	10560
	ATTTAGCAAC	CTAGAAACAC	ACATTTCTTT	GAATTTAGGT	GATACCTAAA	TCTTCTTTAT	10620
	GTCTCTAAAT	TTTGTGATTC	TATAAAACAC	ATCATCAATA	AAATAATGAC	ATAAAATCAT	10680
	TTTTGCTTTA	CCGTGTTTCT	CTCTGGAAG	GGCAAGTGTC	CAGTTACACA	TAGGAAAGAT	10740
65	AATTTAGAGA	TATATTAATC	ATATATAAAG	GAAAAATAAA	AACAGAGTAG	TTCATGATGA	10800
	GCCTGGAGTA	GAAAGGCATAT	CCCAGAACAG	GAGGAGCCTT	GTAAACCACA	TAGGAACTTC	10860
	CTATTTTATG	CTAAAGGGAT	AAGAAACTCA	TTACAGGCTT	TGATGGTTGT	TTGTCAAAGA	10920
	GGGGCATAAA	ATTATCATAT	CCACATCTAG	AAAATACATC	TCTGGCTACG	CTGATATCAA	10980
	TGGATGCGAG	GAAAGAACAG	TGTGGTTACC	ATATATAAAT	TAGGAAATCA	TTAGAGTATT	11040
70	GGGAGTGGAA	ATGGAGAGAA	AGAAAGAGCC	TGGGGGAATT	ATTTAGGAAA	TAATAGTTAC	11100
	AGAAAGACAT	CTAAGTTGCT	GACCTATCTG	ACTGGATGGA	TGGAAGAATA	TCTTGTTTCT	11160
	GAGAGAAAAA	AAGACTTTGG	GTTTAAATTT	GTACTTGATG	AATTAAGGTA	CTTTTAATAT	11220
	TCAAATGGAT	TTGCCCTGGCA	GGCACTTGAA	GATATTAGTC	TAAATCTCAG	AAACAGAATA	11280
	TGATCTGAAG	CTCTAAATTT	GTGATATTCA	ATATAAATAC	TTTAGAGTCA	TTGGGATAAA	11340
	TATGGTAGTT	GTAGCTAAAA	GCAAAAATAA	GATACTAGGG	AGAAAGGATA	AAGTTAGAAG	11400
75	AAAGAAGAAT	CTAGAATTGA	CCTTGAAGTA	TATCAGCATG	TGTAAAGATC	AGGAATTGAT	11460
	CATTTTATT	TTCCAGAAAG	TAGCTTTTCT	TAGGGTTCCA	TATTTACTCC	CATAGATTCT	11520
	TTTT						

Seq ID NO: 465 Protein sequence
Protein Accession #: BAB21525.1

	1	11	21	31	41	51	
85	MNSLSEANTK	FMFDLQFQFR	KSKENNIFYS	PISITSALGM	VLLGAKDNDA	QQISKVLHFD	60
	QVTENTTEKA	ATYHVRDSGN	VHQFQKLLT	EFNKSTDAYE	LKIANKLFGF	KTYQFLQEYL	120
	DAIKKFYQTS	VESTDFANAP	EESRKKINSW	VESQTNEKIK	NLFPPDGTIGN	DTTLVLVNAI	180
	YFKGQWENKF	KKENTKEEKF	WPNKNYTKSV	QMMRQYNSFN	FAILEDVQAK	VLEIPYKSKD	240

LSMIVLLPNE IDGLQKLEEK LTAEKLMEWT SLQNMRETCV DLHLPRFKME ESYDLKDTLR 300
 TMGMVNIENG DADLSGMTWS HGLSVSKVLH KAFVEVTEEG VEAAAATAVV VVELSSPSTN 360
 BEFCNHPFL FFIRQNKINS ILFYGRFSSP

5

Seq ID NO: 466 DNA sequence
 Nucleic Acid Accession #: NM_001910.1
 Coding sequence: 50..1240

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	CCTTCTTTTG	CTGCTGGTGC	TCCTGGAGCT	GGGAGAGGCC	CAAGGATCCC	TTCACAGGGT	120
	GCCCTCAGG	AGGCATCCGT	CCCTCAAGAA	GAAGCTGCGG	GCACGGAGCC	AGCTCTCTGA	180
15	GTTCTGGAAA	TCCCATATTT	TGGACATGAT	CCAGTTCACC	GAGTCTGTCT	CAATGGACCA	240
	GAGTGCCAAAG	GAACCCCTCA	TCAACTACTT	GGATATGGAA	TACTTCGGCA	CTATCTCCAT	300
	TGGCTCCCCA	CCACAGAACT	TCACTGTCTAT	CTTCGACACT	GGCTCCTCCA	ACCTCTGGGT	360
	CCCCTCTGTG	TACTGCACTA	GCCCAGCCTG	CAAGACGCAC	AGCAGGTTCC	AGCCTTCCCA	420
	GTCCAGCAC	TACAGCCAGC	CAGGTCAATC	TTTCTCCATT	CAGTATGGAA	CCGGGAGCTT	480
20	GTCCGGGATC	ATTGGAGCCG	ACCAAGTCTC	TGTGGAAGGA	CTAACCGTGG	TTGGCCAGCA	540
	GTTTGAGAAA	AGTGTACACG	AGCCAGGCCA	GACCTTTGTG	GATGCAGAGT	TTGATGGAAT	600
	TCTGGGCTTG	GGATACCCCT	CCTTGGCTGT	GGGAGGAGTG	ACTCCAGTAT	TTGACAAAT	660
	GATGGCTCAG	AACCTGGTGG	ACTTGCCGAT	GTTTTCTGTC	TACATGAGCA	GTAACCCAGA	720
	AGGTGGTGGG	GGGAGCGAGC	TGATTTTTTG	AGGCTACGAC	CACTCCCAT	TCTCTGGGAG	780
25	CTGGAATTGG	GTCCAGTTC	CCAAGCAAGC	TACTTGGCAG	ATTGCACTGG	ATAACATCCA	840
	GGTGGGAGGC	ACTGTATATG	TCTGCTCCGA	GGGCTGCCAG	GCCATTGTGG	ACACAGGGAC	900
	TTCCCTCATC	ACTGGCCCTT	CCGACAAGAT	TAAGCAGCTG	CAAAACGCCA	TTGGGGCAGC	960
	CCCCGTGGAT	GGAGAATATG	CTGTGGAGTG	TGCCAACCTT	AACGTCATGC	CGGATGTGAC	1020
	CTTCAACATT	AACGAGTCTC	CCTATACCTT	CAGCCCAACT	GCCTACACCC	TACTGGACTT	1080
	CGTGATGGA	ATGCCAGTTCT	GCAGCAGTGG	CTTTCAAGGA	CTTGACATCC	ACCCTCCAGC	1140
30	TGGGCCCCCT	TGGATCCTGG	GGGATGTCTT	CATTGACAG	TTTTACTCAG	TCTTTGACCG	1200
	TGGGAATAAC	CGTGTGGGAC	TGGCCCCAGC	AGTCCCCTAA	GGAGGGGCTT	TGTGTCTGTG	1260
	CCTGCCCTGT	TGACAGACCT	TGAATATGTT	AGGCTGGGGC	ATTCTTTTACA	CCTACAAAAA	1320
	GTTATTTTCC	AGAGAATGTA	GCTGTTTCCA	GGGTTGCAAC	TTGAATTAAG	ACCAAACAGA	1380
	ACATGAGAAT	ACACACACAC	ACACACATAT	ACACACACAC	ACACTTCACA	CATACACACC	1440
35	ACTCCCAACA	CGTCTATGAT	GGAGGAATTA	CGTTATACAT	TCATATTTTG	TATTGATTTT	1500
	TGATTATGAA	AATCAAAAAA	TTTCAATTTT	GATTATGAAA	ATCTCCAAC	ATATGCACAA	1560
	GCAGAGATCA	TGGTATAATA	AATCCCTTTG	CAACTCCACT	CAGCCCTGAC	AACCATCCA	1620
	CACACGGCCA	GGCCTGTTTA	TCTACACTGC	TGCCCCACTC	TCTCTCCAGC	TCCCATGCT	1680
	GTACCTGGAT	CATTCTGAAG	CAAAATCCGA	GCATTACATC	ATTTTGTCCA	TAAATATTTC	1740
40	TAACATCCCT	SLAVAGVTVP	TCGGAATTCA	AGCATCTCCC	ATTGTCCCAC	AAATGTTTGG	1800
	CTGTTTTTGT	AGTTGGATTG	TTTGTATTAG	GATTCAAGCA	AGGCCCATAT	ATTGCATTTA	1860
	TTTGAATGT	CTGTAAGTCT	CTTTCCATCT	ACAGAGTTTA	GCACATTTGA	ACGTTGCTGG	1920
	TTGAATCCC	GAGGTGTCTAT	TTGACATGGT	TCTCTGAAC	TATCTTTCTC	ATAAAATGGT	1980
	AGTTAGATCT	GGAGGTCTGA	TTTTGTGGCA	AAAAACTTTC	CTAGGTGGTG	CTGGGTACTT	2040
45	CTTGTGTCAT	CCTGTGAGGA	GGCAGATAAT	GCTGGTGCCT	CTCTATTGGT	AATGTTAAGA	2100
	CTGCTGGGTG	GGTTTGGAGT	TCTTGGCTTT	AATCATTCTAT	TACAAAGTTC	AGCATTTT	

Seq ID NO: 467 Protein sequence
 Protein Accession #: NP_001901.1

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55	SMDQSAKEPL	INYLDMEYFG	TISIGSPPQN	FTVIFDTGSS	NLWVPSVYCT	SPACKTHSRF	120
	QPSQSSYSYQ	PGQSFSIQYG	TGSLSGIIGA	DQVSVEGLTV	VGQQPGESVT	EPGQTFVDAE	180
	FDGILGLGVP	SLAVAGVTVP	FDNMMQAQNLV	DLPMFSVYMS	SNPEGAGSE	LIFGGYDHS	240
	FSGSLNWVVP	TQATYQIAL	DNIQVGGTVM	FCSEGCQAI	DTGTSITIGP	SDKIKQLQNA	300
	IGAAPVDGEY	AVECANLNV	PDVTFITINGV	PYTLSPATY	LLDFVDGMQF	CSSGFQGLDI	360
60	HPPAGFLWLL	GDVFRQFYS	VFDGRNNRVG	LAPAVF			

Seq ID NO: 468 DNA sequence
 Nucleic Acid Accession #: NM_018058.1
 Coding sequence: 319..1575

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	TACACCGACA	AGTTGTTCAA	GTTCCGCAAT	AACCGGTGGG	AAGACATCCT	GAGCGATGAG	180
70	GTCAACGTGG	CCCGTGGTGT	GGCCAGCCTC	TTTGCCGGAC	GCTCTGTGGC	CTGTGTGGAC	240
	AGAAAGGGCT	CTGGACGCTA	CTCTATCTAC	ATTGCCAATT	ACGCCCTACG	TAATGTGGGC	300
	CCTGATGCCC	TCAATTGAAAT	GGACCCGTAG	GCCAGTGACC	TCTCCCGGGG	CATTCTGGCG	360
	CTCAGAGATG	TGGCTGCTGA	GGCTGGGGTC	AGCAAATATA	CAGGGGGCCG	AGGCGTCAGC	420
	GTGGGCCCCA	TCCTCAGCAG	CAGTGCCTCG	GATATCTTCT	GGCACAATGA	GAATGGGCCT	480
75	AACTTCCTTT	TCCACAACCG	GGGCGATGGC	ACCTTTGTGG	ACGCTGCGGC	CAGTGTGGT	540
	GTGGACGACC	CCCACACGCA	TGGGCGAGGT	GTGCGCCTGG	CTGACTTCAA	CCGTGATGGC	600
	AAAGTGGACA	TCGTCTATGG	CAACTGGAAT	GGCCCCCACC	GCCTCTATCT	GCAAAATGAGC	660
	ACCCATGGGA	AGGTCGCTTT	CCGGGACATC	GCCTCACCCA	AGTTCTCCAT	GCCCTCCCT	720
	GTCCGCACGG	TCATCACCAG	CGACTTTGAC	AATGACCAGG	AGCTGGAGAT	CTTCTTCAAC	780
80	AACATGCTCT	ACCGCAGCTC	CTCAGCCAAC	CGCCTCTTCC	CGGTATCCG	TAGAGAGCAC	840
	GGAGACCCCC	TCATCGAGGA	GCTCAATCCC	GGCGACGCTT	TGGAGCCTGA	GGGCCGGGGC	900
	ACAGGGGGTG	TGGTGACCGA	CTTCGACGGA	GACGGGATGC	TGGACCTCAT	CTTGTCCCAT	960
	GGAGAGTCCA	TGGCTCAGCC	GCTGTCCGTC	TTCCGGGGCA	ATCAGGGCTT	CAACAACAAC	1020
	TGGCTGCGAG	TGGTGCCAGC	CACCCGGGTT	GGGGCCTTTG	CCAGGGGAGC	TAAGGTCTGT	1080
85	CTCTACACCA	AGAAAGATGG	GGCCACCTTG	AGGATCATCG	ACGGGGGCTC	AGGCTACCTG	1140
	TGTGAGATGG	AGCCCGTGGC	ACACTTTGGC	CTGGGGAAAG	ATGAAGCCAG	CAGTGTGGAG	1200
	GTGACGTGGC	CAGATGGCAA	GATGGTGAGC	CGGAACGTGG	CCAGCGGGGA	GATGAACTCA	1260

GTGCTGGAGA TCCTCTACCC CCGGGATGAG GACACACTTC AGGACCCAGC CCCACTGGAG 1320
 ACACCAATGA ATGCATCCAG TTCCCATTCG TGTGCCCTCG AGACAAGCCC GTATGTGTCA 1380
 AACCTATGG AAGCTTACAG TGCCGGACCA ACAAGAAGTG CAGTCGGGGC TACGAGCCCA 1440
 ACGAGGATGG CACAGCCTCG GTGGGGGACTC TCGGCCAGTC ACCGGGCCCC CGCCCCACCA 1500
 CCCCACCCGC TGCTGCTGCC ACTGCCGCTG CTGCTGCCGC TGCTGGAGCT GCCACTGCTG 1560
 CACCGGTCTCT CGTAGATGGA GATCTCAATC TGGGGTCGGT GGTAAAGGAG AGCTGCGAGC 1620
 CCAGCTGCTG AGCAGGGGGT GGACATGAAC CAGCGGATGG AGTCCAGCAG GGGAGTGGGA 1680
 AAGTGGGCTT GTGCTGCTGC CTAGACAGTA GGGATGTAAA GGCTTGGGAG CTAGACCCCTC 1740
 CCAAGGCCCA TCCATGCACA TTACTTAGCT AACAAATTAG GAGACTCGTA AGGCCAGGCC 1800
 CTGTGCTGGG CACATAGCTG TGATCACAGC AGACAGGGTC GCTGCCCTGA TGGCGCTTAC 1860
 ATTCCAGTGG GTCTAATGAC CATATCTTAG GACACAGATG TGCCGAGGGA GGTGGTGTCA 1920
 CTGCACAGGA AGTATGAGGA CTTTAGTGTC CTGAGTTCAA ATCCTGATTG AGGAACCTCAC 1980
 AAAGCTATGT GACCTTACAC CAGTCACTTA ACTTGTTAGC CATCCATTAT CGCATCTGCA 2040
 AAATGGGGAT TAAGAATAGA ATCTTGGGGT TAGTGTGGAG ATTAGATTAA ATGTATGTAA 2100
 GCACATTGGC ACAAACCTG GCACATAGTA AAGGCTCAAT AAAAAACAAG GCCTCTCACT 2160
 GGGCTTTGTC AACACGTG

Seq ID NO: 469 Protein sequence
 Protein Accession #: NP_060528.1

1 11 21 31 41 51
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 MDPEASDLR GILALRDVAA EAGVSKYTGG RGVSVGPILS SSASDIFCDN ENGNPFLFHN 60
 RGDGTFVDA ASAGVDDPHQ HGRGVALADF NRDGKVDIVY GNWNGPHRLY LQMSTHGKVR 120
 FRDIASPKFS MPSPVRTVIT ADFDNDQELE IFNNIAYRS SSANRLFRVI RREHGDPLIE 180
 ELNPGDALEF EGRGTGGVVT DFDGDGMLDL ILSHGESMAQ PLSVFRGNQG FNNNWLRVVP 240
 RTRVGAFARG AKVLYTKKS GAHLRIIDGG SGYLCMEFV AHFGLGKDEA SSVEVTPWDG 300
 KMSVRNVASG EMNSVLEILY PRDEDTLQDP APLETMPNAS SSHSCALET SYPVSTPMEAT 360
 GAGPTRSAVG ATPSPRMAQP AWGLSASHRA PAPPPPPPLL PLPLLLPLLE LPLLLHRSS

Seq ID NO: 470 DNA sequence
 Nucleic Acid Accession #: AJ279016
 Coding sequence: 1..1962

1 11 21 31 41 51
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 TTTGAGATCG TCGTGGCGGG GTACAAATGGA CCAACCTGG TTCTGAAGTA TGACCGGGCC 240
 CAGAAGCGGC TGGTGAACAT CGCGGTCGAT GAGCGCAGCT CACCTACTA CGCGCTGCGG 300
 GACCGGCAGG GGAACGCCAT CGGGTTCACA GCTGCGACA TCGACGGGA CGGCGGGAG 360
 GAGATCTACT TCCCAACAC CAATAATGCC TTCTCGGGGG TGCCACGTA CACCGACAAG 420
 TTGTTCAAGT TCCGCAATAA CCGGTGGGAA GACATCCTGA GCGATGAGGT CAACGTGGCC 480
 CGTGGTGTGG CAGCGCTCTT TGCCGAGCGC TCTGTGGCCT GTGTGGACAG AAAGGGCTCT 540
 GGACGCTACT CTATCTACAT TGCCAATTAC GCCTACGGTA ATGTGGGCCC TGATGCCCTC 600
 ATTGAAATGG ACCCTGAGCG CAGTGACCTC TCCCGGGGCA TTCTGGCGCT CAGAGATGTG 660
 CTGCTGTAGG TCGGGGTGAG CAAATATACA GGGGGCCGAG GCGTCAGCGT GGGGCCCATC 720
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 CACCAAGCAT GCGAGGTGTG GCCTTGGCT GACTTCAACC GTGATGGCAA AGTGGACATC 900
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 ATCACCGCCG ACTTTGACAA TGACCAGGAG CTGGAGATCT TCTTCAACAA CATTGCCTAC 1080
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 AACAGAAGT GCAGTCGGGG CTACGAGCCC AACGAGGATG GCACAGCCTG CGTGGGGACT 1800
 CTCGGCCAGT CACCGGGCCC CCGCCCCACC ACCCCACCGC CTGCTGCTGC CACTGCCGCT 1860
 GCTGTGCGG CTGCTGGAGC TGCCACTGCT GCACCGGTCC TCGTAGATGG AGATCTCAAT 1920
 CTGGGGTCGG TGGTTAAGGA GAGCTGCGAG CCCAGCTGCT GAGCAGGGGT GGGACATGAA 1980
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 CAGACAGGGT CGCTGCCCTG ATGGCGCTTA CATTCAGTGG GGTCTAATGA CCATATCTTA 2220
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 AACTTGTTAG CCATCCATT TCGCATCTGC AAAATGGGGA TTAAGAAATG AATCTTGGGG 2400
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Seq ID NO: 471 Protein sequence
 Protein Accession #: CAC08451

1 11 21 31 41 51
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 FEIVVAGYNG PNLVLKYDRA QKRLVNIADV ERSSPYALR DRQGNAGIVT ACDIDGDGRE 120
 EIFYFLNTNNA FSGVATYTDK LFKFRNNRWE DILSDEVNVA RGVASLFAGR SVACVDRKGS 180

GRYSIIYANY AYGNVGPDAL IEMDPEASDL SRGILALRDV AAEAGVSKYT GGRGVSVGPI 240
 LSSASDIFC DNENGNPNFLF HNRGDGTFVD AAASAGVDDP HQHGRGVALA DFNRDGKVDI 300
 VYGNWNGPHR LYLQMSHGHK VRFRDIASPK FSPSPVVRTV ITADFDNDQE LEIFFNNIAY 360
 RSSSANRLFR VIRREHGDPL IEELNPGDAL EPEGRGTGGV VTDFFDGDML DLILSHGESM 420
 AQPLSVFRGN QGFNNWNLRV VPRTRFGAFA RGAKVVLVTK KSGAHLRIID GSGSYLCEME 480
 PVAHFGLGKD EASSVEVTWP DGKMSVRNVA SGEMNSVLEI LYPRDEDTLQ DPAPLECGQG 540
 FSQQENGHGM DTNECQFPF VCPDRDKPVCV NTYGSYRCRT NKKCSRGYEP NEDGTACVGT 600
 LQSPGPRPT TPTAAATAA AAAAAGAATA APVLVDGDLN LGSVVKESCE PSC

Seq ID NO: 472 DNA sequence
 Nucleic Acid Accession #: FGENESHH
 Coding sequence: 1..4794

15 1 11 21 31 41 51
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 GTTCTGAAGT ATGACCGGG CCAGAAGCGG CTGGTGAACA TCGCGTCTGA TGAGCGCAGC 180
 TCACCTACT ACGCCGTGGC GGACCGGCAG GGAACGCCA TCGGGGTGAC AGCCTGCGAC 240
 20 ATCGACGGGS AGGCCGGGA GGAGATCTAC TTCTCAACA CCAATAATGC CTCTCGGGC 300
 CACAGCAGCT CAGCGCAGGT CCCTCTGGG CTCCACAGAA ACAGGCCTGT GCTGAGCCT 360
 CCACCTACAA CCCCTGCAGG CCTCCTGGGT CTGCCTCCAC TCAGCGGAAG GGACTTTTCC 420
 TCCTCCTGG GTACAGCTTC TCCGACAGC AGGCAGGGAG AGAGGGTGCC GGTCCCTGTC 480
 25 TGTCCGGGTG GACTGAGACC TACCATGAA CCAGAACCAT TTCTTCTGAG ACCCAAATCA 540
 GGGGTGGCCA CGTACACCGA CAGTTGTTT AAGTTCCGCA ATAACCGGTG GGAAGACATC 600
 CTGAGCGATG AGGTCAACGT GGCCTGGTGT GTGGCCAGCC TCTTTGCCGG ACGCTCTGTG 660
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 GGTAATGTGG GCCCTGATGC CCTCATGAA ATGGACCTG AGGCCAGTGA CCTCTCCCGG 780
 30 GGCATTCTGG CGCTCAGAGA TGTGGCTGCT GAGGCTGGGG TCAGCAAATA TACAGAAGGC 840
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 GGAGGAGACC CAGAGGAGGC AGATGAGGAG CACAGTGGGG ATGGAAGCAC CAGCCAACTG 960
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 CAGAGGGAGG CTGGGGCAGC TGGCGTGCCC AGAGGACGTG TTCGAACAGC TCTGCAGACT 1080
 TCCAAAGGCC ATTTGGCTGA CAAGAACCTA TTTGGCCAC CATGTTACTA TTCTGTCTGC 1140
 35 GCGCCTTCTC CAGCCACCCC TTTCCCTGCC CGCCAAGCCC CCCAACACTA CCTGTAGCC 1200
 CCCCTTGTCA CTCAGTAAAT GACACATGGA CGTCTGGCTG GAAAACCTAGC CCGGAGTGTC 1260
 CCCACCCCC GAGCCCCAGG AATGGACCCC AAATGTAAGG GCGCCATGCT TGAGCCCGGC 1320
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 40 CTGAGAAGCT GGGAGGAAAG CAGGCAGAGG GGGCAGGCCA TGTCAGATG TGCACTCAGG 1440
 GAGCTGGGAG GTCCCTGGA GCAAGCCACA CAGCACCTGC TGCTAGAGA GCTGTATGAC 1500
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 45 CTCTCCCATC CCTGTGCTCC CAACTTCCCC AGCTGCTTGA GGCTCTTGA AGCCGGGACA 1740
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 50 CTGCGCACTC ACTGTGGGTC GATGTCTTTT CTAGGGGGCC GAGGCGTCAG CGTGGGCCCC 2040
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 TTCCACAACC GGGCGCATGG CACCTTTGTG GACGCTGCGG CAGTGTCTGA ACGTCTGTTA 2160
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 55 CCACATTGCC ATCATGTTT GTCTATGAGC TTTACAAGGA CCGGGTCAGC GTTCTATTCA 2340
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 TCACCAAGT TCTCCATGCC CTCCCCTGTC CGCACGGTCA TCACCGCCGA CTTTGACAAT 2760
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 65 GGTCAAGGAG AAGGTTTAA AATCAGAAGG GGAGGGTTCC CAGGGCCAGG GGTGACGGCC 2940
 AAGGTCAACA CAGGTCCCCT GATGAAGAAA CAGAAAGGAA GGAAGGACGA GGAAGGGGCA 3000
 AGAGGCTGTG GGAATGCAGG GCAAAGCCTG GCCAAGGAGC CGGCTCTGCT TATTGACGG 3060
 AAAGGGAAGG GAAATGTGGC CCAAAGTGTG CCCAGAACCC AAGCGCCACA AGATACAAAG 3120
 CCACACTACC AAAAAAGGG GCTACAGGGT CCAATCACTA CCAGGAAAAG GGGCTACGGG 3180
 70 GTCCAATCAC TACCAGGAAA AGGGGCTACG GGTCCAATC ACTACCAGGA AAAGGGGCTA 3240
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 75 CCAGGAAAAG GGGCTACAGG GTCCAATCAC TACCAGGAAA AGGGGCTACG GGTCCAATC 3540
 ACTACCAGGA AAAGGGGCTA CCGGCTCCAA TCACTACCAG GAAAAGGGGC TACGGGGTCC 3600
 AATCACTACC AGGAAAAGGG GCTACAGGGT CCAATCACTA CCAGGAAAAG GGGCTACAGG 3660
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 GCTATGGGGT CCAATCACTA CCAGGAAAAG GGGCTACGGG CTCCAATCAC TACCAGGAAA 3840
 80 AGGGGCTATG GGTCCAATC ACTACCAGGA AAAGGGGCTA CAGGGTCCAA CTCTATCCGT 3900
 AGAGAGCAGC GAGACCCCTC CATCGAGGAG CTCAATCCCG GCGACGCTT GGAGCCTGAG 3960
 GGCGGGGCA CAGGGGGTGT GGTGACCGAC TTCGACGGAG ACGGGATGCT GGAACCTATC 4020
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 85 AACCACAACT GGTCTCGAGT GGTGCCACGC ACCCGGTTTG GGGCCTTTGC CAGGGGAGCT 4140
 AAGGTCTGTC TCTACACCAA GAAGAGTGGG GCCCACTGGA GGATCATCGA CGGGGGCTCA 4200
 GGCTACCTGT GTGAGATGGA GCCCGTGCCA CACTTTGGCC TGGGGAAGGA TGAAGCCAGC 4260
 AGTGTGGAGG TGACGTGGCC AGATGGCAAG ATGGTGAAGC GGAACGTGGC CAGCGGGGAG 4320

ATGAACCTCAG TGCTGGAGAT CCTCTACCCC CGGGATGAGG ACACACTTCA GGACCCAGCC 4380
 CCACTGGAGT GTGGCCAAGG ATTCTCCCAG CAGGAAAATG GCCATTGCAT GGACACCAAT 4440
 GAATGCATCC AGTTCCCATC CGTGTGCCCT CGAGACAAGC CCGTATGTGT CAACACCTAT 4500
 GGAAGCTACA GGTGCCGGAC CAACAAGAAG TGCAGTCCGG GCTACGAGCC CAACGAGGAT 4560
 GGCACAGCCT CGCTGGGTAC TGAGCTAGGC TCTAGGCATA CAATGACGTG GAAACCAAGG 4620
 CCCAAAAAGG AGCTGCAACT TTCCCAAGGC ATCTGCACCC CCGTCTGTGC CTTTTTCTCT 4680
 CCGGTTTGCC GGCTGCTCCT CAAAAGAGCT CAGCTCCAGG CTGCTCCCAG CACCCTTCTC 4740
 CAGAAAGCTC CAGGTATTCC AGAAGCCCAA GTGTATGAAC AAGATCAGGA ATAA

Seq ID NO: 473 Protein sequence
 Protein Accession #: FGENESH predicted

1 11 21 31 41 51
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 SPYYALRDRQ GNAIGVTACD IDGDGREEIY FLNTNNAFSG HSSSAQVPSG LHRNRPVLKP 120
 PPTTLAGLLG LPPLSGRDFS SSLGQASPDG RQGERVPVPC CRGGLRPTHE PEPFLLRPKS 180
 GVATYTDKLF FRNNRWEDL LSDEVNVARG VASLFAGRSV ACVDRKGSGR YSIYIANYAY 240
 GNVGPDALIE MDPEASDLRS GILALRDVAA EAGVSKYTEG FSHTASPSIG EISGRTEERE 300
 GGDPEADEEE HSGDGSTSQL CRLGWKDGQF KEEAALVEE QREAGAAGVP RGRVRTALQT 360
 SKSHLADKNL FGPPCYVSGP APSAPHPFPA RQAPQHYPPA PLVTQLMTHG RLAKGLARSV 420
 PHPRAPGMDP KCKGRHAEFG LMAEALGAWP ALSTTVVPGG LRSWEESRQK GQAMSRCALR 480
 ELGGPWSQAT QHLPAARELYD LGEPPILQRT DGDPRRRRDS PKVTQECHLV ATPALGGLE 540
 GPRVAKREI GRETAGVGRF LSHPLVPNFP SCLRPLEAGT VPGAALPGNP GNWVLDMAKA 600
 LAWNQMEKEE GKIHDHEPR FRLRKAREAE FPPGSSEEP LQFPSSGLRGS PVLQVGLGLA 660
 SATHCSSMSF LGGRGVSVGP ILSSASDIF CNENGNPNFL FHNRGDGTFFV DAAASAERRL 720
 AFIVHLKYHL CRDFPHSLCH LAETGPSSSC CPWHARLLQA PHCHGLSMS FTRTGSRFYS 780
 FLTQGLASSA HRRTSLSQGS QGAPPCLLAR APCVLGSLIP TAYYIVLWSA IPESLMTHSY 840
 LSSERVNVGV DDPHQHGRGV ALADFNDRDGK VDIVYGNWNG PHRLYLQMS T HGKVRFRDIA 900
 SPKFSMPSPV RTVITADFDN DQELEIFFNN IAYRSSANR LFRCSILARG SSSLTAGGRN 960
 GQGEGLRIRR GFFPGGQQA KVTGTPMKK QKGRKDEDWA RGCGNAGQSL AKEPASAIAG 1020
 KGKGNVAQSV PRTQAPQDTK PHYHKKGLQG PITTRKRGY VQSLPGKGAT GSNHYQEKGL 1080
 RGPITTRKRG YGVQSLPGKG ATGSNHYQEK GLQGPITTRK RGYGLQSLPG KGATGSNHYH 1140
 RKGLRAPITT RKRGVGVQSL PGKGATGSNH YQEKGLRGPI TTRKRGYGLQ SLPGKGATGS 1200
 NHYQEKGLQG PITTRKRGYR VQSLPGKGAT GSNHYQEKGL RGPITTRKRG YGLQSLPGKE 1260
 AMGSNHYQEK GLRAPITTRK RGYGVQSLPG KGATGSNVIR REHGDPLIEE LNPGDALPEE 1320
 GRGTGGVVTD FDGDMGLDLI LSHGESMAQP LSVFRGNQGF NNNWLRVVR TRFGAFARGA 1380
 KVVLYTKKSG AHLRIIDGGS GYLCMEPVA HFGLGKDEAS SVEVTWPDGK MVSRRNVASGE 1440
 MNSVLBILYP RDEDTLQDPA PLECGQGSFQ QENGHCMDTN ECIQFFVCP RDKPVCVNTY 1500
 GSYRCRTNKK CSRGYEPNED GTACVGTTELG SRHTMTWKPR PKKELQLSQG ICTPVWSFFL 1560
 PGCRLLLKRA QQAAPSTLL QKAPGIPEAQ VYEQDQE

Seq ID NO: 474 DNA sequence
 Nucleic Acid Accession #: NM_003661.1
 Coding sequence: 1..1152

1 11 21 31 41 51
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 ACACAAGCCC AAGCCCACGA CCTGGTCATC AAAAGCCTTG ACAAATTGAA GGAGGTGAGG 720
 GAGTTTGTGG GTGAGAACAT ATCCAACTTT CTTTCTTAG CTGGCAATAC TTACCAACTC 780
 ACACGAGGCA TTGGGAAGGA CATCCGTGCC CTCAGACGAG CCAGAGCCAA TCTTCAGTCA 840
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 CAAGAACTGT GA

Seq ID NO: 475 Protein sequence
 Protein Accession #: NP_003652.1

1 11 21 31 41 51
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 MSALFLGVGV RAEAGARVQ QNVPSGTDGT DPOSKPLGDW AAGTMDPESS IFIEDAIKYF 60
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 YRNWFLKEFP RLKSELEDNI RRLRALADGV QVHKGTITIA NVVSGSLSS SGILTLVGMG 180
 LAFTEGGGL VLEPGMEIG ITAALTGITS STMDYGKKWW TQAQAHDLVI KSLDKLKEVR 240
 EFLGENISNF LSLAGNTYQL TRGIGDIRA LRRARANLQS VPHASASRPR VTEPISAESG 300
 EQVERVNEPS ILEMSRGVKL TDVAPVSFFL VLDVVVLVYE SKHLHEGAKS ETAELKKVA 360
 QELEEKLNL NNNYKILQAD QEL

Seq ID NO: 476 DNA sequence
 Nucleic Acid Accession #: NM_014452.1
 Coding sequence: 1..1968

1 11 21 31 41 51

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5	GCTCAGCCAG	AACAGAAGGC	CTCGAATCTC	ATTGGCACAT	ACCGCCATGT	TGACCGTGCC	180
	ACCGGCCAGG	TGCTAACCTG	TGACAAGTGT	CCAGCAGGAA	CCTATGTCTC	TGAGCATTGT	240
	ACCAACACAA	GGCTGCGCGT	CTGCAGCAGT	TGCCCTGTGG	GGACCTTTAC	CAGGCATGAG	300
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	TTACCTTTGT	CTGCCCTTGC	TGACCGAGAA	TGCACTTGCC	CACCTGGCAT	GTTCCAGTCT	420
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10	ACAGAGACTG	AGGATGTGCG	GTGTAAGCAG	TGTGCTCGGG	GTACCTTCTC	AGATGTGCCT	540
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	ACCTCACCTT	CCCCTGCCAC	AGCCATCTTT	CCACGCCCTG	AGCACATGGA	AACCCATGAA	720
	GTCCCTTCCT	CCACTTATGT	TCCCAAAGGC	ATGAACCTCA	CAGAAATCCA	CTCTTCTGCC	780
15	TCTGTTAGAC	CAAAGTACT	GAGTAGCATC	CAGGAAGGGA	CAGTCCCTGA	CAACACAAGC	840
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	CAGCAAGGCC	CCCACACAG	ACACATCCTG	AAGCTGCTGC	CGTCCATGGA	GGCCACTGGG	960
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	CACAAGCATT	TTGACATCAA	TGAGCATTTG	CCCTGGATGA	TTGTGCTTTT	CCTGTGCTGT	1080
20	GTGCTTGTGG	TGATTGTGGT	GTGCAGTATC	CGGAAAAGCT	CGAGGACTCT	GAAAAAGGGG	1140
	CCCCGGCAGG	ATCCACGTGC	CATTGTGGAA	AAGGCAGGGC	TGAAGAAATC	CATGACTCCA	1200
	ACCCAGAACC	GGGAGAAATG	GATCTACTAC	TGCAATGGCC	ATGGTATCGA	TATCCTGAAG	1260
	CTTGTAGCAG	CCCAAGTGGG	AAGCCAGTGG	AAAGATATCT	ATCAGTTTCT	TTGCAATGCC	1320
25	AGTGAGAGGG	AGGTTGCTGC	TTTCTCCAAT	GGGTACACAG	CCGACCACGA	GCGGGCCTAC	1380
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	GCCTTCGCGC	AGCACCGGAG	AAACGATGTT	GTGGAGAAAG	TTCGTGGGCT	GATGGAAGAC	1500
	ACCACCCAGC	TGAAACTGA	CAAACTAGCT	CTCCCGATGA	GCCCCAGCCC	GCTTAGCCCG	1560
	AGCCCCATCC	CCAGCCCCAA	CGCGAAACTT	GAGAATTCGG	CTCTCCTGAC	GGTGGAGCCT	1620
30	TCCCCACAGG	ACAAGAACAA	GGGCTTCTTC	GTGGATGAGT	CGGAGCCCTT	TCTCCCTGT	1680
	GACTCTACAT	CCAGCGGCTC	CTCCGCGCTG	AGCAGGAACG	GTTCCTTTAT	TACCAAGAA	1740
	AAGAAGGACA	CAGTGTTCGG	GCAGGTACGC	CTGGACCCCT	GTGACTTGCA	GCCTATCTTT	1800
	GATGACATGC	TCCACTTTCT	AAATCCTGAG	GAGCTGCGGG	TGATTGAAGA	GATTCCCCAG	1860
	GCTGAGGACA	AACTAGACCG	GCTATTTCGA	ATTATTGGAG	TCAAGAGCCA	GGAAGCCAGC	1920
35	CAGACCCCTC	TGACTCTGT	TTATAGCCAT	CTTCTGACC	TGCTGTAG		

Seq ID NO: 477 Protein sequence

Protein Accession #: NP_055267.1

	1	11	21	31	41	51	
40	MGTSPPSSSTA	LASCSRIARR	ATATMIAGSL	LLLGFLSTTT	AQPEQKASNL	IGTYRHVDRA	60
	TGQVLTCDDK	PAGTVYSEHC	TNTSLRVCSS	CPVGTFTRHE	NGIEKCHDCS	QPCPWPMEIK	120
	LPCAALTDRE	CTCPPGMFQS	NATCAPHTVC	PVGWGVRRKK	TETEDVRCKQ	CARGTFSQVP	180
	SSVMKCKAYT	DCLSNQLVVI	KPGTKETDNV	CGTLPSFSSS	TSPSPGTAIF	PRPEHMETHE	240
45	VPSSTYVPKG	MNSTESNSSA	SVRPKVLSSI	QEGTVPDNTS	SARGKEDVNK	TLPNLQVNVH	300
	QQGPHRRHIL	KLLPSMEATG	GEKSSTPIKG	PKRGHPRQNL	HKHFDINEHL	PWMIVLFLLL	360
	VLVVIVVCSI	RKSSRTLKKG	PRQDPSAIVE	KAGLKKSMTP	TQNRKWIYY	CNGHGIDILK	420
	LVAAGVGSQW	KDIYQFLCNA	SEREVAAFSN	GYTADHERAY	AALQHWITRG	PEASLAQLIS	480
	ALRQHRNDV	VKIRGLMED	TTQLETDKLA	LPMSPSPLSP	SPIPSNAKL	ENSALLTVEP	540
50	SPQDKNKFF	VDESEPLLR	DSTSSGSSAL	SRNGSFITKE	KKDTVLQRVR	LDPCLQPIF	600
	DDMLHFLNPE	ELRVIEIPQ	AEDKLDRLFE	IIGVKQSEAS	QTLDSVYSH	LPDLL	

Seq ID NO: 478 DNA sequence

Nucleic Acid Accession #: XM_044533

Coding sequence: 238..2751

	1	11	21	31	41	51	
60	GCTCTGCCCA	AGCCGAGGCT	GCGGGGCGGG	CGCCGGCGGG	AGGACTGCGG	TGCCCGCGCG	60
	AGGGGCTGAG	TTTGCCAGGG	CCCACCTTGC	CCTGTTTCCC	ACCTCCCGCC	CCCCAGGTCC	120
	GGAGGCGGGG	GCCCCCGGGG	CGACTCGGGG	GCGGACCGCG	GGGCGGAGCT	GCCCGCCGTC	180
	AGTCCGGCGG	AGCCACCTGA	CGCCGAGCCG	CGGGACACCG	TGCTCCTGCT	TCTCCGAATG	240
	CTGCGCACCG	CGATGGGCGT	GAGGAGCTGG	CTCGCCGCCC	CATGGGGCGC	GCTGCCGCGT	300
	CGGCCACCGC	TGCTGCTGCT	CCTGTGCTGT	CTGCTCCTGC	TGCAGCCGCC	GCCTCCGACC	360
65	TGGGCGCTCA	GCCCCCGGAT	CAGCCTGCCT	CTGGGCTCTG	AAGAGCGGGC	ATTCCTCAGA	420
	TTCGAAGCTG	AACACATCTC	CAACTACACA	GCCCTTCTGC	TGAGCAGGGA	TGGCAGGACC	480
	CTGTACGTGG	GTGCTCGAGA	GGCCCTCTTT	GCACTCAGTA	GCAACCTCAG	CTTCTGTCCA	540
	GGCGGGGAGT	ACCAGGAGCT	GCTTTGGGGT	GCAGACGCAG	AGAAGAAACA	GCAGTGCAGC	600
70	TTCAAGGGCA	AGGACCCACA	GCGCGACTGT	CAAAACTACA	TCAAGATCCT	CCTGCCGCTC	660
	AGCGGCAGTC	ACCTGTTTAC	CTGTGGCACA	GCAGCCTTCA	GCCCCATGTG	TACCTACATC	720
	AACATGGAGA	ACTTCACCTT	GGCAAGGGAC	GAGAAGGGGA	ATGTCCTCCT	GGAAGATGGC	780
	AAGGGCCGTT	GTCCCTTCGA	CCCGAATTTT	AAGTCCACTG	CCCTGGTGGT	TGATGGCGAG	840
	CTCTACACTG	GAACAGTCAG	CAGCTTCCAA	GGGAATGACC	CGGCCATCTC	GCGGAGCCAA	900
75	AGCCTTCGCC	CCACCAAGAC	CGAGAGCTCC	CTCAACTGGC	TGCAAGACCC	AGCTTTTGTG	960
	GCCTCAGCCT	ACATTCTCTA	GAGCCTGGGC	AGCTTGCAAG	GCGATGATGA	CAAGATCTAC	1020
	TTTTTCTTCA	GCGAGACTGG	CCAGGAATTT	GAGTTCCTTG	AGAACACCAT	TGTGTCCCGC	1080
	ATTGCCCGCA	TCTGCAAGGT	CGATGAGGGT	GGAGAGCGGG	TGCTACAGCA	GCGCTGGACC	1140
	TCCTTCTCTA	AGGCCAGCTG	GCTGTGCTCA	CGGCCGACG	ATGGCTTCCC	CTTCAACGTG	1200
	CTGCAAGATG	TCTTACAGCT	GAGCCCCAGC	CCCCAGGACT	GGCGTGACAC	CCTTTTCTAT	1260
80	GGGGTCTTCA	CTTCCCAGTG	GCACAGGGGA	ACTACAGAAG	GCTCTGCCGT	CTGTGTCTTC	1320
	ACAATGAAGG	ATGTGCAGAG	AGTCTTCAGC	GGCCTCTACA	AGGAGGTGAA	CCGTGAGACA	1380
	CAGCAGTGGT	ACACCGTGAC	CCACCCGGTG	CCACACCCCC	GCCCTGGAGC	GTGCATCACC	1440
	AACAGTGCCC	GGGAAGAGAA	GATCAACTCA	TCCCTGCAGC	TCCCAGACCG	CGTGTGAAC	1500
	TTCTCTAAGG	ACCACTTCTT	GATGGACGGG	CAGGTCCGAA	GCCGCATGCT	GCTGCTGCAG	1560
85	CCCCAGGCTC	GCTACCAAGC	CGTGGCTGTA	CACCCGCTGC	CTGGCCTGCA	CCACACCTAC	1620
	GATGTCTCTT	TCTTGGGCAC	TGGTGACGGC	CGGCTCCACA	AGGCAGTGAG	CGTGGGCCCC	1680
	CGGGTGACCA	TCATTGAGGA	GCTGCAGATC	TTCTCATCGG	GACAGCCCGT	GCAGAATCTG	1740

CTCCTGGACA CCCACAGGGG GCTGCTGTAT GCGGCCTCAC ACTCGGGCGT AGTCCAGGTG 1800
 CCCATGGCCA ACTGCAGCCT GTACAGGAGC TGTGGGGACT GCCTCCTCGC CCGGACCCCC 1860
 TACTGTGCTT GGAGGGGCTC CAGCTGCAAG CACGTGAGCC TCTACCAGCC TCAGCTGGCC 1920
 ACCAGGCCGT GGATCCAGGA CATCGAGGGA GCCAGCGCCA AGGACCTTTG CAGCGCGTCT 1980
 5 TCGGTTGTGT CCCCGTCTTT TGTACCAACA GGGGAGAAGC CATGTGAGCA AGTCCAGTTC 2040
 CAGCCCAACA CAGTGAAACAC TTTGGCCTGC CCGCTCCTCT CCAACCTGGC GACCCGACTC 2100
 TGGCTACGCA ACGGGGCCCC CGTCAATGCC TCGGCCTCCT GCCACGTGCT ACCCACTGGG 2160
 GACCTGCTGC TGGTGGGCAC CCAACAGCTG GGGGAGTTCC AGTGCTGGTC ACTAGAGGAG 2220
 10 GGCTTCCAGC AGCTGGTAGC CAGCTACTGC CCAGAGGTGG TGGAGGACGG GGTGGCAGAC 2280
 CAAACAGATG AGGGTGGCAG TGTACCCGTC ATTATCAGCA CATCGCGTGT GAGTGCACCA 2340
 GCTGGTGGCA AGGCCAGCTG GGGTGCAGAC AGGTCTTACT GGAAGGAGTT CCTGGTGATG 2400
 TGCACGCTCT TTGTGCTGGC CGTGTGCTC CCAGTTTAT TCTTGCTCTA CCGGCACCGG 2460
 AACAGCATGA AAGTCTTCTT GAAGCAGGGG GAATGTGCCA GCGTGCACCC CAAGACCTGC 2520
 15 CCTGTGGTGC TGCCCCCTGA GACCCGCCCA CTCAACGGCC TAGGGCCCCC TAGCACCCCG 2580
 CTCGATCACC GAGGGTACCA GTCCCTGTCA GACAGCCCCC CCGGGTCCCC AGTCTTCACT 2640
 GAGTCAGAGA AGAGGCCACT CAGCATCCAA GACAGCTTCG TGGAGGTATC CCCAGTGTGC 2700
 CCCCCGCCCC GGGTCCGCCT TGGCTCGGAG ATCCGTGACT CTGTGGTGTG AGAGCTGACT 2760
 TCCAGAGGAC GCTGCCCTGG CTTCAGGGGC TGTGAATGCT CGGAGAGGGT CAACTGGACC 2820
 TCCCTCCGCG TCTGCTCTTC GTGGAACACG ACCGTGGTGC CCGGCCCTTG GGAGCCTTGG 2880
 20 GGCCAGCTGG CCTGTGCTC TCCAGTCAAG TAGCGAAGCT CCTACCACCC AGACACCCAA 2940
 ACAGCCGTGG CCCACAGAGT CCGGCCAAA TATGGGGGCC TGCTAGGTT GGTGGAACAG 3000
 TGCTCCTTAT GTAAACTGAG CCCTTTGTTT AAAAAACAAT TCCAARTGTG AACTAGAAAT 3060
 GAGAGGGAAG AGATAGCATG GCATGCAGCA CACACGGCTG CTCCAGTTCA TGGCCTCCCA 3120
 GGGGTGCTGG AGATAGCATC AAAGTGGTTG TCTGAGACAG AGTTGGAAC CACTACCAAC 3180
 25 TGGCCTCTTC ACCTTCCACA TTATCCCGCT GCCACCGGCT GCCCTGTCTC ACTGCAGATT 3240
 CAGGACCCAGC TTGGGCTCGG TGCGTCTGCG CTGCGCAGTC AGCCGAGGAT GTAGTTGTTG 3300
 CTGCGTCTCGT CCCACCACT CAGGGACCG AGGGCTAGGT TGGCACTGCG GCCCTCACCA 3360
 GGTCTTGGGC TCGGACCCAA CTCTCGGACC TTTCAGCCT GTATCAGGCT GTGGCCACAC 3420
 30 GAGAGGACAG CGCGAGCTCA GGAGAGATT CTGACAAATG TACGCCTTTC CCTCAGAAAT 3480
 CAGGGAAGAG ACTGTCGCCT GCCTTCTCTC GTTGTGCGT GAGAACCCTG GTGCCCTTTC 3540
 CCACCATATC CACCTCGCT CCATCTTTGA ACTCAAACAC GAGGAAGTAA CTGCACCTG 3600
 GTCTCTCCCG CAGTCCCCAG TTCACCTCC TTCCCTCCACT CTAAGGGATA 3660
 TCAACACTGC CCAGCACAGG GGCCTGAAT TTATGTGGT TTTATACATT TTTTAATAAG 3720
 ATGCACCTTA TGTCAATTTT TAATAAAGTC TGAAGAATTA CTGTTT

Seq ID NO: 479 Protein sequence
 Protein Accession #: XP_044533.3

1 11 21 31 41 51
 MLRTAMGLRS WLAAPWGALP PRPPLLLLLL LLLLLQPPPP TWALSPRISL PLGSEERPFL 60
 RFEAEHISNY TALLLSRDGR TLYVGAREAL FALSSNLSFL PGGEYQELLW GADAEKKQQC 120
 SFKGDQPD RD CQNYIKILLP LSGSHLFTCG TAAPSPMCTY INMENFTLAR DEKGNVLLED 180
 45 GKGRCPFDPN FKSTALVVDG ELYTGTVSSF QGNDPAISRS QSLRPTKTES SLNWLQDPAF 240
 VASAYIPESL GSLQGGDDKI YFFSFETGQE FEFENTIVS RIRARICKGE GGERVLQQRW 300
 TSFLKAQLLC SRPDDGFPPN VLQDVFTLSP SPQDWRDTLF YGVFTSQWHR GTTEGSAVCV 360
 FTMKDVQRFV SGLYKEVNRE TQQWYTVTHP VPTPRPGACI TNSARERKIN SSLQLPDRVL 420
 NFLKDHFLMD GGVRSRMLLL QPQARYQORVA VHRVPLHHT YDVLFLGTGD GRLHKAIVSG 480
 50 PRVHIIEELQ IFSSGQPVQN LLLDTHRGLL YAASHSGVVQ VPMANCSLYR SCGDCLLARD 540
 PYCAWSSGSS KHVSLYQPL ATRPWIQDIE GASAKDLCSA SSVVSPSFVP TGEKPCQEVQ 600
 FQPNVTNTLA CPLLNSLATR LWRNGAPVN ASASCHVLPT GDLLLVGTQQ LGEFQCSWLE 660
 EGFQQLVASV CPEVVEDGVA DQTDGEGSVF VIISTSRVSA PAGGKASWGA DRSYWKFEFLV 720
 MCTLFLVAL LPLVFLLYRH RNSMKVFLKQ GECASVHPKT CPVVLPPETR PLNGLGPPST 780
 55 PLDHRGYQSL SDSPPGSRVF TESEKRPLSI QDSFVEVSPV CPRPRVRLGS EIRDSVV

Seq ID NO: 480 DNA sequence
 Nucleic Acid Accession #: NM_004217.1
 Coding sequence: 58..1092

1 11 21 31 41 51
 GGCCGGGAGA GTAGCAGTGC CTTGGACCCC AGCTCTCCTC CCCCTTTCTC TCTAAGGATG 60
 GCCCAGAAGG AGAAGCTCCTA CCCCTGGCCC TACGGCCGAC AGACGGCTCC ATCTGGCCTG 120
 AGCACCTGCG CCCAGCGAGT CCTCCGGAAG GAGCCTGTCA CCCCATCTGC ACTTGTCTCT 180
 65 ATGAGCCGCT CCAATGTCCA GCCACAGCT GCCCCTGGCC AGAAGGTGAT GGAGAATAGC 240
 AGTGGGACAC CCGACATCTT AACCGGGCAC TTCACAATTG ATGACTTTGA GATTGGCGT 300
 CCTCTGGGCA AAGGCAAGTT TGGAAACGTG TACTTGGCTC GGGAGAAGAA AAGCCATTTC 360
 ATCGTGGCGC TCAAGTCTCT CTTCAGTCC CAGATAGAGA AGGAGGGCGT GGAGCATCAG 420
 70 CTGCGCAGAG AGATCGAAAT CCAGGCCAC CTGCACCATC CCAACATCCT CGCTCTCTAC 480
 AACTATTTTT ATGACCGGAG GAGGATCTAC TTGATTCTAG AGTATGCCCC CCGCGGGGAG 540
 CTCTACAAGG AGCTGCAGAA GAGCTGCACA TTTGACGAGC AGCGAACAGC CACGATCATG 600
 GAGGAGTTGG CAGATGCTCT AATGTACTGC CATGGGAAGA AGGTGATTCA CAGAGACATA 660
 AAGCCAGAAA ATCTGCTCTT AGGGCTCAAG GGAGAGCTGA AGATTGCTGA CTTCGGCTGG 720
 75 TCTGTGCATG CGCCCTCCCT GAGGAGGAAG ACAATGTGTG GCACCTGCGA CTACCTGCCC 780
 CCAGAGATGA TTTGAGGGCG CATGCACAA TGTGAGGTG ATCTGTGGTG CATTTGGAGT 840
 CTTTGCTATG AGCTGCTGGT GGGGAACCCA CCCTTTGAGA GTGCATCACA CAACGAGACC 900
 TATCGCGCAT TCGTCAAGT GGACCTAAAG TTCCCGCTT CTGTGCCAC GGGAGCCAG 960
 80 GACCTCATCT CCAAAGTCT CAGGCATAAC CCCTCGGAAC GGCTGCCCTT GGCCAGGTC 1020
 TCAGCCCACT CTTGGGTCGG GGCCAACTCT CGGAGGGTGC TGCTCCCTCT TGCCCTTCAA 1080
 TCTGTGCGCT GATGGTCCCT GTCAATCACT CGGGTGCCTG TGTTTGTATG TCTGTGTATG 1140
 TATAGGGGAA AGAAGGATC CTAATCTGTT CCCTTATCTG TTTTCTACCT CCTCCTTTGT 1200
 TTAATAAAGG CTGAAGCTTT TTGT

Seq ID NO: 481 Protein sequence
 Protein Accession #: NP_004208

1 11 21 31 41 51

MAQKENSYPW	PYGRQTPAPSG	LSTLPQVRVLR	KEPVTSPSALV	LMSRSNVQPT	AAPGQKVMEN	60
SSGTPDILTR	HFTIDDFEIG	RPLGKGKFGN	VYLAREKKSH	FIVALKVLFK	SQIEKEGVEH	120
QLRREIEIQA	HLHHNPILRL	YNYFYDRRRI	YLILEYAPRG	ELYKELQKSC	TFDEQRTATI	180
MEELADALMY	CHGKKVIVHR	IKPENLLGL	KGELKIADFG	WSVHAPSLRR	KTMCGTLDYL	240
PFEMIEGRMH	NEKVDLWCIG	VLCYELLVGN	PPFESASHNE	TYRRIVKVDL	KFPASVPTGA	300
QDLISKLLRH	NPSERLPLAQ	VSAHPWVRAN	SRRVLPPSAL	QSV		

Seq ID NO: 482 DNA sequence
Nucleic Acid Accession #: AK055663
Coding sequence: 38..1423

1	11	21	31	41	51	
AGAACGGCTT	CCGGCGGGAG	CTGTGCAGCT	CCTTATCATG	GGGACAAATC	ATCTCTTTTCG	60
AAAACCCCAA	AGATCCTTTT	TTGGCAAGTT	GTTACGGGAA	TTTAGACTGT	TAGCAGCTGA	120
CCGAAGGTCC	TGGAAGATAC	TGCTCTTTGG	TGTAATAAAC	TTGATATGTA	CTGGCTTCCT	180
GCTTATGTGG	TGCAGTCTTA	CTAATAGTAT	AGCTTTAACT	GCCTATACCT	ACCTGACCAT	240
TTTGTATCTT	TTTAGTTTAA	TGACATGTTT	AATAAGTTAC	TGGGTAACAT	TGAGGAAACC	300
TAGCCCTGTC	TATTCAATTG	GGTTTGAAG	ATTAGAAGTC	CTGGCTGTAT	TTGCCCTCCAC	360
AGTCTTGGCA	CAGTTGGGAG	CTCTCTTTAT	ATTAAAAGAA	AGTGACAGAAC	GCTTTTGGGA	420
ACAGCCCAG	ATACACACGG	GAAGATTATT	AGTTGGTACT	TTTGTGGCTC	TTTGTTCCTCA	480
CCTGTTCACG	ATGCTTTCTA	TTCCGAATAA	ACCTTTTGCT	TATGTCTCAG	AAGCTGCTAG	540
TACGAGCTGG	CTTCAAGAGC	ATGTTGCAGA	TCTTAGTCGA	AGCTTGTGTG	GAATTATTCC	600
GGGACTTAGC	AGTATCTTCC	TTCCCGAAT	GAATCCATT	GTTTGTATG	ATCTTGCTGG	660
AGCATTGTCT	CTTTGTATTA	CATATATGCT	CATTGAAATT	AATAATTATT	TTGCCGTAGA	720
CACCTGCTCT	GCTATAGCTA	TTGCCCTGAT	GACATTTGGC	ACTATGTATC	CCATGAGTGT	780
GTACAGTGGG	AAAGTCTTAC	TCCAGACAA	ACCACCCCAT	GTTATGTGTC	AGTTGGACAA	840
ACTCATCAGA	GAGGTATCTA	CCTTAGATGG	AGTTTATAGAA	GTCCGAAATG	AACATTTTGG	900
GACCCTAGGT	TTTGGCTCAT	TGGCTGGATC	AGTGCATGTA	AGAATTCGAC	GAGATGCCAA	960
TGAACAAATG	GTTCTTGCTC	ATGTGACCAA	CAGGCTGTAC	ACTCTAGTGT	CTACTCTAAC	1020
TGTTCAAATT	TTCAAGGATG	ACTGGATTAG	GCCTGCCTTA	TTGCTGGGCG	CTGTTGCAGC	1080
CAATGCTCTA	AACCTTTCAG	ATCATCACGT	AATCCCAATG	CCTCTTTTAA	AGGGTACTGA	1140
TGATTTGAAC	CCAGTTACAT	CAACTCCAGC	TAAACCTAGT	AGTCCACCTC	CAGAATTTTC	1200
ATTTAACACT	CCTGGGAATA	ATGTGAACCC	AGTTATTCTT	CTAAACACAC	AAACAAGGCC	1260
TTATGGTTTT	GGTCTCAATC	ATGGACACAC	ACCTTACAGC	AGCATGCTTA	ATCAAGGACT	1320
TGGAGTTCCA	GGAATTTGGG	CAACTCAAGG	ATTGAGGACT	GGTTTATACAA	ATATACCAAG	1380
TAGATATGGA	ACTAATAATA	GAATTGGACA	ACCAAGACCA	TGATAGACTC	TAACCTATTT	1440
TTATAAGGAA	TATTGACTCC	TTGGCTTCCA	ATTTATTTAG	TAATCCAAC	TTGCATTGAC	1500
TGTTTAATCA	TTTACTCTAA	ATGTTAGATA	ATAGTAGTCT	TGTTACATTT	TCATGAAACC	1560
TATGAACTA	TATTTTGTGA	AAATGTATTT	GTGACAGTGA	AATCCTCGTA	AATGTTAAAG	1620
GCTTTAAATA	GGCTTCCTTT	AGAAAATGTG	TTTCTTTAAA	TTTGGATTTT	GGTATCTTTG	1680
GTTTTGTAGT	TGACTGCACT	GTGATGTGAC	CTTACCTTTA	TAAGAGCCAC	TTGATGGAGT	1740
AGATCTGTCA	CATTACTAAG	ATACGATATT	TCTTTTTTTT	TCCGAGACGG	AGTCTTGCTC	1800
TGCCACTGTG	CCCGGCCAAT	ACATTATTAT	TAACCTAAGG	CTGTACTTTA	TTAAGGCTTC	1860
CTTAGTTTTT	GTTTTGTTTT	GTTTTTTGAG	ATGGAGTCTC	ACTCTGTGCG	CCAGGCTGGA	1920
ATGCAGTGGC	ATGATCTCAG	CTCAGTGC	CCTCTGCCTC	CTGAGTTC	ATGATTCTCC	1980
TGCCCTCAGC	TCCCGAGTAG	CTGGGATTAC	AGGCACCTGC	CACCACGCCC	AGCTAATTTT	2040
TGTATTTTGA	GTAAAGACGG	GGGATTTTCA	CATGTTGGCC	AGGCTGGTCT	TGAATCCTG	2100
ACCTCATGAT	CCACCCACCT	TAGCCTCCCA	AAGTGTCTGG	ATTAGGTGTG	AGCCACCGCA	2160
CCTGGCCGAT	ATTTTCTTTA	ATGAAATTTA	TAAATATGCT	TCTTGAATAA	TACACATTTT	2220
GGGAAAGGGA	AAAAATGCTG	TTCAAAAAGT	AAAGGTCTCT	TTTATAGCTT	TTCCAAACTT	2280
AATTGCTAAA	TTTTTCTTTG	AGGTTCTCCT	GAATTATGTC	TTACAAACTA	AAAGCAAAA	2340
TTTTTAGCAG	AAATTTTGGG	ATACATTCTA	TCTAGCACAA	TTTGAATTTT	TAATTATCAA	2400
GATTTTGTGT	AAAGTTTCTC	TCCTTTAAAA	ATTTTAGTAC	ATTTGTAAAT		

Seq ID NO: 483 Protein sequence
Protein Accession #: BAB70980.1

1	11	21	31	41	51	
MGTIHLFRKP	QRSFFGKLLR	EFRLVAADRR	SWKILLFGVI	NLICTFGLLM	WCSSTNSIAL	60
TAYTYLTIKD	LFSLMTCLIS	YVVTLRKPS	VYSFGFERLE	VLAVFASTVL	AQLGALFILK	120
ESAERFLEQP	EIHTRGLLVG	TFVALCFNLF	TMLSIRNKPF	AYVSEAASTS	WLQEHVADLS	180
RSLCGIIPGL	SSIFLPRMNP	FVLIDLAGAF	ALCITYMLIE	INNYFAVDTA	SAIAIALMTF	240
GTMYPMSVYS	GKVLQLQTPP	HVIGQLDKLI	REVSTLDGVL	EVNREHFWTL	GFGSLAGSVH	300
VRIRRDANEQ	MVLAHVITNRL	YTLVSTLTQV	IFKDDWIRPA	LLSGPVAANV	LNFSDDHVIP	360
MPLLKGTDDL	NPVTSTPAKP	SSPPPEFSFN	TPGKNVNPVI	LLNTQTRFYG	FGLNHGHTFY	420
SSMLNQLGLV	PGIGATQGLR	TGFTNIPSR	GTNNRIGQPR	P		

Seq ID NO: 484 DNA sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..900

1	11	21	31	41	51	
ATGCCGCCGC	GGGAGCTGAG	CGAGGCGGAG	CGGCCCCGCG	TCCGGGCCCC	GACCCCTCCC	60
CCGCCGCCGC	GTAGCGCGCC	CCCAGAGCTG	GGCATCAAGT	GCGTGTCTGT	GGGCGACGGC	120
GCCGTGGGCA	AGAGCAGCCT	CATCGTCAGC	TACACCTGCA	ATGGGTACCC	CGCGCGCTAC	180
CGGCCCACTG	CAGCTGGACAC	CTTCTCTGGT	ACGTACGTTT	AATCGCCCGT	GCGGCCGCGT	240
GGCTGCGGGG	GGGCTGTGCA	CGGGGAGCT	GGGGCGGGCG	TCTCGGCGGG	AGGGCGCAGA	300
GGACCCCGGG	GAGGAGACTG	GAGCAGGCCC	CGAGGTGGCG	CTGGTGGCGG	CCAGGACGCT	360
CTTCTTAAC	CAGGCTCTCC	CGGCCCGGCC	CCTGCAGTGC	AAGTCTCTGT	GGATGGAGCT	420
CGGGTGGCGA	TTGAGCTCTG	GGACACAGCG	GGACAGGAGG	ATTTTGAACG	ACTTGTGTTCC	480
CTTTGTCTAC	CGGATACCGA	TGTCTTCTG	GCGTGTCTCA	GCGTGGTGCA	GCCAGCTCC	540
TTTCAAAACA	TCACAGAGAA	ATGGCTGCCC	GAGATCCGCA	CGCACAAACC	CCAGGCGCCT	600
GTGCTGCTGG	TGGGCACCCA	GGCCGACCTG	AGGACGATG	TCAACGTACT	AATTCAGCTG	660

GACCAGGGGG GCCGGGAGGG CCCCGTGCCC CAACCCAGG CTCAGGGTCT GGCCGAGAAG 720
 ATCCGAGCCT GCTGCTACCT TGAGTGCTCA GCCTTGACGC AGAAGAAGTT GAAGGAAGTA 780
 TTTGACTCGG CTATTCTCAG TGCCATTGAG CACAAAGCCC GGCTGGAGAA GAAACTGAAT 840
 GCCAAAGGTG TGCACACCT CTCCCGCTGC CGCTGGAAGA AGTTCCTCTG CTTCTGTTGA

Seq ID NO: 485 Protein sequence
 Protein Accession #: FGENESH predicted

1 11 21 31 41 51
 | | | | | |
 MPPRELSEAE PPPLRAPTPP PRRRSAPPEL GIKCVLVGDG AVGKSSLIVS YTCNGYPARY 60
 RPTALDTFSG TYVQSPVRRP GCGGAVHRGA GAGVSAGGRR GPRGGDWSRP RGGAGAAQDA 120
 LPNSGSPRPA PAVQVLVDGA PVRIELWDTA GQEDFDRLRS LCYPDTDVFL ACFVSVQPSS 180
 FQNITEKWLP EIRTHNPQAP VLLVGTQADL RDDVNVLIQL DQGGREGPVP QPQAQGLAEK 240
 IRACCYLECS ALTQKNLEKEV FDSAILSAIE HKARLEKKLN AKGVRTL SRC RWKFFCFV

Seq ID NO: 486 DNA sequence
 Nucleic Acid Accession #: XM_063832.2
 Coding sequence: 1..711

1 11 21 31 41 51
 | | | | | |
 ATGCCGCGCG GGGAGCTGAG CGAGGCCGAG CCGCCCCCGC TCCGGGCCCC GACCCCTCCC 60
 CCGCGGCGGC GTAGCGCGCC CCCAGAGCTG GGCATCAAGT GCGTGCTGCT GGGCGACGGC 120
 GCCGTGGGCA AGAGCAGCCT CATCGTCAGC TACACCTGCA ATGGGTACCC CGCGCGCTAC 180
 CGGCCCACTG CGCTGGACAC CTTCTCTGTG CAAGTCTCTG TGGATGGAGC TCCGGTGGCG 240
 ATTGAGCTCT GGGACACAGC GGGACAGGAG GATTTTGACC GACTTCGTTC CTTTGTCTAC 300
 CCGGATACCG ATGTCTTCTT GGCCTGCTTC AGCGTGGTGC AGCCGAGCTC CTTTCAAAAC 360
 ATCAGAGAGA AATGGCTCCG CGAGATCCGC ACGCACAAAC CCCAGGCGCC TGTGCTGCTG 420
 GTGGGCACCC AGGCCGACCT GAGGGACGAT GTCAACGTAC TAATTACGCT GGACCAAGGG 480
 GGCCTGGGAG GCGCCGCTGC CCAACCCAG GCTCAGGGTC TGGCCGAGAA GATCCGAGCC 540
 TGCCTGCTACC TTGAGTGCTC AGCCTTGACG CAGAAGAACT TGAAGGAAGT ATTTGACTCG 600
 GCTATTCTCA GTGCCATTGA GCACAAAGCC CGGCTGGAGA AGAAACTGAA TGCCAAAGGT 660
 GTGCGCACCC TCTCCCGCTG CCGCTGGAAG AAGTCTCTCT GCTTCGTTTG A

Seq ID NO: 487 Protein sequence
 Protein Accession #: XP_063832.1

1 11 21 31 41 51
 | | | | | |
 MPPRELSEAE PPPLRAPTPP PRRRSAPPEL GIKCVLVGDG AVGKSSLIVS YTCNGYPARY 60
 RPTALDTFSV QVLVDGAPVR IELWDTAGQE DFDRLRLSLCY PDTDVFLACF SVVQPSSEFQN 120
 ITEKWLPEIR THNPQAPVLL VGTQADLRDD VNVLIQLDQG GREGPVPQFQ AQGLAEKIRA 180
 CCYLECSALT QKNLEKEVFDS AILSAIEHKA RLEKKLNAGK VRTL SRCRWK KFFCFV

Seq ID NO: 488 DNA sequence
 Nucleic Acid Accession #: NM_014398.1
 Coding sequence: 64..1314

1 11 21 31 41 51
 | | | | | |
 GGCACCGATT CGGGGCTTGC CCGGACTTCG CCGCACGCTG CAGAACCTCG CCCAGCGCCC 60
 ACCATGCCCC GGCAGCTCAG CGCGCGGCGC GCGCTCTTCG CGTCCCTGGC CGTAATTTTG 120
 CACGATGGCA GTCAAATGAG AGCAAAAGCA TTTCCAGAAA CCAGAGATTA TTCTCAACCT 180
 ACTGCAGCAG CAACAGTACA GGACATAAAA AAACCTGTCC AGCAACAGC TAAGCAAGCA 240
 CCTCACCAAA CTTTAGCAGC AAGATTCTAT GATGGTCATA TCACCTTTCA AACAGCGGCC 300
 ACAGTAAAAA TTCCAACAAC TACCCAGCA ACTACAAAAA AACTTGCAAC CACCAGCCCA 360
 ATTACCTACA CCCTGGTCAC AACCAGGCC ACACCCAACA ACTCACACAC AGCTCCTCCA 420
 GTTACTGAAG TTACAGTCGG CCCTAGCTTA GCCCTTTAT CACTGCCACC CACCATCACC 480
 CCACGAGCTC ATACAGCTGG AACCAGTTCA TCAACCGTCA GCCACACAAC TGGGAACACC 540
 ACTCAACCCA GTAACAGAC CACCCTTCCA GCAACTTTAT CGATAGCACT GCACAAAGC 600
 ACAACCGGTC AGAAGCCTGA TCAACCCACC CATGCCCCAG GAACAACGCG AGCTGCCACC 660
 AATACCAACC GCACAGCTGC ACCTGCCTCC ACGGTTCTCG GGCCACCCCT TGCACCTCAG 720
 CCATCGTCAG TCAAGACTGG AATTATCAG GTTCTAAACG GAAGCAGACT CTGTATAAAA 780
 GCAGAGATGG GGATACAGCT GATTGTTCAA GACAAGGAGT CGGTTTTTTC ACCTCGGAGA 840
 TACTTCAACA TCGACCCCAA CGCAACGCAA GCCTCTGGGA ACTGTGGCAC CCGAAAATCC 900
 AACCTTCTGT TGAATTTTCA GGGCGGATTT GTGAATCTCA CATTATACCA GGATGAAGAA 960
 TCATATTATA TCAGTGAAGT GGGAGCCTAT TTGACCGTCT CAGATCCAGA GACAGTTTAC 1020
 CAAGGAATCA AACATGCGGT GGTGATGTTT CAGACAGCAG TCGGGCATTC CTTCAAGTGC 1080
 GTGAGTGAAC AGAGCCTCCA GTTGTGAGCC CACCTGACAG TGAACAACAC CGATGTCCAA 1140
 CTTCAAGCCT TTGATTTTGA AGATGACCAC TTTGGAAATG TGGATGAGTG CTCGTCTGAC 1200
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 GGTGTCTATA AAATCCGCTT AAGGTGTCAA TCATCTGGAT ACCAGAGAAT CTAATTGTTG 1320
 CCCGGGGGGA ATGAAAATAA TGGAAATTTAG AGAACTCTTT CATCCCTTCC AGGATGGATG 1380
 TTGGGAAATT CCCTCAGAGT GTGGGTCTTT CAAACAATGT AAACCACCAT CTTCTATTCA 1440
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 GTTATTTTGA TGAAGATAT AGTGAGCTGT TTATTTCTTA GTTTCCTTTA GAATATTTTA 1560
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 AGCCTTCAAA TTATAAACCA AGGGTCAATT GTAACATAA CTACTGTGTG TGCATTGAAG 1680
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 GCTTTTACTA TCTGTGTTTT ATGGTTTCAT GTAACATACA TATTCCTGGT GTAGCACTTA 1800
 ACTCCTTTTC CACTTTAAAT TTGTTTTTGT TTTTGTGAGC GGAGTTTACC TCTGTCAACC 1860
 CAGGCTGGAG TACAGTGGCA CGATCTCGGC TTATGGCAAC CTCCGCCCTC CGGGTTCAAG 1920
 TGATTCTCCT GCTTCAGCTT CCCGAGTAGC TGGGATTACA GGCACACACT ACCAGCCTG 1980
 GCTAATTTT GTATTTTAT TATAGACGGG TTTCAACATG TTGGCCAGAC TGGTCTTGAA 2040
 CTCTTGACCT CAGGTGATCC ACCCACCTCA GCCTCCCAA GTGCTGGGAT TACAGGCATG 2100
 AGCCATTGCG CCGGCTTTA AATGTTTTT TTAATCATCA AAAAGAACA CATATCTCAG 2160

GTTGTCTAAG TGTTTTATG TAAACCAAC AAAAGAACA AATCAGCTTA TATTTTTTAT 2220
 CTTGATGACT CCTGCTCCAG AATTGCTAGA CTAAGAATTA GGTGGCTACA GATGGTAGAA 2280
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 TAGGCTAAGC ACTTTATCTA TATCTCATTT CATCTCACAC ACTTATAAGT GAATGAGTAA 2400
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 GAGCTTGAAT TCATGTTGGT CTGACATCAA GGTCTTTGGT CTTCTCCCTA CACCAAGTTA 2520
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 TCACCTTACA GGGAAAATGGG TTTATCCAGG ATCATGAGAC ATTAGGGTAG ATGAAAGGAG 2640
 AGCTTTGCAG ATAAACAAAT AGCCTATCCT TAATAAATCC TCCACTCTCT GGAAGGAGAC 2700
 TGAGGGGCTT TGTAAAACAT TAGTCAGTTG CTCATTTTAA TGGGATTGCT TAGCTGGGCT 2760
 GTAAAGATGA AGGCATCAAA TAAACTCAAA GTATTTTAA ATTTTGTGA TAATAGAGAA 2820
 ACTTCGCTAA CCAACTGTTC TTTCTTGAGT GTATAGCCCC ATCTTGTTGGT AACTTGCTGC 2880
 TTTCTGCACTT CATATCCATA TTTCTTATG TTTCACTTAT TCTGTAGAGC AGCCTGCCAA 2940
 GAATTTTATT TCTGCTGTTT TTTTGTGCTG TAAAGAAAGG AACTAAGTCA GGATGTTAAC 3000
 AGAAAAGTCC ACATAACCCT AGAATCTTAA GTCAAGGAAT AATCAAGTC AGCCTAGAGA 3060
 CCATGTTGAC TTTCTCATG TGTTCCTTAA TGACTCAGTA AGTTGGCAAG GTCCTGACTT 3120
 TAGTCTTAAT AAAACATTGA ATTGTAGTAA AGGTTTTTGC AATAAAAACT TACTTTGG

Seq ID NO: 489 Protein sequence
 Protein Accession #: NP_055213.1

1 11 21 31 41 51
 MPRQLSAAAA LFASLAVILH DGSQMRKAF PETRDYSQPT AAATVQDIK PVQPPAKQAP 60
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 TEVTVGSPSL PYSLPPTITP PAHTAGTSSS TVSHTTGNNT QPSNQTTLPA TLSIALHKST 180
 TGQKPDQPTH APGTTAAAHN TTRTAAPAST VPGPTLAPQP SSVKTGIYQV LNSRLCIKA 240
 EMGQLIVQD KESVFSPPRY FNIDPNATQA SGNCGTRKSN LLLNFQGGFV NLFTTKDEES 300
 YYISEVGAYL TVSDPETVYQ GIKHAVVMFQ TAVGHSFKCV SEQSLQSAH LQVKTDDVQL 360
 QAFDFEDDHF GNVDECSSDY TIVLPVIGAI VVGLCLMGGM VYKIRLRCQS SGVQRI

Seq ID NO: 490 DNA sequence
 Nucleic Acid Accession #: NM_005409.3
 Coding sequence: 94..378

1 11 21 31 41 51
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 TTGGCTGTGA TATTGTGTGC TACAGTTGTT CAAGGCTTCC CCATGTTCAA AAGAGGACGC 180
 TGTCTTTGCA TAGGCCCTGG GGTAAAAGCA GTGAAAAGTG CAGATATTGA GAAAGCCTCC 240
 ATAAATGTACC CAAGTAACAA CTGTGACAAA ATAGAAGTGA TTATTACCTT GAAAGAAAAA 300
 AAAGGACAAC GATGCCTAAA TCCCAATCG AAGCAAGCAA GGCTTATAAT CAAAAAAGTT 360
 GAAAGAAAAG ATTTTAAAAA ATATCAAAAC ATATGAAGTC CTGGAAAAGG GCATCTGAAA 420
 AACCTAGAAC AAGTTTAACT GTGACTACTG AAATGACAAG AATCTACAG TAGGAAACTG 480
 AGACTTTTCT ATGTTTTTGT GACTTTCAAC TTTTGTACAG TTATGTGAAG GATGAAAGGT 540
 GSGTGAAAGG ACCAAAAACA GAAATACAGT CTTCTGAAT GAATGACAAT CAGAATTCCA 600
 CTGCCCAAAG GAGTCCAGCA ATTTAAATGGA TTTCTAGGAA AAGCTACCTT AAGAAAGGCT 660
 GGTTACCATC GGAAGTTTACA AAGTGCTTTC ACGTCTTAC TTGTGTGATT ATACATTCAT 720
 GCATTTCTAG GCTAGAGAAC CTTCTAGATT TGATGCTTAC AACTATTCTG TTTGTACTAT 780
 GAGAACATTT CTGTCTCTAG AAGTTATCTG TCTGTATTGA TCTTTATGCT ATATTACTAT 840
 CTGTGGTTAC AGTGGAGACA TTGACATTAT TACTGGAGTC AAGCCCTTAT AAGTCAAAAG 900
 CATCTATGTG TCGTAAAGCA TTCTCAAAC ATTTTTCAT GCAAAATACAC ACTTCTTTC 960
 CCAAATATCA TGTAAGCACAT CAATATGTAG GGAACCATTC TTATGCATCA TTTGGTTTGT 1020
 TTTATAACCA ATTCATTAAA TGTAATTCAT AAAATGTACT ATGAAAAAAA TTATACGCTA 1080
 TGGGATACTG GCAACAGTGC ACATATTTC TAACCAAAAT AGCAGCACCG GTCTTAATTT 1140
 GATGTTTTTC AACTTTTAT CATTGAGATG TTTTGAAGCA ATTAGGATAT GTGTGTTTAC 1200
 TGTACTTTTT GTTTTGTATC GTTTGTATAA ATGATAGCAA TATCTTGGAC ACATTTGAAA 1260
 TACAAAATGT TTTTGTCTAC CAAAGAAAAA TGTGAAAAA TAAGCAAATG TATACCTAGC 1320
 AATCACTTTT ACTTTTGTGA ATTCTGTCTC TTAGAAAAAT ACATAATCTA ATCAATTTCT 1380
 TTGTTTATGC TATATACTG TAAAATTTAG GTATACTCAA GACTAGTTTA AAGAATCAAA 1440
 GTCATTTTTT TCTCTAATAA ACTACCACAA CCTTCTTTT TTAACAAAAA AAA

Seq ID NO: 491 Protein sequence
 Protein Accession #: NP_005400.1

1 11 21 31 41 51
 MSVKGMAIAL AVILCATVVQ GPFMPKRGRC LCIGPGVKAV KVADIEKASI MYPSNNDCKI 60
 EVIITLKENK GQRCLNPKSK QARLIILKVE RKNF

Seq ID NO: 492 DNA sequence
 Nucleic Acid Accession #: NM_000577.1
 Coding sequence: 41..520

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 GAAGACCTTC TATCTGAGGA ACAACCAACT AGTTGCCGGA TACTTGCAAG GACCAATATG 180
 CAATTTAGAA GAAAGATAG ATGTGGTACC CATTGAGCCT CATGCTCTGT TCTTGGGAAT 240
 CCAATGGAGG AAGATGTGCC TGTCTGTGT CAAGTCTGGT GATGAGACCA GACTCCAGCT 300
 GGAGGCAGTT AACATCACTG ACCTGAGCGA GAACAGAAAG CAGGACAAGC GCTTCGCCTT 360
 CATCCGCTCA GACAGTGGCC CCACCACCG TTTTGAGTCT GCCCCTGCC CCGTTGGTT 420
 CCTCTGCACA GCGATGGAGC CTGACCGCC CGTCAGCCTC ACCAATATGC CTGACGAAGG 480
 CGTCATGGTC ACCAAATCT ACTTCCAGGA GGACGAGTAG TACTGCCCGG GCCTGCCTGT 540
 TCCATTCTT GCATGGCAAG GACTGCAGG ACTGCCAGT CCCCTGCCCC AGGCTCCCC 600

GCTATGGGG CACTGAGGAC CAGCCATTGA GGGGTGGACC CTCAGAAGGC GTCACAACAA 660
 CCTGGTCACA GGACTCTGCC TCCTCTTCAA CTGACCAGCC TCCATGCTGC CTCCAGAATG 720
 GTCTTTCTAA TGTGTGAATC AGAGCACAGC AGCCCTGCA CAAAGCCCTT CCATGTCGCC 780
 TCTGCATTCA GGATCAAAAC CCGACCACCT GCCCAACCTG CTCTCTCTCT GCCACTGCCT 840
 CTCTCTCCCT CATTCACCTT TCCATGCCCC TGGATCCATC AGGCCACTTG ATGACCCCA 900
 ACCAAGTGGC TCCCACACCC TGTTTTACAA AAAAGAAAAG ACCAGTCCAT GAGGGAGGTT 960
 TTTAAGGGTT TGTGAAAAAT GAAAAATAGG ATTTTCATGAT TTTTTTTTTT CAGTCCCCGT 1020
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 ATTCCTGCAT TTGTGAAATG ATGGTGAAAG TAAGTGGTAG CTTTTCCCTT CTTTTCTTC 1140
 TTTTTTTGTG ATGTCCCAAC TTGTAAAAAT TAAAAGTTAT GGTACTATGT TAGCCCCATA 1200
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 CCCAGCTCC AAGCTCCATC TCCACTCCAG ATTTTTTACA GCTGCCTGCA GTACTTTACC 1320
 TCCATACAGA AGTTTCTCAG CTCCAAGGC TCTGAGCAAA TGTGGCTCCT GGGGGTTCTT 1380
 TCTTCTCTG CTGAAGGAAT AAATTGCTCC TTGACATTGT AGAGCTTCTG GCACTTGAG 1440
 ACTTGTATGA AAGATGGCTG TGCTCTGCCC TGTCTCCCC ACCAGGCTGG GAGCTCTGCA 1500
 GAGCAGGAAA CATGACTCGT ATATGTCTCA GGTCCCTGCA GGGCCAAGCA CTAGCCTCG 1560
 CTCTTGGCAG GTACTCAGCG AATGAATGCT GTATATGTTG GGTGCAAAAT TCCCTACTTC 1620
 CTGTGACTTC AGCTCTGTTT TACAATAAAA TCTTGAATAA GCCTAAAAAA AAAAAAAA 1680
 AAAAAAAA AAAAAAAA AAAAAAAA AAAAAA

Seq ID NO: 493 Protein sequence
 Protein Accession #: NP_000568.1

1 11 21 31 41 51
 MALETICRPS GRKSSKMQAF RIWDVNQKTF YLRNNQLVAG YLQGPVNLE EKIDVVPIEP 60
 HALFLGIHGG KMCLSCVKSG DETRLQLEAV NITDLSENRK QDKRFVAFIRS DSGPTTSFES 120
 AACPGWFLCT AMEADQPVSL TNMPDEGVMV TKFYFQEDE

Seq ID NO: 494 DNA sequence
 Nucleic Acid Accession #: NM_002081.1
 Coding sequence: 222..1898

1 11 21 31 41 51
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 CGGGACCTTG GCTCTGCCCT TCGCGGGCGG GAACTGCGCA GGACCGGCC AGGATCCGAG 180
 AGAGGCGCGG CGGGGTGGCC GGGGGCGCG CCGGCCCGCG CATGGAGCTC CGGGCCGAG 240
 GCTGGTGGCT GCTATGTGCG GCGCAGCGC TGGTCTGCTG CGCCGCGCGG GACCCGCGCA 300
 GCAAGAGCCG GAGCTCGCGG GAGGTCCGCC AGATCTACGG AGCCAAGGGC TTCAGCCTGA 360
 GCGACGTGCC CCAGGCGGAG ATCTCGGGTG AGCACCTGCG GATCTGTCCC CAGGGCTACA 420
 CCTGCTGCAC CAGCGAGATG GAGGAGAACC TGGCCAACCG CAGCCATGCC GAGCTGGAGA 480
 CGCGCTCCG GGACAGCAGC CGCGTCTGCG AGGCCATGCT TGCCACCCAG CTGCGCAGCT 540
 TCGATGACCA CTTCACGAC CTGCTGAACG ACTCGGAGCG GACGCTGCAG GCCACCTTCC 600
 CCGGCGCCTT CCGAGAGCTG TACACGCAGA ACGCGAGGGC CTTCGCGGAC CTGTACTCAG 660
 AGCTGCGCCT GTACTACCGC GGTGCCAACC TGCACTGGA GGAGACGCTG GCCGAGTTCT 720
 GGGCCGCGCT GCTCGAGCGC CTCTCAAGC AGCTGCACCC CAGCTGCTG CTGCGCTGATG 780
 ACTACCTGGA CTGCTGGGCG AAGCAGGCGG AGCGCTGCGG GCCCTTCGGG GAGGCCCGCA 840
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 CATCGGGTGT GGAGAGTGTC ATCGGCAGCG TGCAACGCTG GCTGGCGGAG GCCATCAACG 1200
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 AGGTCAACCC CAGGGCCCTT GGGCCTGAGG AGAAGCGCGC CCGGGCAAG CTGGCCCCGC 1320
 GGGAGAGGCC ACCTTCAGGC ACGCTGGAGA AGCTGGTCTC TGAAGCCAAG GCCCAGCTCC 1380
 GCGACGTCCA GGACTTCTGG ATCAGCTCC CAGGGACACT GTGCAGTGAG AAGATGGCCC 1440
 TGAGCACTGC CAGTGATGAC CGCTGTGGA ACGGGATGGC CAGAGGCCGG TACCTCCCCG 1500
 AGGTGATGGG TGACGGCTTG GCCAACCCG CAGGTGGAG GTGGACATCA 1560
 CCAAGCCGGA CATGACCATC CGGCAGCAGA TCATGCAGCT GAAGATCATG ACCAACCGGC 1620
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 GCTCGGGCAG CGGTGATGGC TGTCTGGATG ACCTCTGCGG CCGGAAGGTC AGCAGGAAGA 1740
 GCTCCAGCTC CCGGACGCCC TTGACCCATG CCTCCAGG CCTGTGAGAG CAGGAAGGAC 1800
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 TCCTGGCCCT TACAGTAGCC AGGCCCGGT GCGGTAACT GCGCCAGGC CCCAGGGACA 1920
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 TGGAGAGGCC TGGGTGGGA CAGGAGGGC CGGCGCTCT GAGCAGGGGC AGGCGCAGAG 2040
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 TCCGGCTGCC TAGCCCTCCC CCCAGCTCCC TGCAACGCGC CAGAAGCAGC CCTCGAGGC 2220
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 CGCCTCTCC CACTGGGACT CCCAGCAGAG CCCACAGCC AGCCTTGGCC CACCCCCAG 2340
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 CACCTTGGAC CTGTTGAGC TCCTGTCACT CACTGAGGCC ATCAGGGGCC TGCCCCAGGC 3120

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TCCTGAACCG ACTGACCCCTG AGGAGGCCGC TTAGTGCTGC TTGTCTTTTC ATCACCCTCC 3300
CGCACAGTGG ACGGAGGTCC CCGGTTGCTG GTCCAGGTCCC CATGGCTTGT TCTCTGGAAC 3360
CTGACTTTAG ATGTTTTGGG ATCAGGAGCC CCCAACACAG GCAAGTCCAC CCCATAATAA 3420
CCCTGCCAGT GCCAGGGTGG GCTGGGGACT CTGGCACAGT GATGCCGGGC GCCAGGACAG 3480
CAGCACTCCC GCTGCACACA GACGGCCTAG GGGTGGCGCT CAGACCCAC CCTACGCTCA 3540
TCTCTGGAAG GGGCAGCCCT GAGTGGTCAC TGGTCAGGGC AGTGGCCAAG CCTGCTGTGT 3600
CCTTCTCCA CAAGGTCCCC CCACCGCTCA GTGTACGCGG GTGACGTGTG TTCTTTTGAG 3660
TCCTTGATG AATAAAGGC TGGAAACCTA AA

Seq ID NO: 495 Protein sequence
Protein Accession #: NP_002072.1

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1 11 21 31 41 51
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ICPQGYTCCT SMEEENLANR SHAELATALR DSSRVLQAML ATQLRSFDDH FQHLNDSER 120
TLQATFPFAGF GELYTQNARA FRDLVSELRL YYRGANLHLE ETLAEFWARL LERLFKQLHP 180
QLLLPDDYLD CLGKQAEALR PFGEAPRELRL LRATRAFVAA RSFVQQLGVA SDVVRKVAQV 240
PLGPECSRRAV MKLVYCAHCL GVPGARPCPD YCRNVLKGL ANQADLDAEW RNLLDSMVL 300
TDKFWTSGV ESVGISVHTV LAEAINALQD NRDTLTAKVI QCGGNPKVNP QGPGEPEKRR 360
RGKLAERERF PSGLLEKLVS EAKAQLRDVQ DFWSLPGTL CSEKMALSTA SDDRCWNGMA 420
RGRYLPVEMG DGLANQINNP EVEVDITKPD MTIRQQIMQL KIMTNRLRSA YNGNDVDFQD 480
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Seq ID NO: 496 DNA sequence
Nucleic Acid Accession #: NM_001650.2
Coding sequence: 40.1011

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GGGGTCTGGA CTCAAGCTTT CTGGAAGCA GTACAGCGG AATTTCTGGC CATGCTTAT 180
TTTGTCTCC TCAGCCTGGG ATCCACCATC AACTGGGGTG SAACAGAAAA GCCTTTACCG 240
GTGCACATGG TTCTCATCTC CCTTTGCTTT GGACTCAGCA TTGCAACCAT GGTGCAGTGC 300
TTTGGCCATA TCAGCGGTGG CCACATCAAC CCTGCAGTGA CTGTGGCCAT GGTGTGCACC 360
AGGAAGATCA GCATCGCCAA GTCTGTCTTC TACATCGCAG CCCAGTGCCT GGGGGCCATC 420
ATTGGAGCAG GAATCCTCTA TCTGGTCACA CCTCCAGTG TGGTGGGAGG CCTGGGAGTC 480
ACCATGGTTC ATGGAATATCT TACCGCTGGT CATGGTCTCC TGGTTGAGTT GATAATCACA 540
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ACTGGTGCCA GCATGAATCC CGCCCGATCC TTTGGACCTG CAGTTATCAT GGGAAATTGG 720
GAAAACCAAT GGATATATTG GGTGGGCCCC ATCATAGGAG CTGTCCTCGC TGGTGGCCTT 780
TATGAGTATG TCTTCTGTCC AGATGTTGAA TTCAAACGTC GTTTTAAAGA AGCCTTCAGC 840
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GAGACGGATG ACCTGATTCT AAAACCTGGA GTGGTGCATG TGATTGACGT TGACCGGGGA 960
GAGGAGAAGA AGGGGAAAGA CCAATCTGGA GAGGTATTGT CTTCAGTATG ACTAGAAGAT 1020
CGCACTGAAA GCAGACAAGA CTCCTTAGAA CTGTCTCAG ATTTCTTCC ACCCATTAAG 1080
GAAACAGATT TGTATATAAT TAGAAATGTG CAGGTTGTGT GTTTCATGTC ATATTACTCA 1140
GTCTAAACAA TAAATATTTT ATAATTTACA AAGGAGGAAC GGAAGAAACC TATTGTGAAT 1200
TCCAAATCTA AAAAAAGAAA TATTTTAAAG ATGTTCTTAA TCCAAATATAT ACCTATTTTA 1260
TCTAGTTACC TTTCATTAAC AACCAATTTT AACCGTGTGT CAAGATTTGG TTAAGTCTTG 1320
CTGCACAGAA CTCAAAGACA CGTCTATCAG CTTATTCCCT CTCTACTGGA ATATTGGTAT 1380
AGTCAATTCT TATTTGAATA TTTATTCTAT TAACTGAGT TTAACAATGG C

Seq ID NO: 497 Protein sequence
Protein Accession #: NP_001641.1

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1 11 21 31 41 51
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GTEKPLPVDV VLISLCFGLS IATMVQCFGH ISGGHINPAV TVAMVCTRKI SIAKSVFYIA 120
AQCLGAIIGA GILYLVTPPS VVGGLGVMTV HGNLTAGHGL LVELIITFQL VFTIFASCD 180
KRDTVTSIA LAIGFSAVIG HLFAINYTGA SMNPARSFGP AVIMGNWENH WIYWVGPIIG 240
AVLAGGLYEV VFPCDVEFKR RFKEAFSKAA QQTGGSYMEV EDNRSQVETD DLILKPGVVH 300
VIDVDRGEEK KGKDQSGEVL SSV

Seq ID NO: 498 DNA sequence
Nucleic Acid Accession #: AB020684.1
Coding sequence: 1..1744

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GACGGTTACC AGAGGAGAGG GACTCAGTCC TATTGAAAGC TGTGAAGGAT TGGGAGATCC 180
TGCTTGCTTT TATGTTGCTG TAATTTTAT TTTAAATGGA CTAATGATGG CATTATTCTT 240
CATATATGGC ACATATTTAA GTGGCAGCCG ATTAGGAGGC CTGGTTACAG TGTGTGCTT 300
CTTTTTCAT CATGGAGAGT GTACCGTGT AATGTGGACA CCACCTCTCC GTGAAAGCTT 360
CTCATATCCA TTTCTTGTTC TTCAGATGTT GCTAGTGACT CATATTCTCA GGGCTACAAA 420
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GCAGTTTGCT CAGTTTGTAC TTCTTACTCA GATTGCATCA TTATTGTCAG TATATGTTGT 540
CGGGTACATT GATATATGTA AATTACGGAA GATCATTTAT ATACACATGA TTTCTCTTGC 600
ACTTTGTTTT GTTTTGATGT TTGGGAACCT AATGTTATTA ACTTCTTAT ATGCTTCTTC 660
TTTGGTAATT ATTTGGGGTA TTCTGGCAAT GAAACCACAT TTCCTGAAAA TAAATGTATC 720

	TGAACCTAGT	TTATGGGTTA	TTCAAGGATG	TTTTTGGTTA	TTTGGAAC TG	TCATACTTAA	780
	ATACTTGACA	TCTAAAAATT	TTGGTATTGC	AGATGACGCT	CATATTGGCA	ACTTACTAAC	840
	ATCAAAATTC	TTTAGTTTGA	AGGATTTTGA	TACCTTTATTG	TATACCTGTG	CAGCGGAGTT	900
5	TGACCTTTATG	GAAAAAGAGA	CTCCACTGAG	ATACACAAAG	ACATTATTGC	TTCCAGTTGT	960
	TCTTGTAGTG	TTTGTGCTA	TTGTTAGAAA	GATTATTAGT	GATATGTGGG	GTGTCTTAGC	1020
	TAAACAACAG	ACACATGTAA	GAAAAACCCA	GTTTGATCAT	GGAGAGCTGG	TTTACCATGC	1080
	ATTGCAATTG	TTAGCATATA	CAGCCCTTGG	TATTTTAATT	ATGAGACTAA	AACTCTTCTT	1140
	GACACCACAC	ATGTGTGTTA	TGGCATCACT	GATCTGCTCA	AGACAGCTAT	TTGGATGGCT	1200
10	CTTTTGCAAA	GTACATCC TG	GTGCTATTGT	GTTTGCTATA	TTAGCAGCAA	TGTCAATACA	1260
	AGGTTTCAGCA	AATCTGCAAA	CCCAGTGGAA	TATTGTAGGG	GAGTTCAGCA	ATTTGCCCCA	1320
	AGAAGAAGCT	ATAGAATGGA	TCAAATATAG	TACTAAACCA	GATGCAGTGT	TTGCGGGTGC	1380
	CATGCCACAG	ATGGCAAGTG	TTAAGCTCTC	TGCACCTCGG	CCCATTGTGA	ATCATCCACA	1440
	TTATGAAGAC	GCAGGCTTGA	GAGCCAGAAC	AAAAATAGTA	TACTCAATGT	ATAGTCGGAA	1500
15	AGCAGCCGAA	GAAGTGAAGC	GAGAAGTATG	AAAGTTAAAA	GTGAAGTATT	ACATTCTAGA	1560
	AGAGTCATGG	TGTGTAAGAA	GATCCAAGCC	TGGTTGCAGT	ATGCCTGAAA	TTTGGGATGT	1620
	AGAAGATCCT	GCCAATGCTG	GGAAAACTCC	CTTATGTAAC	CTCTTGGTGA	AGGATTCCAA	1680
	ACCTCACTTC	ACCACTGTAT	TCCAGAACAG	TGTTTACAAA	GTCCCTAGAA	TTGTAAAAGA	1740
	ATGACTGCTA	CATGACCTGC	TGCCTACGGA	GAAGTACATC	TGTAATGGTT	TTAATGTTTT	1800
20	GCTAAGTCAT	GTGTTGTTCA	TATCCCAAAA	ACTTTTATAG	GTAAGTGT	TCAATAGAAA	1860
	AACGTTTTAT	TGGTCAAT	TGAATGTCAT	TCTAATTATA	AAAAAGACTT	ACACCTTTAT	1920
	CAATTGGTTA	CTATTCAAT	GCACCCCTTA	AAATTGCTA	TGCAAAATGAG	TATATGCTTG	1980
	TACTTGACTT	TAATATTTGT	GCTAAAGTGA	GCAAAGCTAC	CTGTATAAAG	AAAACACAGT	2040
	GGGTTGTGAC	AAGGATGACA	TGAAAATACA	GGACAATTCT	GACAATGTAG	GGGCTGATTT	2100
25	TATAGTGTA	GAACATTTAA	TGCCCTTGC	TTCTTTTTTC	TGCCCTGTG	TCTTGTCTTT	2160
	TGGACATTTC	AGTGATTGTA	AGTTCCTCGG	TCATGTCAGC	CCCTGTCTC	AACCTGAGTT	2220
	ACAGTAGATG	GGGCAGACAT	GGAGTGTTTG	CTATATAAAA	CTATCTGTTT	GTTTACTTTC	2280
	CTTGTGCGCT	TTTTTCTCT	TGTTCTCTTG	TTAATGAAGC	TTTTCTCTGC	CATTATTAA	2340
	CCAACTCTCT	GGACCTTGTG	GTTAGGAAAT	TCCCTTAACT	TCCAGCCATA	TGGCATTATC	2400
30	GTGTCTCTTT	CTCTCTCTCT	CTTGCTCTCT	CTCTCTCTCT	CTTCCCATTA	TTTTCTGTCA	2460
	AATAAGTACT	GTTTACTCAT	TTAGTTGCTT	ATCAAGTACT	TATTCTTGTT	TTTAAAAAAA	2520
	ATTAATGGTA	ACTGTATTTT	TCTCATTTTT	AGCATTTATC	AAATGTTTAT	ATTTTAATAC	2580
	CTTTAAACCA	CTTTAAAGTT	TTTTCAATGT	TAATTATAGT	TTTAAAGAAA	ACTATTTTGA	2640
	ACAACCCCAA	ATATAGTGCA	TCTAGAAACT	AATGTATATT	TGATTAGACA	TCATTATATG	2700
35	TGGAACAGTA	GACTGTAGTA	CATGGTAATT	TTTCTTTTAC	TATTAAGATA	CAATAAAACA	2760
	TGACTAAATTT	TGCTGTCAAA	AATGTAAAGA	ATAATGATAA	ATGGAGTTT	TTATATTTTA	2820
	CTTTTAAGAT	TGCCCTGTCT	TAATAAGACA	AAGCCTTAAG	CCTTATGTGA	TAATTTTGGT	2880
	TCTAAAAACC	ATCATTTTCA	TATAAGGAAT	AAGTATATTT	CGTCTCTCT	TTTAGTTTTT	2940
	TTCTTCTCTAT	TTATTTTAT	TTTGAAAAAT	TTCTACACCT	TCTTTGAATT	CCTTGTATGA	3000
40	ATTTTGTGTT	CTTAGAAGTT	AATTTGTGTG	AAATGAGATT	CTTCAAAACG	ATGAAACCTC	3060
	ATAGCTCTGA	GAAAAGGTTT	TAGGGTTTTA	AATTTCTAAGC	AAAGCGTGAC	TATGGCTGAC	3120
	AGACTACACA	TTAATTTATA	CAGCTTCTCT	TTCTTAACCA	CAGGCAGATT	AACCTCATTG	3180
	TGGATTGTCC	TTAGACCTTC	AGTCTCTCAG	CATGGTTTCT	GGTGGCCACT	CCTGGAAGCC	3240
45	GCTGTTCCCT	TTCTACCTTC	TTACCAGAGC	CCAAGGGCAG	GCCTGGTCCC	GGGGAAGCAG	3300
	CAGCTTGCTG	ACATAAGTCA	GCTGCAAAAG	CTGAGGAGTG	TGCCCTCAGA	GAAGCACCOC	3360
	CCCCAGTCT	TGTGCCAGCG	CCTAGAGCCG	CAGCTCCACG	GGATGCTCCT	TCCCTGGAGG	3420
	CAGCCCAGGA	GAGGGACTCT	GGCAGCGTTC	TTAGATTG	TGGCCACTGT	TTCTCATTTG	3480
	CTGGTTGACT	GTTTTTATTT	CTTAGGCTTT	TGCTAGTTTT	AGAAAATAGG	GAAGCAGCCC	3540
50	TTGATTGTG	GATTAAGAGC	AACATTGAG	CGATGATGCA	CAACAGTCCA	GGAAAATGGG	3600
	CGGTGGACAC	TTGAGGCTGA	GGATGGGAGT	TGACATGAGC	AGGGAGAGGG	AGGTGCGCGC	3660
	TGCTTATCTG	TGATTGTTGC	TACCTGAGT	GTGGCTGATT	GTGTACATCC	AGCAGTTACA	3720
	ATTTTAAAAA	ATTATACCTT	TACATTATTT	TTATATTTTT	CTCACCCCCA	GTAATTTCTC	3780
	TCCAAAGAAG	TTACATGTGA	ATAAGTAGAA	ATTCTGTATA	GGAAAAAAGC	ATTAAAAATA	3840
55	CTATTATAAC	TGCTTCATT	GCTGGGAACC	ATTAAAAAGTA	ATATAAAATTA	GCTTTTTCCT	3900
	GAAGGATCCT	TTGTAGCAG	TGTTTATGAA	TGTAACCCCC	AGCAAAATAT	GGCTATATAT	3960
	TAGGGGAGCC	AGTTTGGAGC	AGAGGCTGGA	AGGTCCCTGC	TATGCAGCCG	TGGCCACAGC	4020
	TGCGACCCCA	AGCATCTGTG	AGCATCCACA	CCTTTGATGG	CAATGCAGAT	TGGTAGCAGG	4080
	TTCCATAGGC	GTACAAAACA	GTATTAAAGC	TCAGTGTGTT	GCATATTGTT	AGCATTTTACA	4140
	AATATTTTTC	CTTTAGTATG	AGGAAAGTAA	GGATGGGCAA	AGAAGCGATC	AAAATAGCTA	4200
60	TTGTACAAC	ATTTTGCAAA	ACAAAGTTGG	GGCTGTATTT	CTTTAAAAAG	ATAAGCCTCT	4260
	AAAAATGCTT	GGCAAAAAAA	ATATAGTGTT	AAAAATAGGC	AGTGATATTA	ATGAGAAAAA	4320
	GAAAGTATGT	ATCAGGAATA	AAGTGATATT	GCATAGGAGT	ATTGTATTTT	TATGAATTTT	4380
	ATGCCAGTTG	TTTACATGTA	CTATATATGT	TAAATTAATA	AAAATCATGA	GAAATG	

Seq ID NO: 499 Protein sequence
Protein Accession #: BAA74900.1

	1	11	21	31	41	51	
70	PLVINTLKRF	NLYPEVILAS	WYRIYTKIMD	LIGIQTKICW	TVTRGEGLSL	IESCEGLGDP	60
	ACFYVAVIFI	LNGLMMALFF	IYGTYLSGSR	LGLLVTVLCF	PFNHGECTRV	MWTPPLRESF	120
	SYFFLVQLML	LVTHILRATK	LYRGLIALC	ISNVFFMLPW	QFAQFVLLTQ	IASLFAVYV	180
	GYIDICKLRK	IYIHMISLA	LCFVLMFGNS	MLLTSYYASS	LVIIWIGILAM	KPHFLKINVS	240
	ELSLWVIQGC	FWLFGTVILK	YLTSLKIFGIA	DDAHIGNLLT	SKFFSYKDFD	TLTYTCAAEF	300
75	DFMEKETPLR	YTKTLPLPVV	LUVFVAIVRK	IISDMWGVLA	KQQTHVRKHQ	FDHGLVLYHA	360
	LQLLAYTALG	ILIMRLKSLF	TPHMCVMASL	ICSRQLFGWL	FCKVHPGAIV	FAILAAMSIQ	420
	GSANLQQTWN	IVGEPSNLQP	EELIEWIKYS	TKPDVAFAGA	MPTMASVKLS	ALRPVNVHPH	480
	YEDAGLRART	KIVYSMYSRK	AAEIVKRELI	KLKVNYYILE	ESWCVRRSKP	GCSMPEIWDV	540
	EDPANAGKTP	LCNLVLVKDSK	PHFTTVFQNS	VYKVLVVKE			

Seq ID NO: 500 DNA sequence
Nucleic Acid Accession #: NM_001276.1
Coding sequence: 127..1278

	1	11	21	31	41	51	
85	AGTGGAGTGG	GACAGGTATA	TAAAGGAAGT	ACAGGGCCTG	GGGAAGAGGC	CCTGTCTAGG	60
	TAGCTGGCAC	CAGGAGCCGT	GGGCAAGGGA	AGAGGCCACA	CCCTGCCCTG	CTCTGCTGCA	120

5
10
15
20
25
30

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GCCAGAAATGG GTGTGAAGGC GTCTCAAACA GGCTTTGTGG TCCTGGTGTCT GCTCCAGTGC 180
TGCTCTGCGAT ACAAACTGGT CTGCTACTAC ACCAGCTGGT CCCAGTACCG GGAAGGCGAT 240
GGGAGCTGCT TCCCAGATGC CCTTGACCGC TTCTCTGTGA CCCACATCAT CTACAGCTTT 300
GCCAATATAA GCAACGATCA CATCGACACC TGGGAGTGGG ATGATGTGAC GCTCTACGGC 360
ATGCTCAACA CACTCAAGAA CAGGAACCCC AACCTGAAGA CTCTCTGTCT TGTCCGAGGA 420
TGGAACCTTG GGTCTCAAAG ATTTTCCAAG ATAGCCTCCA ACACCCAGAG TCGCCGGACT 480
TTTCATCAAGT CAGTACCGCC ATTCCTGCGC ACCCATGGCT TTGATGGGCT GGACCTTGCC 540
TGGCTCTACC CTGGACGGAG AGACAAACAG CATTTTACCA CCCTAATCAA GGAATGAAG 600
GCCGAATTTA TAAAGGAAGC CCAGCCAGGG AAAAAGCAGC TCCTGCTCAG CGCAGCACTG 660
TCTGCGGGGA AGGTCAACAT TGACAGCAGC TATGACATTG CCAAGATATC CCAACACCTG 720
GATTTTCATTA GCATCATGAC CTACGATTTT CATGGAGCCT GGCCTGGGAC CACAGGCCAT 780
CACAGTCCCC TGTTCGAGG TCAGGAGGAT GCAAGTCCCT ACAGATTGAG CAACACTGAC 840
TATGCTGTGG GGTACATGTT GAGGCTGGGG GCTCCTGCCA GTAAGCTGGT GATGGGCATC 900
CCCACCTTCG GGAGGAGCTT CACTCTGGCT TCTTCTGAGA CTGGTGTGG AGCCCCAATC 960
TCAGGACCGG GAATTCACAG CCGGTTCCAC AAGGAGGCGG GGACCTTGCT CTACTATGAG 1020
ATCTGTGACT TCTCCGCGG AGCCACAGTC CATAGAACCC TCGGCCAGCA GGTCCCCTAT 1080
GCCACCAAGG GCAACCAAGT GGTAGGATAC GACGACCAGG AAAGCGTCAA AAGCAAGGTG 1140
CAGTACCTGA AGGATAGGCA GCTGGCAGGC GCCATGGTAT GGGCCCTGGA CCTGGATGAC 1200
TTCCAGGGCT CCTTCTGCGG CCAGGATCTG CGCTTCCCTC TCACCAATGC CATCAAGGAT 1260
GCACCTCGTG CAACGTAGCC CTCTGTTCTG CACACAGCAC GGGGGCCAGG GATGCCCCGT 1320
CCCCCTCTGG CTCCAGCTGG CCGGAGCCCT GATCACCTGC CCTGCTGAGT CCCAGGCTGA 1380
GCCTCAGTCT CCCTCCCTTG GGGCCTATGC AGAGGTCCAC AACACACAGA TTTGAGCTCA 1440
GCCCTGGTGG GCAGAGAGGT AGGGATGGGG CTGTGGGGAT AGTGAGGCAT CGCAATGTAA 1500
GACTCGGGAT TAGTACACAC TTGTTGATGA TTAATGGAAA TGTTTACAGA TCCCAAGGCC 1560
TGGCAAGGGA ATTTCTTCAA CTCCCTGCCC CTTAGCCCTC CTTATCAAAG GACACCATT 1620
TGGCAAGCTC TATCACAAG GAGCCAAACA TCCTACAAGA CACAGTGACC ATACTAATTA 1680
TACCCCTGCG AAAGCCCTTC TGAAACCTTC ACTTAGGAAC GTAATCGTGT CCCCTATCCT 1740
ACTTCCCTCT CCTAATTCAC CAGCTGCTCA ATAAAGTACA AGAGTTTAA AGTGTGTTGG 1800
CGCTTTGCTT TGGTCTATCT TTGAGCGCCC ACTAGACCCA CTGAGCTCAC CTCGCCATC 1860
TCTTCTGGGT TCCTTCTCTT GAGCCTTGGG ACCCTGAGC TTGCAGAGAT GAAGCGCCG 1920
ATGTT

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Seq ID NO: 501 Protein sequence
Protein Accession #: NP_001267.1

35
40
45

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1 11 21 31 41 51
| | | | |
MGVKASQTGF VVLVLQCCS AYKLVCYYS WSQYREGDGS CFPDALDRFL CTHIIYSFAN 60
ISNDHIDTWE WNDVTLYGML NTLKNRNPNL KTLLEVGGWN FGSQRFASKIA SNTQSRRTFI 120
KSVPPFLRTH GFDGLDLAWL YPGRDQKHF TTLIKEMKAE FIKEAQPQKK QLLLSAALSA 180
GKVTIDSSVD IAKISQHLDF ISIMTYDFHG AWRGTGHHHS PLFRGQEDAS PDRFSNTDYA 240
VGMYLRLGAP ASKLVMIPT FGRSFTLASS ETGVGAPISG PGIPGRFTKE AGTLAYYEIC 300
DPLRGATVHR TLGQVVPYAT KGNQWVGYDD QESVKSQVQY LKDRQLAGAM VWALDLDFFQ 360
GSFCGQDLRF PLTNAIKDAL AAT

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Seq ID NO: 502 DNA sequence
Nucleic Acid Accession #: NM_006474.1
Coding sequence: 181..669

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55
60
65

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1 11 21 31 41 51
| | | | |
GCTGCCTAGG GTCTGGAAG CTGCGGCACC CTCCCTCTCC GGGGCTCCTG CTCCCACCCC 60
TCCGGCCCCC CCACGCTCGC GCTCCTCCAG GCTGGGCTG TGGCCGCGGT GCTTTTAATT 120
TTCCCCCAGC TCAGAATCTT GCTGCTCGGC CCCAGGAGA GCAACAATC AACGGGAACG 180
ATGTGGAAGG TGTCAGCTCT GCTCTTCGTT TTGGGAAGCG CGTCGCTCTG GGTCTTGGCA 240
GAAGGAGCCA GCACAGGCCA GCCAGAAGAT GACACTGAGA CTACAGGTTT GGAAGGCGGC 300
GTTGCCATGC CAGGTGCCGA AGATGATGTG GTGACTCCAG GAACCAAGCA AGACCGCTAT 360
AAGTCTGGCT TGACAACCTT GGTGGCAACA AGTGTCAACA GTGTAACAGG CATTTCGCATC 420
GAGGATCTGC CAACTTTCAGA AAGCACAGTC CACGCGCAAG AACAAAGTCC AAGCGCCACA 480
GCCTCAAAGC TGGCCACCAG TCACTCCACG GAGAAAGTGG ATGGAGACAC ACAGACACA 540
GTTAGAAAG ATGGTTGTG AACAGTGACC CTGGTTGGAA TCATAGTTGG GGTCTTACTA 600
GCCATCGGTT TCATTGGTGG AATCATCGTT GTGGTTATGC GAAAAATGTC GGAAGGTAC 660
TCGCCCTAAA GAGCTGAAGG GTTACGCCCT GCTTGCCAAC GTGCTTTAAA AAAAGACCGT 720
TTCTGACTCT GTGGCCCTGT CCCTGAGCTC GTGGGGAGAA GATGACCTG GGAACATTG 780
CGGGCCCATC CAGATTCAC GGTGACTTTC CGTTTGCCAA ATTAACCGAG GAAAGACCTT 840
TCACCAGATT TGGTCTTTAA ACTTT

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Seq ID NO: 503 Protein sequence
Protein Accession #: NP_006465.1

70
75

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1 11 21 31 41 51
| | | | |
MWKVSALLFV LGSASLWVLA EGASTGQPED DTETTGLEGG VAMPGAEDDV VTPGTSEDYR 60
KSLTLTLVAT SVNSVTGIRI EDLPTSESTV HAQEQSPSAT ASNVAISHST EKVDGDTQTT 120
VEKDLSTVT LVGIIVGVLL AIGFIGIIV VVMRKMSGRY SP

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Seq ID NO: 504 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 62..895

80
85

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1 11 21 31 41 51
| | | | |
CACTGCTCTG AGAATTGTG AGCAGCCCCT AACAGGCTGT TACTTCACTA CAACTGACGA 60
TATGATCATC TTAATTACT TATTTCTCTT GCTATGGGAA GACACTCAAG GATGGGGATT 120
CAAGGATGGA ATTTTTCATA ACTCCATATG GCTTGAACGA GCAGCCGGTG TGTACCACAG 180
AGAAGCACGG TCTGGCAAT ACAAGCTCAC CTACGCAGAA GCTAAGGCGG TGTGTGAATT 240
TGAAGGCGGC CATCTCGCAA CTTACAAGCA GCTAGAGGCA GCCAGAAAAA TTGGATTTC 300

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TGTCTGTGCT GCTGGATGGA TGGCTAAGGG CAGAGTTGGA TACCCCATTG TGAAGCCAGG 360
 GCCCAACTGT GGATTGGGAA AAACCTGGCAT TATTGATTAT GGAATCCGTC TCAATAGGAG 420
 TGAAAGATGG GATGCCATT GCTACAAACC ACACGCAAAAG GAGTGTGGTG GCGTCTTTAC 480
 AGATCCAAAG CAAATTTTTA AATCTCCAGG CTTCCTCAAAT GAGTACGAAG ATAACCAAAT 540
 CTGCTACTGG CACATAGAC TCAAGTATGG TCAGCGTATT CACCTGAGTT TTTTAGATT 600
 TGACCTTGAA GATGACCCAG GTTGCTTGGC TGATTATGTT GAAATATATG ACAGTTACGA 660
 TGATGTCCAT GGCTTTGTGG GAAGATACCTG TGGAGATGAG CTTCAGATG ACATCATCAG 720
 TACAGGAAAT GTCATGACCT TGAAGTTTCT AAGTGATGCT TCAGTGACAG CTGGAGGTTT 780
 CCAATCAAA TATGTGCAA TGGATCCTGT ATCCAAATCC AGTCAAGGAA AAAATACAAG 840
 TACTACTTCT ACTGGAATA AAACTTTTT AGCTGGAAGA TTTAGCCACT TATAAAAAA 900
 AAAAAAGGA TGATCAAAAC ACACAGTGT TATGTTGGAA TCTTTTGGAA TCCTTTTGAT 960
 CTCACGTGTA TTATTAACAT TTATTATTA TTTTCTAAA TGTGAAAGCA ATACATAATT 1020
 TAGGGAAAT TGGAAATAT AGGAACTTT AAACGAGAAA ATGAAACCTC TCATAATCCC 1080
 ACTGCATAGA AATAACAAGC GTTAACATTT TCATATTTTT TTCTTTCAGT CATTTTTCTA 1140
 TTTGTGGTAT ATGTATATAT GTACCTATAT GTATTTCGAT TTGAAATTTT GGAATCCTGC 1200
 TCTATGTACA GTTTTGTATT ATACTTTTA AATCTTGAAC TTTATAAACA TTTTCTGAAA 1260
 TCATTGATTA TTCTACAAA ACATGATTTT AAACAGCTGT AAAATATTCT ATGATATGAA 1320
 TGTTTTATGC ATTATTAAAG CCTGTCTCTA TTGTTGGAAT TTCAGGTCAT TTTCAATAAT 1380
 ATTGTTGCAA TAAATATCCT TGAACACACA AAAAAAAA AA

Seq ID NO: 505 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 | | | | |
 MIILYLFLL LWEDTQGWGF KDGFHNSIW LERAAGVYHR EARSQKYKLT YAEAKAVCEF 60
 EGGHLATYKQ LEAARKIGHF VCAAGWMAKG RVGYPIVKPG PNCGFGKGTGI IDYGIRLNRS 120
 ERWDAYCYNP HAKECGGVPT DPKQIFKSPG FPNEYEDNQI CYWHIRLKYG QRIHLSFLDF 180
 DLEDDPGCLA DYVEIYDSYD DVHGFVGRYC GDELPPDIIIS TGNVMTLKFLL SDASVTAGGF 240
 QIKYVAMDPV SKSSQGKNYS TTSTGNKNFL AGRFSLH

Seq ID NO: 506 DNA sequence
 Nucleic Acid Accession #: NM_007115.1
 Coding sequence: 69..902

1 11 21 31 41 51
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 CTGACGATAT GATCATCTTA ATTTACTTAT TTCTCTTGCT ATGGGAAGAC ACTCAAGGAT 120
 GGGGATTCAA GGATGGAATT TTTCATAACT CCATATGGCT TGAACGAGCA GCCGGTGTGT 180
 ACCACAGAGA AGCAGCGTCT GGCAATACA AGCTCACCTA CGCAGAAGCT AAGGCGGTGT 240
 GTGAATTGA AGGCGGCCAT CTCGCAACTT ACAAGCAGCT AGAGGCAGCC AGAAAAATTG 300
 GATTTCATGT CTGTCTGTCT GGATGGATGG CTAAGGGCAG AGTTGGATAC CCCATTGTGA 360
 AGCCAGGGCC CAACGTATGA TTGGAAAAA CTGGCATTAT TGATTATGGA ATCCGTCTCA 420
 ATAGGAGTGA AAGATGGGAT GCCTATTGCT ACAACCCACA CGCAAGGAG TGTGGTGGCG 480
 TCTTTACAGA TCCAAAGCGA ATTTTAAAT CTCCAGGCTT CCCAAATGAG TACGAAGATA 540
 ACCAAATCTG CTACTGGCAC ATTAGACTCA AGTATGGTCA GCGTATTCAC CTGAGTTTTT 600
 TAGATTTTGA CCTTGAAGAT GACCCAGGTT GCTTGGCTGA TTATGTTGAA ATATATGACA 660
 GTTACGATGA TGTCCATGCG TTTGTGGGAA GATACTGTGG AGATGAGCTT CCAGATGACA 720
 TCATCAGTAC AGGAAATGTC ATGACCTTGA AGTTTCTAAG TGATGCTTCA GTGACAGCTG 780
 GAGGTTTCCA AATCAAAATAT GTTGCAATGG ATCCTGTATC CAAATCCAGT CAAGGAAAAA 840
 ATACAAGTAC TACTTCTACT GGAAATAAAA ACTTTTATAG TGGAAAGATT AGCCACTTAT 900
 AAAAAAAGAA AAGGATGATC AAAACACACA GTGTTTATGT TGGAACTCTT TGGAACTCCT 960
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 TAAATTAGGG AAAATTGGAA AATATAGGAA ACTTTAAACG AGAAAATGAA ACCTCTCATA 1080
 ATCCCACTGC ATAGAAATAA CAAGCGTTAA CATTTCATA TTTTTTCTT TCAGTCATT 1140
 TTGTATTTGT GGTATATGTA TATATGTACC TATATGTATT TGCATTGAA ATTTTGGAA 1200
 CCTGCTCTAT GTACAGTTT GTATTATACT TTTTAAATCT TGAACCTTAT GAACATTTTC 1260
 TGAAATCATT GATTATTCTA CAAAACATG ATTTTAAACA GCTGTAAAT ATTCTATGAT 1320
 ATGAATGTTT TATGCATTAT TTAAGCCTGT CTCTATTGTT GGAATTCAG GTCATTTTCA 1380
 TAAATATTGT TGCAATAAAT ATCCTTCGGA ATTC

Seq ID NO: 507 Protein sequence
 Protein Accession #: NP_009046.1

1 11 21 31 41 51
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 MIILYLFLL LWEDTQGWGF KDGFHNSIW LERAAGVYHR EARSQKYKLT YAEAKAVCEF 60
 EGGHLATYKQ LEAARKIGHF VCAAGWMAKG RVGYPIVKPG PNXXFGKGTGI IDYGIRLNRS 120
 ERWDAYCYNP HAKECGGVPT DPKRIFKSPG FPNEYEDNQI CYWHIRLKYG QRIHLSFLDF 180
 DLEDDPGCLA DYVEIYDSYD DVHGFVGRYC GDELPPDIIIS TGNVMTLKFLL SDASVTAGGF 240
 QIKYVAMDPV SKSSQGKNYS TTSTGNKNFL AGRFSLH

Seq ID NO: 508 DNA sequence
 Nucleic Acid Accession #: NM_001044.1
 Coding sequence: 129..1991

1 11 21 31 41 51
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 ACCGCTCCGG AGCGGGAGGG GAGGCTTCGC GGAACGCTCT CGGCGCCAGG ACTCGCGTGC 60
 AAAGCCCAGG CCCGGGCGGC CAGACCAAGA GGAAGAAGC ACAGAATTCC TCAACTCCCA 120
 GTGTGCCCAT GAGTAAGAGC AAATGCTCCG TGGGACTCAT GTCTTCCGTG GTGGCCCCGG 180
 CTAAGGAGCC CAATGCCGTG GGCCCGAAGG AGGTGGAGCT CATCTTGTG AAGGAGCAGA 240
 ACGGAGTGCA GCTCACCAAG TCCACCCTCA CCAACCCGCG GCAGAGCCCC GTGGAGGCC 300
 AGGATCGGGA GACCTGGGCG AAGAAGATCG ACTTCTCTCT GTCCGTCATT GGCTTTGCTG 360
 TGGACCTGCG CAACGCTCTG CGGTTCCCTT ACCTGTGCTA CAAAATGGT GCGGTGCTCT 420

	TCTCTGGTCCC	CTACTGTGCTC	TTCATGGTCA	TTGCTGGGAT	GCCACTTTTC	TACATGGAGC	480
	TGGCCCTCGG	CCAGTTCAAC	AGGGAAGGGG	CCGCTGGTGT	CTGGAAGATC	TGCCCCATAC	540
	TGAAGGTGT	GGGCTTCAAG	GTCACTCTCA	TCTCACTGTA	TGTCGGCTTC	TTCTACAACG	600
5	TTCATCATCG	CTGGGCGCTG	CACATATCTCT	TCTCTCTCCT	CACCAACGAG	CTCCCTCGGA	660
	TCCACTGCAA	CAACTCCTTG	AACAGCCCCA	ACTGCTCGGA	TGCCCATCCT	GGTGACTCCA	720
	GTGGAGACAG	CTCGGCGCTC	AACGACACTT	TTGGGACCAC	ACCTGCTGCC	GAGTACTTTG	780
	AACGTGGCGT	GCTGACCTTC	CACCGAGAGC	ATGGCATCGA	CGACCTGGGG	CCTCCGCGGT	840
	GGCAGCTCAC	AGCCTGCTCG	GTGCTGGTCA	TGCTGCTGCT	CTACTTCAGC	CTCTGGAAGG	900
	GGGTGAAGAC	CTCAGGGAAG	GTGGTATGGA	TCACAGCCAC	CATGCCATAC	GTGGTCTCTA	960
10	CTGCCCTGCT	CCTGCGTGGG	GTCACCTTCC	CTGGAGCCAT	AGACGGCATC	AGAGCATACC	1020
	TGAGCGTTGA	CTTCTACCGG	CTCTGCGAGG	CGTCTGTTTG	GATTGACGCG	GCCACCCAGG	1080
	TGTGCTTCTC	CCTGGGCGTG	GGGTTCCGGG	TGCTGATCGC	CTTCTCCAGC	TACAACAAGT	1140
	TCACCAACAA	CTGCTACAGG	GACGCGATTG	TCACCACCTC	CATCAACTCC	CTGACGAGCT	1200
15	TCTCTCTCGG	CTTCGTCGTC	TTCTCCTTCC	TGGGGTACAT	GGCACAGAAG	CACAGTGTGC	1260
	CCATCGGGGA	CGTGCCCAAG	GACGGGCCAG	GGCTGATCTT	CATCATCTAC	CCGGAAGCCA	1320
	TGCCCCAGCT	CCCTCTGTCC	TCAGCCTGGG	CCGTGGTCTT	CTTCATCATG	CTGCTCACCC	1380
	TGGGTATCGA	CAGCGCCATG	GGTGGTATGG	AGTCAGTGAT	CACCGGGCTC	ATCGATGAGT	1440
	TCCAGCTGCT	GCACAGACAC	CGTGAGCTCT	TCACGCTCTT	CATCGTCTTG	GCGACCTTCC	1500
20	TCTGTCCCT	GTTCGTGCGT	ACCAACGGTG	GCATCTACGT	CTTCACGCTC	CTGGACCATT	1560
	TTGACGCCGG	CACGTCCAAT	CTCTTTGGAG	TGCTCATCGA	AGCCATCGGA	GTGGCCTGGT	1620
	TCTATGGTGT	TGGGCAGTTG	AGCGACGACA	TCCAGCAGAT	GACCGGGCAG	CGGCCACAGC	1680
	TGTACTGGCG	GCTGTGCTGG	AAGCTGGTCA	GCCCCTGCTT	TCTCCTGTTC	GTGGTCTGTG	1740
	TGAGCATTTG	GACCTTCAGA	CCCCCCCCT	ACGGAGCCTA	CATCTTCCCC	GACTGGGCCA	1800
25	ACGCGCTGGG	CTGGGTCAAT	GCCACATCCT	CCATGGCCAT	GGTGCCCATC	TATGCGGCCT	1860
	ACAAGTTCTG	CAGCTGCGCT	GGGTCTCTTC	GAGAGAAACT	GGCCTACGCC	ATTGCACCCG	1920
	AGAAGGACCG	TGAGCTGGTG	GACAGAGGGG	AGGTGCGCCA	GTTACGCTC	CGCCACTGGC	1980
	TCAAGGTGTA	GAGGGAGCAG	AGACGAAGAC	CCCAGGAAGT	CATCTGCAA	TGGGAGAGAC	2040
	ACGAACAAAC	CAAGGAAATC	TAAGTTTCGA	GAGAAAGGAG	GGCAACTTCT	ACTCTTCAAC	2100
30	CTCTACTGAA	AACACAAATC	ACAAAGCAGA	AGACTCTCTT	CTTCTGACTG	TTTACACCTT	2160
	TCCGTGCCGG	GAGCGCACCT	CGCCGTGTCT	TGTGTGCTG	TAATAACGAC	GTAGATCTGT	2220
	CGAGCGAGGT	CCACCCCGTT	GTGTCTCTTG	CAGGGCAGAA	AAACGTCTAA	CTTCATGCTG	2280
	TCTGTGTGAG	GCTCCCTCCC	TCCCTGCTCC	CTGCTCCCGG	CTCTGAGGCT	GCCCCAGGGG	2340
	CACGTGTGTT	TCAGGCGGGG	ATCACGATCC	TTGTAGACGC	ACCTGCTGAG	AATCCCCGTG	2400
35	CTCACAGTAG	CTTCTAGAC	CATTTACTTT	GCCCCATATTA	AAAAGCCAAG	TGTCCTGCTT	2460
	GGTTTAGCTG	TGCAGAAGGT	GAAATGGAGG	AAACCACAAA	TTCATGCAAA	GTCTTTTCCC	2520
	GATGCGTGGC	TCCCAGCAGA	GGCCGTAAAT	TGAGCGTTCA	GTTGACACAT	TGCACACACA	2580
	GTCTGTTTCA	AGGCATTGGA	GGATGGGGGT	CCTGGTATGT	CTCACCAGGA	AATTCTGTTT	2640
	ATGTTCTTGC	AGCAGAGAGA	AATAAACTC	CTTGAAACCA	GCTCAGGCTA	CTGCCACTCA	2700
40	GGCAGCCTGT	GGGTCTCTGT	GGTGTAGGGA	ACGGCCTGAG	AGGAGCGTGT	CCTATCCCCG	2760
	GACGCATGCA	GGCCCCCAG	AGGAGCGTGT	CCTATCCCCG	GACGCATGCA	GGGCCCCCAC	2820
	AGGAGCATGT	CCTATCCCCG	GACGCATGCA	GGGCCCCCAC	AGGAGCGTGT	ACTACCCACG	2880
	AACGCATGCA	GGGCCCCCAC	AGGAGCGTGT	ACTACCCACG	GACGCATGCA	GGGCCCCCAC	2940
	TGGAGCGTGT	ACTACCCACG	GACGCATGCA	GGGCCCCCAC	AGGAGCGTGT	CCTATCCCCG	3000
45	GACCGGACGC	ATGCAGGGCC	CCCCACAGGAG	CGTGTACTAC	CCCAGGACGC	ATGCAGGGCC	3060
	CCCCACAGGAG	CGTGTACTAC	CCCCACAGGAG	ATGCAGGGCC	CCCCACAGGAG	CGTGTACTAC	3120
	CCCAGGACGC	ATGCAGGGCC	CCCATGCAGG	CAGCCTGCAG	ACCAACACTC	TGCCTGGCCT	3180
	TGAGCCGTGA	CCTCCAGGAA	GGGACCCAC	TGGAATTTTA	TTTCTCTCAG	GTGCGTGCCA	3240
	CATCAATAAC	AACAGTTTTT	ATGTTTGCGA	ATGGCTTTTT	AAAATCATAT	TTACCTGTGA	3300
50	ATCAAACAA	ATTCAAGAA	GCAGTATCCG	CGAGCCTGCT	TGCTGATATT	GCAGTTTTTG	3360
	TTTACAAGAA	TAATTAGCAA	TACTGAGTGA	AGGATGTTGG	CCAAAAGCTG	CTTTCCATGG	3420
	CACACTGCCC	TCTGCCACTG	ACAGGAAAGT	GGATGCCATA	GTTTGAATTC	ATGCCTCAAG	3480
	TGGTGGGGG	TGCCCTACGT	CTGCCCGAGG	GCAGGGGCGG	TGCAGGGCCA	GTCATGGCTG	3540
	TCCCTGCAA	GTGGACGTGG	GCTCCAGGGA	CTGGAGTGTA	ATGCTCGGTG	GGAGCCGTCA	3600
55	GCCTGTGAAC	TGCCAGGCGG	CTGCAGTTAG	CACAGAGGAT	GGCTTCCCCA	TGCTCTCTG	3660
	GGGAGGGGCA	CAGAGGACCG	CTTCCCCATC	GCCTTCTGGC	CGCTGCAGTC	AGCACAGAGA	3720
	GGCGCTTCCC	CATTGCCTTC	TGGGGAGGGA	CACAGAGGAC	AGTTTCCCCA	TGCGCTTCTG	3780
	GTTGTGTAAG	ACAGCACAGA	GAGCGGCTTC	CCCATCGCCT	TCTGGGGAGG	GGCTCCGTGT	3840
60	AGCAACCCAG	GTGTTGTCCG	TGTCTGTTGA	CCAATCTCTA	TTCAGCATCG	TGTGGGTCCC	3900
	TAAGCACAA	AAAAGACATC	CACAATGGAA	AAAAAAAAG	GAATTC		

Seq ID NO: 509 Protein sequence
Protein Accession #: NP_001035.1

65	1	11	21	31	41	51	
	MSKSKCSVGL	MSSVVAPAKE	PNAVGPKEVE	LILVKEQNGV	QLTSSTLTNP	RQSPVEAQDR	60
	ETWKKIDFL	LSVIGFAVDL	ANVWRPPYLC	YKNGGGAFLV	PYLLFMVIAG	MPLFYMELAL	120
	QQFNREGAAG	VWKICPILKG	VGFTVILISL	YVGFFYNVIL	AWALHYLFSS	FTTELPWIHC	180
70	NNSWNPNCS	DAHPPDSSGD	SSGLNDTFGT	TPAAEYFERG	VLHLHQSHGI	DDLGPFRWQL	240
	TACLVLVIVL	LYFSLWKGVK	TSKVVVWITA	TMPIVVLTLA	LLRGVTLPGA	IDGIRAYLSV	300
	DFYRLCEASV	WIDAATQVCF	SLGVGFGVLI	AFSSYNKFTN	NCYRDAIVTT	SINSLTSFSS	360
	GFVVSFSLGY	MAQKHSVPIG	DVAKDGPGLI	FIIYPEAIAT	LPLSSAWAVV	FFIMLLTLGI	420
	DSAMGMESEV	ITGLIDEFQL	LHRHRELFTL	FIVLATFLLS	LFCVTNGGIY	VFTLLDHFAA	480
75	GTSILFGVLI	EAIGVAWFYQ	VQQFSDDIQQ	MTGQRPSLYW	RLCWKLVSFC	FLLFVVVSI	540
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	RELVDREGEV	QFTLRHNLKV					

Seq ID NO: 510 DNA sequence
Nucleic Acid Accession #: NM_001216.1
Coding sequence: 43..1422

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	CTGTCACTGC	TGCTTCTGAT	GCCTGTCCAT	CCCCAGAGGT	TGCCCCGGAT	GCAGGAGGAT	180
	TCCCCCTTGG	GAGGAGGCTC	TTCTGGGGAA	GATGACCCAC	TGGGCGAGGA	GGATCTGCCC	240

5 AGTGAAGAGG ATTCACCCAG AGAGGAGGAT CCACCCGGAG AGGAGGATCT ACCTGGAGAG 300
 GAGGATCTAC CTGGAGAGGA GGATCTACCT GAAGTTAAGC CTAAATCAGA AGAAGAGGGC 360
 TCCCTGAAGT TAGAGGATCT ACCTACTGTT GAGGCTCCTG GAGATCCTCA AGAACCCCGAG 420
 AATAATGCCC ACAGGGACAA AGAAGGGGAT GACCCAGATC ATTGGCGCTA TGGAGGCGAC 480
 CGCCCTGGC CGCCGGGTGTC CCCAGCCTGC CGCGGGCGCT TCCAGTCCCC GGTGGATATC 540
 CGCCCCCAGC TCGCCGCTTT CTGCCCGGCC CTGCCCGCCC TGGAACTCCT GGGCTTCCAG 600
 CTCCCGCCGC TCCAGAACT GCGCCTGCGC AACAAATGGCC ACAGTGTGCA ACTGACCCCTG 660
 CCTCTGGGC TAGAGATGGC TCTGGGTCCC GGGCGGGAGT ACCGGGCTCT GCAGCTGCAT 720
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 10 CCTGCGAGA TCCACGTGGT TCACCTCAGC ACCGCCTTTC CCAGAGTTGA CGAGGCCTTG 840
 GGGCGCCCGG GAGGCCTGGC CGTGTGGCC GCCTTTCTGG AGGAGGGCCC GGAAGAAAC 900
 AGTGCCTATG AGCAGTTGCT GTCTCGCTTG GAAGAAATCG CTGAGGAAGG CTCAGAGACT 960
 CAGGTCCAG GACTGGACAT ATCTGCACTC CTGCCCTCTG ACTTCAGCCG CTACTTCCAA 1020
 15 TATGAGGGGT CTCTGACTAC ACCGCCCTGT GCCCAGGGTG TCATCTGGAC TGTGTTTAA 1080
 CAGACAGTGA TGCTGAGTGC TAAGCAGCTC CACACCTCT CTGACACCCT GTGGGGACCT 1140
 GGTGACTCTC GGCTACAGCT GAACCTCCGA GCGACGAGC CTTTGAATGG GCGAGTGATT 1200
 GAGGCCTCCT TCCCTGCTGG AGTGGACAGC AGTCTCGGG CTGCTGAGCC AGTCCAGCTG 1260
 AATTCCTGCC TGGCTGCTGG TGACATCCTA GCCCTGGTTT TTGGCCTCCT TTTTGTGTG 1320
 20 ACCAGCGTCG CGTTCCTTGT GCAGATGAGA AGGCAGACA GAAGGGGAAC CAAAGGGGGT 1380
 GTGAGTACC GCCCAGCAGA GGTAGCCGAG ACTGGAGCCT AGAGGCTGGA TCTTGGAGAA 1440
 TGTGAAGAG CAGCCAGAGG CATCTGAGG GGAGCCGTA ACTGTCTGT CCTGTCTATT 1500
 ATGCCACTTC CTTTAACTG CCAAGAAAT TTTTAAATA AATATTATA AT

Seq ID NO: 511 Protein sequence
 Protein Accession #: NP_001207.1

30 1 11 21 31 41 51
 MAPLCPSWL PLLIPAPAPG LTVQLLSLL LLMPVHPQL PRMQEDSPLG GSSGEDDPL 60
 GEEDLPSEED SPREEDPPGE EDLPGEEDLP GEEDLPVEKP KSEEEGSLKL EDLPTVEAPG 120
 DPQEPQNNH RKEGDDQSH WRYGGDPPWP RVSPACAGRF QSPVDIRPOL AAFCPALRPL 180
 ELLGFLQPL PBLRLRNNGH SVQLTLPPGL EMALGPGRY RALQLHLHWG AGRPGSEHT 240
 VEGHREPAEI HVVHLSTAFV RVDEALGRPG GLAVLAAFL EGPENSAEY QLLSLREEIA 300
 35 EEGSETQVPG LDISALLPSD FSRFYQYEGS LTPPCAQGV IWTVFNQTM LSAQLHLTL 360
 DTLWGPDSR LQNFNFRATQ LNRGRVIRASF PAGVDSFRA AEPVQLNSCL AAGDILALVF 420
 GLLFAVTSVA FLVQMRQRH RGTGKGVSYR PAEVAETGA

Seq ID NO: 512 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..3978

45 1 11 21 31 41 51
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 TTTGCAGAAA GATATGACCC CAGCCTGAAG ACCATGATCC CAGTGCAGAC CTGTGCAAGG 120
 TTAGCACCCA ACCCGGTGGA TGATGCCGGG CTACTCTCCT TCGCCACATT TTCCTGGCTC 180
 ACCCGGTGTA TGGTGAAGG CTACCGGCAA AGGCTGACCG TAGACACCCT GCCCCATTG 240
 TCGACATATG ACTCATCTGA CACCAATGCC AAAAGATTTC GAGTCCTTTG GGATGAAGAG 300
 50 GTAGCAAGGG TGGTCTCTGA GAAGGCCTCT CTGAGCCACG TGGTGTGGAA ATTCCAGAGG 360
 ACACGCGTGT TGATGACAT CGTGGCCAAC ATCCTGTGCA TCATCATGGC AGCCATAGGG 420
 CCGACAGTTC TCATTACCA AATCCTCCAG CAGACTGAGA GGACCTCTGG GAAAGTCTGG 480
 GTTGGCATTG GACTGTGCT AGCCCTTTTT GCCACCGAGT TTACCAAAGT CTTCTTTTGG 540
 GCCCTTGGCT GAGCCATCAA CTACCGCACG GCCATCCGGT TGAAGGTGGC GCTCTCCACC 600
 TTTGTTTTTG AAAACCTAGT GTCTTCAAG ACATTGACCC ACATCTCTGT TGGCGAGGTG 660
 55 CTCATATATC TGTCAGTGA TAGCTATTCT TTGTTTGAAG CTGCCTTGT TTGTCTTTG 720
 CCAGCCACCA TCCCGATCCT AATGGTCTTT TGTGCGCGCT ACGCCTTTT CATTCCTGGG 780
 CCCACAGCTC TCATCGGGAT ATCAGTGTAT GTCATATTCA TACCCGTCCA GATGTTTATG 840
 GCCAAGCTCA ATTCAGCTTT CCGAAGGTCA GCAATTTTGG TGACAGACAA GCGAGTTCAG 900
 60 ACAATGAATG AGTTTCTGAC CTGCATCAGG CTGATCAAAA TGTATGCCTG GGAGAAATCT 960
 TTTACCAACA CTATCCAAGA TATAAAGAGG AGGGAAGAA AATTACTGGA AAAAGCTGGA 1020
 TTTGTCCAAA GTGGAACTC TGCCCTGGCC CCCATCGTGT CCACCATAGC CATCGTGTG 1080
 ACATTATCCT GCCACATCCT CTTGAGACGC AAATCAACCG CACCCGTGGC ATTTAGTGTG 1140
 ATTGCCATGT TTAATGTAAT GAAGTTTTTC ATTGCAATCT TGCCCTTCTC CATCAAAGCA 1200
 65 ATGGCTGAAG CGAATGTCTC TCTAAGGAGA ATGAAGAAAA TTCTCATAGA TAAAAGCCCC 1260
 CCATCTTACA TCACCCAACC AGAAGACCCA GATACTGTCT TGCTTTTAGC AAATGCCACC 1320
 TTGACATGGG AGCATGAAGC CAGCAGGAAA AGTACCCCAA AGAAATTGCA GAACCAAGAA 1380
 AGGCATTAT GCAAGAAACA GAGGTGAGAG GCATACAGTG AGAGGAGTCC ACCAGCCAAG 1440
 GGAGCCACTG GCCCAGAGGA GCAAGGTGAC AGCCTCAAA CCGTTCTGCA CAGCATAAGC 1500
 70 TTTGTGGTGA GAAAGTTATG TCGTTATCCC GAAGCCGAGC TCCTGGCTTG GAGGTGGCCA 1560
 GCAGTGTGTT TTTGGAGAA CATCAGAGGA TACAGGCCTC ATGGATTTTC TGCTAAAGAC 1620
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 GCCAAATACC TTGGGAAGAT CTTGGGAATA TGTGGGAATG TGGGAAGTGG AAAGAGCTCC 1740
 CTCCTTGCAG CTCCTCTAGG ACAGATGCAG CTGCAGAAAG GGGTGGTGGC AGTCAATGGA 1800
 75 ACTTTGGCCT ACGTTTCACT CAGGCATGG ATCTTTATG GAAATGTGAG AGAAAACATA 1860
 CTCTTTGGAG AAAAGTATGA TCACCAAGG TATCAGCACA CAGTCCCGCT CTGTGGCCTC 1920
 CAGAGGAGC TGAGCAACCT CCCCTATGGA GACCTGACTG AGATTGGGGA GCGGGGCCCTC 1980
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 CAGCTCTACC TGCTGGACGA CCCCTGTCTG CCGGTGGACG CCCACGTGGG GAAGCACGTC 2100
 TTTGAGGAGT GCATTAAAGG GAGGCTCAGG GGAAGACAG TCGTCTTGGT GACCCACCAG 2160
 80 CTACAGTTCT TAGATCTTGT TGTGAAGTT ATTTTATTAG AAGATGGAGA GATTTGTGAA 2220
 AAGGGAACCC ACAGGAGTT AATGGAGGAG AGAGGGCGCT ATGCAAAACT GATTCACAAC 2280
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 TTCAAGGAGA GCCCTGCTGA GAGAGAGGAA GATGCTGGTA TAATCGGTA CCTCCTTTCT 2400
 CTCTTCACTG TGTTCCTCTT CCTCCTGATG ATTGGCAGCG CTGCCCTTCA CAACTGGTGG 2460
 85 CTGGGTCTCT GGTGTGACAA GGGCTCACGG ATGACCTGTG GGGCCAGGG CAACAGGACC 2520
 ATGTGTGAGG TCGGCGCGGT GCTGGCAGAC ATCGGTGAGC ATGTGTACCA GTGGGTGTAC 2580
 ACTGCAAGCA TGGTGTTCAT GCTGGTGTGTT GCGCTCACCA AAGGCTTCGT CTTACCAAG 2640

	ACCACACTGA	TGGCATCTC	CTCTCTGCAT	GACACGGTGT	TTGATAAGAT	CTTAAAGAGC	2700
	CCAATGAGTT	TCTTTGACAC	GACTCCCCT	GGCAGGCTAA	TGAACCGTTT	TTCCAAGGAT	2760
	ATGGACGAGC	TGGATGTGAG	GCTGCCGTTT	CACGCAGAGA	ACTTCTGCA	GCAGTTTTTT	2820
	ATGGTGGTGT	TTATTTCTCGT	GATCTTGGCT	GCTGTGTTTC	CTGCTGTCTT	TTTAGTCTGT	2880
5	GCCAGCCTTG	CTGTAGGCTT	CTTCATTCTG	TTACGCATTT	TCCACAGAGG	AGTCCAGGAG	2940
	CTCAAGAAGG	TGGAGAATGT	CAGCCGGTCA	CCCTGGTTCA	CCCACATCAC	CTCCTCCATG	3000
	CAGGCGCTGG	GCATCATTTCA	CGCCTATGGC	AAGAAGGAGA	GCTGCATCAC	CTATACTTCA	3060
	TCCAAAGGCC	TGTCAATTGT	ATACATCATC	CAGCTGAGCG	GACTGCTCCA	AGTGTGTGTG	3120
10	CGAACGGGAA	CAGAGACGCA	AGCCAAATTC	ACCTCCGTGG	AGCTGCTCAG	GGAATACATT	3180
	TCGACCTGTG	TTCCTGAATG	CACTCATCCC	CTCAAAGTGG	GGACCTGTCC	CAAGGACTGG	3240
	CCCAGCTGTG	GGGAGATCAC	CTTCAGAGAC	TATCAGATGA	GATACAGAGA	CAACACCCCC	3300
	CTTGTCTCG	ACAGCCTGAA	CTTGAACATA	CAAAGTGGGC	AGACAGTCCG	GATTGTTGGA	3360
	AGAACAGGTT	CCGGAAAGTC	ATCGTTAGGA	ATGGCTTTGT	TTCGTCTGGT	GGAGCCAGCC	3420
15	AGTGGCACAA	TCTTTATTGA	TGAGTGGAT	ATCTGCATTC	TCAGCTTGGG	AGACCTCAGA	3480
	ACCAAGCTGA	CTGTGATCCC	ACAGGATCCT	GTCTGTGTTG	TAGGTACAGT	AAGGTACAAC	3540
	TTGGATCCCT	TTGAGAGTCA	CACCGATGAG	ATGCTCTGGC	AGGTCTTGGG	GAGAACATTC	3600
	ATGAGAGACA	CAATAATGAA	ACTCCAGGAA	AAATTACAGG	CAGAACTCAC	AGAAATGGA	3660
	GAAACTTCT	CAGTAGGGGA	ACGTCAGCTG	CTTTGTGTGG	CCCGAGCTCT	TCTCCGTAAT	3720
20	TCAAAGATCA	TTCTCCTTGA	TGAAGCCACC	GCCTCTATGG	ACTCCAAGAC	TGACACCCCTG	3780
	GTTCAGAAC	CCATCAAGAA	TGCCTTCAAG	GGCTGCACCTG	TGCTGACCAT	CGCCACCCGC	3840
	CTCAACACAG	TCTCAACTG	CGATCACGTC	CTGGTTATGG	AAAATGGGAA	GGTGATTGAG	3900
	TTTGACAAGC	CTGAAGTCTT	TGCAGAGAAG	CCAGATTCTG	CATTTCGGAT	GTTACTAGCA	3960
	GCAGAAGTCA	GATTGTAG					

Seq ID NO: 513 Protein sequence
Protein Accession #: Eos sequence

	1	11	21	31	41	51	
30	MVGE GPY LIS	DL DQR GRR RS	FAERY DPS LK	TMIPVR PCAR	LAPNPVDDAG	LLSFATFSWL	60
	TPVMVKGYRQ	RLTVDTL PPL	STYDSSDTNA	KRFRVLWDEE	VARVGPEKAS	LSHV VWK FQR	120
	TRVLMDIVAN	ILCIIMAAIG	PTVLIHQILQ	QTER TSGKVW	VGIGLCIALF	ATEPTK VFFW	180
	ALAWAINVRT	AIRLKV ALST	LVFENLV SFK	TLTHISVGEV	LNILSSDSYS	LFEALFCPL	240
	PATIPILMV F	CAAYAFFILG	PTALIGISVY	VIFIPVQMF M	AKLNSAFRRS	AILVTDKRVQ	300
35	TMNEFLT CIR	LIMYAW EK S	FTNTIQDIRR	RERKLEKAG	FVQSGNSALA	PIVSTIAIVL	360
	TLSCHILLRR	KLTA PVA FS V	IAMFNVMKFS	IAILPFSIKA	MAEANVSLRR	MKKILIDKSP	420
	PSYITQPEDP	DTVLLANAT	LWHEHASRK	STPKKLQNKQ	RHLCKKQ RSE	AYSERSPPAK	480
	GATGPPEQSD	SLKSVLHSIS	FVVRKLC RYP	EAQLLAWRWP	AVFVGRIIRG	YRPHGFS AKD	540
	KDESRRLLTW	PQEVDR TQRA	AKYLKGLIGI	CGNVGSGKSS	LLAALLGQM Q	LQKGVVAVNG	600
40	TLAYVQQAW	IFHGNVRENI	LFGEKYDHQR	YQHTVRVCG L	QKDLNLPY G	DLTEIGERGL	660
	NLSGGQRQRI	SLARAVYSDR	QLYLLDDPLS	AVDAHVGKHV	FEECIKKTLR	GKTVVLVTHQ	720
	LQFLESCDEV	ILLEDGEICE	KGTHKELMEE	RGRYAKLIHN	LRGLQFKDPE	HLYNAMVEA	780
	FKESPAEREE	DAGIIGYLLS	LFTVFLFLM	IGSAAFSNWW	LGLWLDKGRS	MTCGPQGNRT	840
	MCEVGA VLAD	IGQHVYQWVY	TASMVFM LVF	GVTKG FVFTK	TTLMASSSLH	DTVFDKILKS	900
45	PMSFFDTTPT	GRLMNRFSKD	MDEL DVRLPF	HAENFLQ QFF	MVVFILVILA	AVFPAVLLV V	960
	ASLAVGFFIL	LRIFHRGQVE	LKKVENVSRS	PWFTHITSSM	OGLGIIHAYG	KKESCITYTS	1020
	SKGLSLSYII	QLSGLLQVCV	RTGTETQAKF	TSVELLREYI	STCVPECTHP	LKVGTCPKDW	1080
	PSCGEITFRD	YQMR YRDNT P	LVLD SLNLNI	QSGQTVGIVG	RTGSGKSSLG	MALFRLVEPA	1140
	SGTIPIDEVD	ICILSLEDLR	TKLTVIPQDP	VLFVGT VRYN	LDPFESH TDE	MLWQVLERTF	1200
50	MRDTIMKLPE	KLQAEVTENG	ENFSVGERQL	LCVARALLRN	SKIILLDEAT	ASMSKTDTL	1260
	VQNTIKDAFK	GCTVLTIAHR	LNTVLNCDHV	LVMENGKVIE	FDKPEVLAEK	PDSAFAMLLA	1320
	AEVRL						

Seq ID NO: 514 DNA sequence
Nucleic Acid Accession #: Z31560
Coding sequence: 1-966

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	ACTTCGCGGG	CGCGCGCGCG	CAACTCCACC	GCGGCGGCGG	CCGCGCGCAA	CCAGAAAAAC	120
	AGCCCGGACC	CGCTAAGCG	GCCATGAAT	GCCTTCATGG	TGTGGTCCCG	CGGGCAGCGG	180
	CGCAAGATGG	CCCAGGAGAA	CCCCAAGATG	CACAACTCGG	AGATCAGCAA	GCGCCTGGGC	240
	GCCGAGTGGA	AACITTTTGT	GGAGACGGAG	AAGCGGCCGT	TCATCGACGA	GGCTAAGCGG	300
65	CTGCGAGCGC	TGCACATGAA	GGAGCACCCG	GATTATAAAT	ACCGGCCCCG	GCGGAAAAAC	360
	AAGACGCTCA	TGAAGAAGGA	TAAGTACACG	CTGCCCGGCG	GGCTGCTGGC	CCCCGGCGGC	420
	AATAGCATGG	CGAGCGGGGT	CGGGGTGGGC	GCCGGCCTGG	GCGCGGGCGT	GAACCAGCGC	480
	ATGGACAGTT	ACGCGCACAT	GAACGGCTGG	AGCAACGGCA	GCTACAGCAT	GATGCAGGAC	540
	CAGCTGGGCT	ACCCGCAGCA	CCCGGCCCTC	AATGCGCACG	GCGCAGCGCA	GATGCAGCCC	600
70	ATGCACCGCT	ACGACGTGAG	CGCCCTGCAG	TACAACTCCA	TGACCAGCTC	GCAGACCTAC	660
	ATGAACGGCT	CGCCACCTA	CAGCATGTCC	TACTCGCAGC	AGGGCACCCC	TGGCATGGCT	720
	CTTGGCTCCA	TGGGTTCGTT	GGTCAAGTCC	GAGGCCAGCT	CCAGCCCCCC	TGTGTTTACC	780
	TCTTCTCTCC	ACTCCAGGGC	GCCCTGCCAG	GCCGGGGACC	TCCGGGACAT	GATCAGCATG	840
	TATCTCCCCG	GCGCCGAGGT	GCCGGAACCC	GCCGCCCCCA	GCAGACTTCA	CATGTCCTCAG	900
75	CACTACCAGA	GCGGCCCGGT	GCCCGGCACG	GCCATTAACG	GCACACTGCC	CCTCTCACAC	960
	ATGTGAGGGC	CGGACAGCGA	ACTGGAGGGG	GGAGAAATTT	TCAAAGAAAA	ACGAGGGGAA	1020
	TGGGAGGGGT	GCAAAAGAGG	AGAGTAAGAA	ACAGCATGGA	GAAAACCCGG	TACGCTCAAA	1080
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Seq ID NO: 515 Protein sequence
Protein Accession #: CAA83435

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	RKMAQENPKM	HNSEISKRLG	AEWKLLSETE	KRPFFIDEAKR	LRALHMKEHP	DYKYRPRRKT	120
	KTLMKDKKYT	LPGGLLAPGG	NSMASGVGVG	AGLGAGVNRQ	MDSYAHMNGW	SNGSYSMMQD	180

QLGYPQHPL NAHGAQMOP MHRVDVSALQ YNSMTSSQTY MNGSPYMS YSQQGTGMA 240
 LGSMGSSVKS EASSSPFVVT SSSHSRAPCQ AGDLRDMISM YLPGAEPPEP AAPSLHMSQ 300
 HYQSGVPVPT AINGTLPLSH M

Seq ID NO: 516 DNA sequence
 Nucleic Acid Accession #: U91618
 Coding sequence: 29..541

1 11 21 31 41 51
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 AGCATTAGAA GCAGATTTCT TGACCAATAT GCATACATCA AAGATTAGTA AAGCACATGT 180
 TCCCTCTTGG AAGATGACTC TGCTAAATGT TTGCAGTCTT GTAAATAATT TGAACAGCCC 240
 AGCTGAGGAA ACAGGAGAAG TTCATGAAAG GGAGCTTGTT GCAAGAAGGA AACTTCTCTAC 300
 TGCTTTAGAT GGTCTTAGCT TGGAAAGCAAT GTTGACAAAT TACCAGCTCC ACAAATCTG 360
 TCACAGCAGG GCTTTTCAAC ACTGGGAGTT AATCCAGGAA GATATCTTGT ATACTGGAAA 420
 TGACAAAAAT GGAAAGGAAG AAGTCATAAA GAGAAAAATT CCTTATATTC TGAACCGGCA 480
 GCTGTATGAG AATAAACCCA GAAGACCCCTA CATACTCAAA AGAGATTCTT ACTATTACTG 540
 AGAGAATAAA TCATTATTAT ACATGTGATG GTGATTCAAT ATCCCTTAAT TAAATATCAA 600
 ATTAATTTTG TGTGAAAATG TGACAAACAC ACTTATCTGT CTCTTCTACA ATTGTGGTTT 660
 ATTGAATGTG TTTTCTGCA CTAATAGAAA TTAGACTAAG TGTTTTCAA TAAATCTAAA 720
 TCTTCAAAAA AAAAAAAAAA AAATGGGGCC GCAATT

Seq ID NO: 517 Protein sequence
 Protein Accession #: AAB50564

1 11 21 31 41 51
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Seq ID NO: 518 DNA sequence
 Nucleic Acid Accession #: NM_006536.2
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Seq ID NO: 519 Protein sequence
 Protein Accession #: NP_006527.1

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Seq ID NO: 520 DNA sequence
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5	GAGGCGGTGC	TGGCCCTGTG	GCTGCCACCA	GACTCAGCTA	CTGTTCTGCA	GAAGATGAAT	2880
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Protein Accession #: NP_000219.1

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	NARLNGGKQV	LNLMLDVSGI	PATQSQKIQE	VGEITNLRVN	FTRLAPVPQR	GYHPPSAYYA	240
	VSQRLRLQSG	FCHGHADRC	PKPGASAGPS	TAVQVHDCV	CQHNTAGPNC	ERCAPFYNNR	300
35	PWRPAEGQDA	HECQRDCDNG	HSETCHFDPA	VFAASQGAAG	GVCNDCRDHT	BGKNCERCQL	360
	HYFRNRPRGA	SIQETCISCE	CDPDGAVPGA	PCDPVTGQCV	CKEHVQGERC	DLCKPGFTGL	420
	TYANPQGCRR	CDCNLLGSR	DMPCEESGR	CLCLPNVVG	KCDQCAPYHW	KLASGQCEP	480
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	TGPGGCDKAS	GRCLCRPGLT	GPCDQCQRG	YCNRYPCVA	CHPCFQTYDA	DLREQALRFG	600
40	RLRNATASLW	SGPGLEDRL	ASRILDASKS	IEQIRAVLSS	PAVTEQEVAV	VASAILSLRR	660
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	VLRPAEKLV	SMTKQLGDFW	TRMEELRHQA	RQGGAEAVQA	QQLABGASEQ	ALSAQEGFER	1080
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	TGGCACTTAT	TAGCTTCTCT	CATAAATGA	TCACGATTAT	AAATTAATG	TTTGGGTTCA	3240
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Seq ID NO: 523 Protein sequence
Protein Accession #: NP_001935.1

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	ATDADEPNHL	NSKIAFKIVS	QEPAGTPMFL	LSRNTGEVRT	LTNSLDREQA	SSYRLVVSGA	240
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	WLAVYFTTSG	NEGNWFEIQT	DPRTNEGILK	VVKALDYEQL	QSVKLSIAVK	NKAEFHQSVI	360
	SRYRVQSTPV	TIQVINVREG	IAFRPASKTF	TVQKGISSKK	LVDYILGTQY	AIDEDTNKAA	420
40	SNVXYVMGRN	DGGYLMIDSK	TAEIKFVKNM	NRDSTFIVNK	TITAEVLAI	EYTGKISTGT	480
	VVVRVPDFND	NCPTAVLEKD	AVCSSSPSVV	VSARTLNNRY	TGPYTFALD	QPVKLPVWS	540
	ITTLNATSAL	LRAQEGIPPG	VVHISLVLT	SDNNRCMPR	SLTLEVQCQD	NRGICGTSYP	600
	TTSPGTRYGR	PHSGRLGPAA	IGLLLLGLLL	LLLAPLLLLT	CDCGAGSTGG	VTGGFIPVPD	660
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45	MTTKLGAATE	SGGAAGFATG	TVSGAASFGG	AATGVGICSS	QGSMTMRTRH	STGGTNKDYA	780
	DGAISMNFLD	SYFSQKAFAC	AEDDDQGEAN	DCLLIYDNEG	ADATGSPVGS	VGCCSFIADD	840
	LDDSFPLDSL	PKFKKLAEIS	LGVDGEGKEV	QPPSKDSGYG	IESCGHPIEV	QQTGFVKCQT	900
	LSGSQSASAL	SASGSVQPAV	SIPDPLQHGN	YLVTEYTSAS	GSLVQPSSTAG	FDPLLTQNV	960
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Seq ID NO: 524 DNA sequence
Nucleic Acid Accession #: XM_058069.2
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	ATTTCTTCTT	TATGGCCAAC	CTTGCCATCT	GGCATTGAAG	CTGCTTATGA	AATTGAAGCC	1020
	AGAAATCAAG	TTTTTCTTTT	TAAAGATGAC	AAATACTGGT	TAATTAGCAA	TTTAAAGACCA	1080
75	GAGCCAAAT	ATCCCAAGAG	CATACATTCT	TTTGGTTTTC	CTAACTTTGT	GAAAAAATTT	1140
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	TGGAGGTATG	ATGAAAGGAG	ACAGATGATG	GACCCCTGGT	ATCCCAAACT	GATTACCAAG	1260
	AACTTCCAAG	GAATCCGGCC	TAAAAATGAT	GCAGTCTTCT	ACTCTAAAAA	CAAACTACTAC	1320
80	TATTTCTTCC	AAGGATCTAA	CCAATTTGAA	TATGACTTCC	TACTCCAACG	TATCACCAAA	1380
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Seq ID NO: 525 Protein sequence
Protein Accession #: P39900

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 EBNYPKSIHS FGFPNFVKIK DAAVFNPRFY RTYFFVDNQY WRDERRQMM DPGYPKLITK 420
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Seq ID NO: 527 Protein sequence
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Seq ID NO: 528 DNA sequence
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	AATGCTGGAT	TTCAAGAATA	TACCATTCCCT	ATTACTGTAA	AAGACAGGCG	CGGCCAAGCT	2040
20	GCAACAAAAT	TATTGAGAGT	TAATCTGTGT	GAATGTACTC	ATCCAACTCA	GTGTCGTGCG	2100
	ACTTCAAGGA	GTACAGGAGT	AATACTTGGA	AAATGGGCAA	TCCTTGCAAT	ATTACTGGGT	2160
	ATAGCACTGC	TCTTTTCTGT	ATTGCTAACT	TTAGTATGTG	GAGTTTGTGG	TGCAACTAAA	2220
	GGGAAACGTT	TTCCTGAAGA	TTTAGCACAG	CAAACTTAA	TTATATCAAA	CACAGAAGCA	2280
	CCTGGAGACG	ATAGAGTGTG	CTCTGCCAAT	GGATTATGA	CCCAAACTAC	CAACAACTCT	2340
25	AGCCAAGGTT	TTGTGGTAC	TATGGGATCA	GGAATGAAAA	ATGGAGGGCA	GGAAACCATT	2400
	GAAATGATGA	AAGGAGGAAA	CCAGACCTTG	GAATCCTGCC	GGGGGGCTGG	GCATCATCAT	2460
	ACCCTGGACT	CCTGCAGGCG	AGGACACACG	GAGGTGGACA	ACTGCAGATA	CACTTACTCG	2520
	GAGTGGCACA	GTTTTACGTA	ACCCGCTCTC	GGTGAAAAAT	TGCATCGATG	TAATCAGAAAT	2580
	GAAGACCCGA	TGCCATCCCA	AGATTATGTC	CTCACTTATA	ACTATGAGGG	AAGAGGATCT	2640
30	CCAGCTGGTT	CTGTGGGCTG	CTGCAGTGAA	AAGCAGGAAG	AAGATGGCCT	TGACTTTTTTA	2700
	AATAATTTGG	AACCCAAAT	TATTACATTA	GCAGAAGCAT	GCACAAGAG	ATAATGTCAC	2760
	AGTGCTACAA	TAGGTCTTTT	GTGAGACATT	CTGGAGGTTT	CCAAAAATAA	TATTGTAAAG	2820
	TTCAATTTCA	ACATGTATGT	ATATGATGAT	TTTTTTCTCA	ATTTTGAATT	ATGCTACTCA	2880
	CCAATTTATA	TTTTTAAAGC	CAGTTGTGTC	TTATCTTTTC	CAAAAAGTGA	AAAATGTTAA	2940
35	AACAGACAAC	TGGTAAATCT	CAAACTCCAG	CACTGGAATT	AAGGTCTCTA	AAGCATCTGC	3000
	TCTTTTTTTT	TTTTACGGAT	ATTTTAGTAA	TAAATATGCT	GGATAAATAT	TAGTCCAACA	3060
	ATAGCTAAGT	TATGCTAATA	TCACATTAT	ATGTATTAC	TTTAAAGTAT	AGTTTAAAAA	3120
	ATAACCAAGA	AATATTGAGT	ATCACTATGT	GAAGAAAGTT	TTGGAAAAAG	AACAATGAAG	3180
	ACTGAATTAA	ATTAAAAATG	TTGCAGCTCA	TAAAGAATTG	GGACTCACCC	CTACTGCAC	3240
40	ACCAAAATCA	TTTGACTTTG	GAGGCAAAAT	GTGTTGAAGT	GCCCTATGAA	GTAGCAATTT	3300
	TCTATAGGAA	TATAGTTTGA	AATAAATGTG	TGTGTGTATA	TTATTATTAA	TCAATGCAAT	3360
	ATTTAAAAATG	AAATGAGAAC	AAAGAGGAAA	ATGGTAAAAA	CTTGAATGA	GGCTGGGGTA	3420
	TAGTTTGTCC	TACAATAGAA	AAAAGAGAGA	GCTTCCTAGG	CCTGGGCTCT	TAAATGCTGC	3480
	ATTATAACTG	AGTCTATGAG	GAAATAGTTC	CTGTCCAATT	TGTGTAATTT	GTTTAAAAAT	3540
45	GTAAATAAAT	TAAACTTTTC	TGGTTTCTGT	GGGAAGGAAA	TAGGGAAATCC	AATGGAAACAG	3600
	TAGCTTTGCT	TGCAAGTCTG	TTTCAAGATT	TCTGCATCCA	CAAGTAGTA	GCAAACTGGG	3660
	GAATACTCGC	TGCAGCTGGG	GTTCCCTGCT	TTTTGGTAGC	AAGGGTCCAG	AGATGAGGTG	3720
	TTTTTTTCCG	GGAGCTAATA	ACAAAAACAT	TTTAAACTT	ACCTTTACTG	AAGTTAAATC	3780
	CTCTATTGCT	GTCTTATAG	TGACCAACAT	CTTTTAAATT	TAGATCCAAA		3840
50	TAACCATGTC	CTCCTAGAGT	TTAGAGGCTA	GAGGGAGCTG	AGGGGAGGAT	CTTACTGAAA	3900
	GCACCTGGGG	GAGATTGATT	GTCCTTAAAC	CTAAGCCCCA	CAAACTTGAC	ACCTGATCAG	3960
	GTCTGGGAGC	TACAAAATTT	CATTTTCTCT	CTCACTGCCC	TCTCTCTGAG	TGGCAATTGGC	4020
	CTGAATCAAG	GAAAGCCAGG	CCTTGTGGGC	CCCTTCTTTT	CGGCTTCTG	CTAAGCAAC	4080
	ACCTCCAGCA	GAGATTCCCT	TAAGTGACTC	CAGGTTTTC	ACCATCCTTC	AGCGTGAATT	4140
55	AATTTTAAAT	CAGTTTGCTT	TCTCCAGAGA	AATTTTAAAA	TAATAGAAGA	AATAGAAAT	4200
	TTGAATGTAT	AAAAGAAAAA	GATCAAGTTG	TCATTTTAGA	ACAGAGGGAA	CTTTGGGAGA	4260
	AAGCAGCCCA	AGTAGGTTAT	TTGTACAGTC	AGAGGGCAAC	AGGAAGATGC	AGGCCTTCAA	4320
	GGGCAAGGAG	AGGCCACAAG	GAATATGGGT	GGGAGTAAAA	GCAACATCGT	CTGCTTCATA	4380
	CTTTTTCCTA	GGCTTGGCAC	TGCCTTTTCC	TTTCTCAGGC	CAATGGCAAC	TGCCATTTGA	4440
60	GTCCGGTGAG	GGATCAGCCA	ACCTCTTCTC	TATGGCTCAC	CTTATTGGA	GTGAGAAATC	4500
	AAGGAGACAG	AGCTGACTGC	ATGATGAGTC	TGAAGGCATT	TGCAGGATGA	GCCTGAACTG	4560
	GTGTGTCAGA	ACAAACAAGG	CATTATGGG	AATTGTTGTA	TTCTTCTGCG	AGCCCTCCTT	4620
	CTGGGCACTA	AGAAGGTCTA	TGAATTAAAT	GCCTATCTAA	AATTCTGATT	TATTCTTACA	4680
	TTTTTCTGTT	TCTAATTTGA	CCCTAAAAAT	TATGTGTTTT	AGACTTAGAC	TTTTTATTGC	4740
65	CCCCCCCCCT	TTTTTTTTTG	AGACGGAGTC	TCGCTCTGAC	GCACAGGCTG	GAGTGCAGTG	4800
	GCTCCGATCT	CTGCTCACTG	AAAGCTCCGC	CTCCCGGGTT	CATGCCATT	TCCTGCCTCA	4860
	GCCTCCTGAG	TAGCTGGGAC	TACAGGCGCC	CACCACCACG	CCCGGCTAAT	TTTTTGATTT	4920
	TTTAATAGAG	ACGGGGTTTC	ACTGTGTTAG	CCAGGATGGT	CTCGATCTCC	TGACCTCTGTG	4980
	ATCCGCGTGC	CTCGGCTCC	CAAAAGTCTG	GGATTACAGG	CATGACCCAC	CGCTCCCGGC	5040
70	CTTGTTTTCC	GTTTAAAGTC	GTCTTCTTTT	AATGTAATCA	TTTTGAACAT	GTGTGAAAGT	5100
	TGATCATACG	AATTGGATCA	ATCTTGAAT	ACTCAACCA	AAGACAGTCG	AGAAGCCAGG	5160
	GGGAGAAAGA	ACTCAGGGCA	CAAAATATTG	GTCTGAGAA	GGAAATCTCT	GTAAGCCTAG	5220
	TTGCTGAAAT	TTCTGCTGT	AACCAGAAAG	CAGTTTATC	TAACGGCTAC	TGAAACACCC	5280
	ACTGTGTTTT	GCTCACTCCC	TCACTCACCG	ATCAAAACCT	GCTACCTCCC	CAAGACTTTA	5340
75	CTAGTGCCGA	TAAACTTTCT	CAAAGAGCAA	CCAGTATCAC	TTCCCTGTTT	ATAAAACCTC	5400
	TAACCATCTC	TTTGTCTTTT	GAACATGCTG	AAAACCACT	GGCTGTCATG	TATGCCCGAA	5460
	TTTGTAAATG	TTTTCTCTCA	AATGAAAAAT	TAATTTTAGG	GATTCATTTT	TATATTTTCA	5520
	CATATGTAGT	ATTATTTATT	CCTTATATGT	GTAAGGTGAA	ATTTATGGTA	TTTGAGTGTG	5580
	CAAGAAAATA	TATTTTAAAA	GCTTTTCAAT	TTCCCCCAGT	GAATGATTTA	GAATTTTFTA	5640
80	TGTAATATA	CAGAATGTTT	TTTTTACTTT	TTATAAGGAA	GCAGCTGTCT	AAAAATGCAGT	5700
	GGGGTTTGT	TTGCAATGTT	TTAAACAGAG	TTTTAGTATT	GCTATTAATA	GAAGTTACTT	5760
	TGCTTTTAAA	GAAACTTGGC	TGCTTAAAA	AAGCAAAAAT	TGGATGCATA	AAGTAATATT	5820
	TACAGATGTG	GGGAGATGTA	ATAAAACAAT	ATTAACCTGG	TTTCTGTGTT	TGCTGTATT	5880
	TAGAGATTAA	ATAATTTCTA	GATGATCACT	TGCAAAAAT	ATGCTTATGG	CTGGCATGGA	5940
	AATAGAAATA	CTCAATATATG	TCTTTGTTGT	ATTAATGGGG	AATATTTTGG	ACAATGTTTC	6000
85	ATTATCAAA	TGTCGACATC	ATTAATATAT	ATTGTAATGT	TGGGAAGAGA	TCACTATTTT	6060
	GAAGCACAGC	TTTACAGATG	AGTATCTATG	ATACATATGT	ATAATAAAT	TTGATCGGGT	6120
	ATTAAAGATA	TTAGAAGGTT	GTTTAAATTT	CAGAGTATTC	CATGAATAGT	ACACTGACAC	6180

AGGGGTTTTA CTTTGAGGAC CAGTGTAGTC AAGGGAAAAC ATGAGTTAAA AAGAAAAGCA 6240
 GGCAATATTG CAGTCTTGAT TCTGCCACTT ACAGGATAGA TAATGCCTGA ACTTTAATGA 6300
 CAAGATGATC CAACCATAAA GGTGCTCTGT GCTTCACAGT GAATCTTTTC CCCATGCAGG 6360
 AGTGTGCTCC CCTACAAACG TTAAGACTGA TCATTTCAAA AATCTATTAG CTATATCAAA 6420
 AGCCTTACAT TTTAATATAG GTTGAACCAA AATTTCAATT CCAGTAACTT CTATTGTAAAC 6480
 CATTATTTT GTGTATGTCT TCAAGAATGT TCATTGGATT TTTGTTTGTG ATAGTAAAAT 6540
 ACCGGATACA TTTCACGTGT CCTTCAGTAT TGATTGGTT GAATATTGGG TCATAATGGT 6600
 TGAGAAGCAT GGACACTAGA GCCAGAATGC TTGGATATGA ATCCTGGATC TGTCACTTAC 6660
 TTCTGTGTGA CCTTTGAAAG GCTACTTATT TCCTCTCTTA GCTTTCTCAT TAAATCAAT 6720
 GAACAATGCC AGCCTCATGG GGTGTGTGAA TGATTAAAT AGTTAATATA CCTAAAGTAC 6780
 ATAGAACACT GCCTGCACAT AGTAAAGAA TTATAAGTGT GAGGTAGTTG GTAAATATAT 6840
 GTAGTTGGAT ATACTACCGA ACAATATCTA ATCTCTTTTT AGGGAAATAA AGTTTGTGCA 6900
 TATATATAAT CCGGAACAT G

Seq ID NO: 529 Protein sequence
 Protein Accession #: NP_001932.1

1 11 21 31 41 51
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 MAAAGPRRSV RGAVCLHLLL TLVIFSRDGE ACKKVILNVP SKLEADKIIG RVNLEECFRS 60
 ADLIRSSDDP FRVLNDGSVY TARAVALS DK KRSFTIWLSD KRKQTQKEVT VLLEHQKKVS 120
 KTRHRTRETVL RRAKRKRWAPI PCSMQENSLG PFPLFLQQVE SDAAQNYTVF YSISGRGVNDK 180
 EPLNLFYIER DTGNLFCTRP VDREYDVDF LIAYASTADG VSADLPLPLP IRVEDENDNH 240
 PVFTEAIYNF EVLESSRPT TVGVVCACTR DEPDTMHTRL KYSILQOTPR SPGLFSVHPS 300
 TGVITTVSHY LDREVVDKYS LIMKVQMDMG QFFGLIGTST CIITVTSND NAPTRFNAY 360
 EAFVVENAFN VEILRIPIED KDLINTANWR VNFTILKGNE NGHFKISTDK ETNEGVLVSV 420
 KPLNYEENRQ VNLEIGVUNE APFARDIPRV TALNRALVTV HVRDLDEGPE CTAAQYVRI 480
 KENLAVGSKI NGYKAYDPEN RENGNGLYRK LHDPKGWITI DEISGSIITS KILDREVETP 540
 KNELYNITVL AIDKDDRSCT GTLAVNIEDV NDNPPPEILQE YVVICKPKMG YTDILAVDPD 600
 EPVHGAPFFY SLPNTSPEIS RLWSLTKVND TAARLSYQKN AGFQYTIPI TVKDRAGQAA 660
 TKLLRVNLCE CTHPTQCRAT SRSTGVILGK WAILAILLGI ALLFSVLLTL VCGVFGATKG 720
 KRFPEDLAQQ NLIISNTEAP GDDRVCSANG FMTQTNNNS QGFCGTMSGG MKNGGQETIE 780
 MMKGNGQTL ESCRAGHHHT LDSCRGGHTE VDNCRITYSE WHSFTQPLRG EKLHRCNQNE 840
 DRMPBQDYVL TYNIEGRGSP AGSVGCCSEK QEEDGLDFLN NLEPKFITLA EACTKR

Seq ID NO: 530 DNA sequence
 Nucleic Acid Accession #: NM_016583.2
 Coding sequence: 72..842

1 11 21 31 41 51
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 GGAGTGGGGG AGAGAGAGGA GACCAGGACA GCTGCTGAGA CCTCTAAGAA GTCCAGATAC 60
 TAAGAGCAAA GATGTTTCAA ACTGGGGGCC TCATTGTCTT CTACGGGCTG TTAGCCAGAG 120
 CCATGGCCCA GTTTGGAGGC CTGCCCGTGC CCCTGGACCA GACCCTGCCC TTGAATGTGA 180
 ATCCAGCCCT GCCCTTGAGT CCCACAGGTC TTGCAGGAAG CTGACAAAT GCCCTCAGCA 240
 ATGGCCTGCT GTCTGGGGGC CTGTTGGGCA TTCTGGAAAA CCTTCCGCTC CTGGACATCC 300
 TGAAGCCTGG AGGAGGTACT TCTGGTGGCC TCCTTGGGGG ACTGCTTGGA AAAGTGACGT 360
 CAGTGATTCC TGGCCTGAAC AACATCATTG ACATAAAGGT CACTGACCCC CAGCTGCTGG 420
 AACTTGGCCT TGTGCAGAGC CTGATGGGCC ACCGTCTCTA TGTCAACATC CCTCTCGGCA 480
 TAAAGTCCCA AGTGAATACG CCCTGGTTCG GTGCAAGTCT GTTGAGGCTG GCTGTGAAGC 540
 TGGACATCAC TGCAGAAATC TTAGCTGTGA GAGATAAGCA GGAGAGGATC CACCTGGTCC 600
 TTGGTGACTG CACCCATTCC CTGGAAGGCC TGCAAAATTC TCTGCTTGAT GGACTTGGCC 660
 CCCTCCCCAT TCAAGTCTT CTGGACAGCC TCACAGGGAT CTGGAATAAA GTCCTGCCTG 720
 AGTTGGTTCA GGGCAACGTG TGCCCTCTGG TCAATGAGGT TCTCAGAGGC TTGGACATCA 780
 CCCTGGTGCA TGACATTGTT AACATGCTGA TCCACGGACT ACAGTTTGTC ATCAAGGTCT 840
 AAGCCTTCCA GGAAGGGGCT GGCCTCTGCT GAGCTGCTTC CCAGTGCTCA CAGATGGCTG 900
 GCCCATGTGC TGGAAAGATG CACAGTTGCC TTCTCTCCGA GGAACCTGCC CCTCTCCTT 960
 TCCCACCAGG CGTGTGTAAC ATCCCATGTG CTCACCTAA TAAATGGCT CTCTCTCTGC 1020
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA

Seq ID NO: 531 Protein sequence
 Protein Accession #: NP_057667.1

1 11 21 31 41 51
 | | | | |
 MFQTGGLIVF YGLLAQTMQA FGGLPVPLDQ TLPLNVNPA LPSPTGLAGS LTNALSNGLL 60
 SGGLLGILEN LPLLDILKPG GGTSGGLLGG LLGKVTSVIP GLNNIIDIKV TDPQLLELGL 120
 VQSPDGHRLY VTIPLGKIKL VNTPLVGASL LRLAVKLDIT ABILAVRDKQ ERIHLVLGDC 180
 THSPGSLQIS LLDGLGFLPI QGLLDLSLTGI LNKVLPELVQ GNVCPVNEV LRGLDITLVH 240
 DIVNMLIHGL QFVIKV

Seq ID NO: 532 DNA sequence
 Nucleic Acid Accession #: NM_004363.1
 Coding sequence: 115..2223

1 11 21 31 41 51
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 CTCAGGGCAG AGGGAGGAAG GACAGCAGAC CAGACAGTCA CAGCAGCCTT GACAAAACGT 60
 TCTTGAACT CAAGCTCTTC TCCACAGAGG AGGACAGAGC AGACAGCAGA GACCATGGAG 120
 TCTCCCTCGG CCCTCCCA CAGATGGTGC ATCCCTGGC AGAGGCTCCT GCTCAGAGCC 180
 TCACTTCTAA CTTCTGGAA CCGCCACACC ACTGCCAAGC TCACTATTGA ATCCAGCCG 240
 TTCAATGTGC CAGAGGGGAA GGAGGTGCTT CTACTTGTC ACAATCTGCC CCAGCATCTT 300
 TTTGGCTACA GCTGGTACAA AGGTGAAAGA GTGGATGGCA ACCGTCAAAT TATAGGATAT 360
 GTAATAGGAA CTCAACAAGC TACCCAGGG CCGCATACA GTGGTGGAGA GATAATATAC 420
 CCCAATGCAT CCTGCTGAT CCAGAATCAT ATCCAGAATG ACACAGGATT CTACACCTTA 480

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CACGTCATAA AGTCAGATCT TGTGAATGAA GAAGCAACTG GCCAGTTCGG GGTATACCCG 540
 GAGCTGCCCA AGCCCTCCAT CTCCAGCAAC AACTCCAAC CCGTGGAGGA CAAGGATGCT 600
 GTGGCCTTCA CCTGTGAACC TGAGACTCAG GACGCAACCT ACCTGTGGTG GGTAAACAAT 660
 CAGAGCCTCC CGGTGAGTCC CAGGCTGCAG CTGTCCAATG GCAACAGGAC CCTCACTCTA 720
 TTCAATGTCA CAAGAAATGA CACAGCAAGC TACAAATGTG AAACCCAGAA CCCAGTGAGT 780
 GCCAGGCGCA GTGATTCACT CATCTGAAT GTCTCTATG GCCCGGATGC CCCCAACCATT 840
 TCCCTCTTAA ACACATCTTA CAGATCAGGG GAAAATCTGA ACCTCTCCTG CCACGCAGCC 900
 TCTAACCCAC CTGCACAGTA CTCTTGGTTT GTCAATGGGA CTTTCCAGCA ATCCACCCAA 960
 GAGCTCTTTA TCCCAACAT CACTGTGAAT AATAGTGGAT CCTATACGTG CCAAGCCCAT 1020
 AACTCAGACA CTGGCCTCAA TAGGACCACA GTCACGACGA TCACAGTCTA TGCAGAGCCA 1080
 CCCAAACCCCT TCATCACCAG CAACAACCTCC AACCCTGTGG AGGATGAGGA TGCTGTAGCC 1140
 TTAACCTGTG AACCTGAGAT TCAGAACACA ACCTACCTGT GGTGGGTAAA TAATCAGAGC 1200
 CTCCCGGTCA GTCCAGGCT GCAGCTGTCC AATGACAACA GGACCTCAC TCTACTCAGT 1260
 GTCACAAGGA ATGATGTAGG ACCCTATGAG TGTGGAATCC AGAACGAAT AAGTGTGTAC 1320
 CACAGCGACC CAGTCATCTT GAATGTCTCT TATGGCCCGAG ACGACCCAC CATTTCCCCC 1380
 TCATACACCT ATTACCGTCC AGGGGTGAAC CTCAGCCTCT CTGCGCATGC AGCCTCTAAC 1440
 CCACCTGCAC AGTATCTCTG GCTGATTGAT GGGAACATCC AGCAACACAC ACAAGAGCTC 1500
 TTTATCTCCA ACATCACTGA GAAGAACAGC GGAATCTATA CCTGCCAGGC CAATAACTCA 1560
 GCCAGTGGCC ACAGCAGGAG TACAGTCAAG ACAATCACAG TCTCTGCGGA GCTGCCCAAG 1620
 CCCTCCATCT CCAGCAACAA CTCCAAACCC GTGGAGGACA AGGATGCTGT GGCCTTCACC 1680
 TGTGAACCTG AGGCTCAGAA CACAACCTAC CTGTGGTGGG TAAATGGTCA GAGCCTCCCA 1740
 GTCAGTCCCA GGCTGCAGCT GTCCAATGGC AACAGGACCC TCACTCTATT CAATGTCCAC 1800
 AGAAATGACG CAAGAGCCTA TGTATGTGGA ATCCAGAACT CAGTGAGTGC AAACCGCAGT 1860
 GACCCAGTCA CCGTCAGTGT CCTCTATGGG CCGGACACCC CCATCATTTT CCCCCAGAC 1920
 TCGTCTTACC TTTCGGGAGC GAACCTCAAC CTCTCTGCC ACTCGGCCTC TAACCCATCC 1980
 CCGCAGTATT CTGGCGTAT CAATGGGATA CCGCAGCAAC ACACACAAGT TCTCTTTATC 2040
 GCCAAATCA CGCCAAATAA TAACGGGACC TATGCTCTGT TTGTCTCTAA CTGGCTACT 2100
 GGCCGCAATA ATTCCATAGT CAAGAGCATC ACAGTCTCTG CATCTGGAAC TTCTCTGGT 2160
 CTCTCAGCTG GGGCCAGTGT CCGCATCATG ATTGGAGTGC TGGTTGGGGT TGCTCTGATA 2220
 TAGCAGCCCT GGTGTAGTTT CTTCATTTCA GGAAGACTGA CAGTTGTTTT GCTTCTTCTT 2280
 TAAAGCATTG GCAACAGCTA CAGTCTAAAA TTGCTTCTTT ACCAAGGATA TTTACAGAAA 2340
 AGACTCTGAC CAGAGATCGA GACCATCCTA GCCAACATCG TGAACCCCA TCTCTACTAA 2400
 AAATACAAAA ATGAGCTGGG CTTGGTGGCG CGCACCTGTA GTCCAGTTA CTCGGGAGGC 2460
 TGAGGCAGGA GAATCGCTTG AACCCTGGGAG GTGGAGATTG CAGTGAGCCC AGATCGCACC 2520
 ACTGCACTCC AGTCTGGCAA CAGAGCAAGA CTCCATCTCA AAAAGAAAAG AAAAGAAGAC 2580
 TCTGACCTGT ACTCTGAAAT ACAAGTTTCT GATACCACCT CACTGTCTGA GAATTTCCAA 2640
 AACTTTAATG AACTAALCTA CAGCTTCATG AAAGTGTCCA CCAAGATCAA GCAGAGAAAA 2700
 TAATTAATTT CATGGGACTA AATGAACTAA TGAGGATTGC TGATTTCTTA AATGTCTTGT 2760
 TTCCAGATT TCAGGAAACT TTTTCTCTT TAAGCTATCC ACTCTACAG CAATTTGATA 2820
 AAATATACTT TTGTGAACAA AAATTGAGAC ATTTACATT TCTCCCTATG TGGTCGCTCC 2880
 AGACTTGGGA AACTATTCAT GAATATTTAT ATTGTATGGT AATATAGTTA TTGCACAAGT 2940
 TCAATAAAAA TCTGCTCTTT GTATAACAGA AAAA

Seq ID NO: 533 Protein sequence
 Protein Accession #: NP_004354.1

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1 11 21 31 41 51
 MESPSAPPHR WCIPWQRLLL TASLLTFWNP PTTAKLTIES TPFNVAEGKE VLLLVHNLPO 60
 HLFYGSWYKG ERVDGNRII GYVIGTQQAT PGPAYSGREI IYPNALLLIQ NIIQNDTGFY 120
 TLHVIKSDLV NEEATGQFRV YPELPKPSIS SNNSKPVEDK DAVAFTCEPE TQDATYLLWV 180
 NNQSLFVSPR LQLSNGNRTL TLFNVTRNDT ASYKCTQNP VSARRSDSVI LNVLYGPDAP 240
 TISPLNTSYR SGENLNLSCB AASNPAPQYS WFNVTGTFQS TQELFIPNIT VNNSGSYTCQ 300
 AHNSTGLNR TTVTTITVYA EPPKPFITSN NSNPVEDEDA VALTCEPEIQ NTYLLWVWNN 360
 QSLFVSPRLQ LSNDRNLTL LSVTRNDVGP YECGIQNELS VDHSDFVILN VLYGPDPTI 420
 SPSYTYRFRG VNLSSLCHAA SNPPAQYSWL IDGNIQOHTQ ELFI SNITEK NSGLVTCQAN 480
 NSASGHSRTT VKTITVSAEL PKPSISSNNS KPVEDKDAVA FTCEPEAQNT TYLWVWNGQS 540
 LPVSPRLQLS NGNRTLTLFN VTRNDARAYV CGIQNSVSAN RSDPVTLDVL YGPDPTIISP 600
 PDSSYLSGAN LNLSCHSASN PSPQYSWRIN GIPQOHTQVL FIAKITPNNN GTYACFVSNL 660
 ATGRNNSIVK SITVSASGTS PGLSAGATVG IMIGVLVGA LI

Seq ID NO: 534 DNA sequence
 Nucleic Acid Accession #: NM_006952.1
 Coding sequence: 11..793

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70
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1 11 21 31 41 51
 AATCCCGACA ATGGCGAAAG ACAACTCAAC TGTTCTGTTG TTCCAGGGCC TGCTGATTTT 60
 TGGAAATGTG ATTATTGGTT GTTGCGGCAT TGCCCTGACT GCGGAGTGCA TCTTCTTTGT 120
 ATCTGACCAA CACAGCCTCT ACCCACTGCT TGAAGCCACC GACAACGATG ACATCTATGG 180
 GGCTGCCTGG ATCGGCATAT TTGTGGGCAT CTGCCTCTTC TGCTGTCTG TTCTAGGCAT 240
 TGTAGGCATC ATGAAGTCCA GCAGGAAAAT TCTTCTGGCG TATTTTCATTC TGATGTTTAT 300
 AGTATATGCC TTGAAGTGG CATCTGTAT CACAGCAGCA ACACACGAG ACTTTTTCAC 360
 ACCCAACCTC TTCCTGAAGC AGATGCTAGA GAGGTACCAA AACACAGCC CTCCAAACAA 420
 TGATGACCAG TGGAAAAACA ATGGAGTCAC CAAAACCTGG GACAGGCTCA TGCTCCAGGA 480
 CAATTGCTGT GGCCTGAAATG GTCCATCAGA CTGGCAAAAA TACACATCTG CCTTCCGGAC 540
 TGGAATAAT ATGCTGACT ATCCCTGGCC TCGTCAATGC TGTGTTATGA ACAATCTTAA 600
 AGAACCTCTC AACCTGGAGG CTTGTAAACT AGGCGTGCCT GGTTTTTATC ACAATCAGGG 660
 CTGCTATGAA CTGATCTCTG GTCCAATGAA CCGACACGCC TGGGGGGTTG CCTGGTTTGG 720
 ATTTGCCATT CTCTGCTGGA CTTTTTGGGT TCTCTGGGT ACCATGTTCT ACTGGAGCAG 780
 AATTGAATAT TAAGAA

Seq ID NO: 535 Protein sequence
 Protein Accession #: NP_008883.1

85

1 11 21 31 41 51

MAKDNSTVRC FQGLLIIFGNV IIGCCGIALT AECIFVSDQ HSLYPLLEAT DNDDIYGAAW 60
 IGIFVGICLF CLSVLGIVGI MKSSRKILLA YFILMFIVYA FEVASCITAA TQRDFFTPNL 120
 FLKQMLERYQ NNSPPNNDQ WKNNGVTKTW DRLMLQDNCC GVNGPSDWQK YTSAPRTENN 180
 DADYPWPRQC CVMNNLKEPL NLEACKLGVP GFYHNGQCYE LISGPMNRHA WGVAVFGFAI 240
 LCWTFWVLLG TMFYWSRIEY

Seq ID NO: 536 DNA sequence
 Nucleic Acid Accession #: NM_002638.1
 Coding sequence: 120..473

1 11 21 31 41 51
 CAATACAGCT AAGGAATTAT CCCTTGTAAT TACCACAGAC CCGCCCTGGA GCCAGGCCAA 60
 GCTGGACTGC ATAAAGATTG GTATGGCCTT AGCTCTTAGC CAAACACCTT CCTGACACCA 120
 TGAGGGCCAG CAGCTTCTTG ATCGTGGTGG TGTTCTCATC CGCTGGGACG CTGGTTCTAG 180
 AGGCAGCTGT CACGGGAGTT CCTGTAAAG GTCAAGACAC TGTCAAAGGC CGTGTTCAT 240
 TCAATGGACA AGATCCCGTT AAAGGACAAG TTTCAGTTAA AGGTCAAGAT AAAGTCAAAG 300
 CGCAAGAGCC AGTCAAAGGT CCAGTCTCCA CTAAGCCTGG CTCCTGCCCC ATTATCTTGA 360
 TCCGTGCGCG CATGTTGAAT CCCCCTAACC GCTGCTTGAA AGATACTGAC TGCCACAGGA 420
 TCAAGAAGTG CTGTGAAGGC TCTTGGGGA TGGCCTGTTT CGTTCGCCAG TGAAGGGAGC 480
 CGGTCTCTGC TGCACCTGTG CCGTCCCCAG AGCTACAGGC CCCATCTGGT CCTAAGTCCC 540
 TGCTGCCCTT CCCCTTCCCA CACTGTCCAT TCTTCTCCCC ATTCAGGATG CCCACGGCTG 600
 GAGCTGCCTC TCTCATCCAC TTTCACATAA A

Seq ID NO: 537 Protein sequence
 Protein Accession #: NP_002629.1

1 11 21 31 41 51
 MRASSFLIVV VFLIAGTLVL EAAVTGVPVK GQDTPVKRVP FNGQDPVKQ VSVKGQDKVK 60
 AQEPVKGPVS TKPGSCPIIL IRCAMLNPPN RCLKDTPCPG IKKCEGSCG MACFVPQ

Seq ID NO: 538 DNA sequence
 Nucleic Acid Accession #: NM_001793.2
 Coding sequence: 71..2560

1 11 21 31 41 51
 AAAGGGGCAA GAGCTGAGCG GAACACCGGC CCGCCGTCGC GGCAGCTGCT TCACCCCTCT 60
 CTCTGCAGCC ATGGGGCTCC CTCGTGGACC TCTCGCTCT CTCTCCTTC TCCAGGTTTG 120
 CTGGCTGCAG TCGCGGCGCT CCGAGCCGTG CCGGGCGGTC TTCAGGGAGG CTGAAGTGAC 180
 CTTGGAGGCG GGAGGCGCGG AGCAGGAGCC CGGCCAGGCG CTGGGAAAG TATTATGGG 240
 CTGCCCTGGG CAAGAGCCAG CTCTGTTTAG CACTGATAAT GATGACTTCA CTGTGCGGAA 300
 TGGCGAGACA GTCCAGGAAA GAAGGTCACT GAAGGAAAGG AATCCATTGA AGATCTTCCC 360
 ATCCAAACGT ATCTTACGAA GACACAAGAG AGATTGGGTG GTTGCTCCAA TATCTGTCCC 420
 TGAAATGGC AAGGCTCCCT TCCCCAGAG ACTGAATCAG CTCAAGTCTA ATAAAGATAG 480
 AGACACCAAG ATTTTCTACA GCATCACGGG GCCGGGGGCA GACAGCCCC CTGAGGGTGT 540
 CTTGCTGTGA GAGAAGGAGA CAGGCTGGTT GTTGTGAAT AAGCCACTGG ACCGGGAGGA 600
 GATTGCCAAG TATGAGCTCT TTGGCCACGC TGTGTGAGAG AATGGTGCCT CAGTGGAGGA 660
 CCCCATGAAC ATCTCCATCA TCGTGACCGA CCAGAATGAC CACAAGCCCA AGTTTACCCA 720
 GGACACCTTC CGAGGGAGTG TCTTAGAGGG AGTCTTACCA GGTACTTCTG TGATGCAGGT 780
 GCAGACCAAG GATGAGGATG ATGCCATCTA CACCTACAAT GGGGTGGTTG CTTACTCCAT 840
 CCATAGCCAA GAACCAAAAG ACCCACACGA CCTCATGTTT ACCATTACCC GGAGCACAGG 900
 CACCATCAGC GTCATCTCCA GTGGCCTGGA CCGGGAAGAA GTCCCTGAGT ACACACTGAC 960
 CATCCAGGCC ACAGACATGG ATGGGGACGG CTCCACCACC ACGGCAGTGG CAGTAGTGGA 1020
 GATCCTTGAT GCCAATGACA ATGCTCCCAT GTTTGACCCC CAGAAGTACG AGGCCCATGT 1080
 GCCTGAGAAT GCAGTGGGCC ATGAGGTGCA GAGGCTGACG GTCACTGATC TGGACGCCCC 1140
 CAACTCACCA GCGTGGCGTG CCACCTACCT TATCATGGGC GGTGACGACG GGGACCATTT 1200
 TACCATCAC ACCCACCTG AGAGCAACCA GGGCATCCTG ACAACACGGA AGGGTTTGGA 1260
 TTTTGAGGCC AAAAACCAAG ACACCTCTGA CGTTGAAAGT ACCAACGAGG CCCCTTTTGT 1320
 GCTGAAGCTC CCAAGCTCCA CAGCCACCAT AGTGGTCCAC GTGGAGGATG TGAATGAGGC 1380
 ACCTGTGTTT GTCCACCCCT CCAAAGTCGT TGAGGTCCAG GAGGGCATCC CCACTGGGGA 1440
 GCCTGTGTGT GTCTACACTG CAGAAGACCC TGACAAGGAG AATCAAAAGA TCAGTACCG 1500
 CATCCTGAGA GACCCAGCAG GGTGGCTAGC CATGGACCCA GACAGTGGGC AGGTACAGC 1560
 TGTGGGCACC CTCGACCGTG AGGATGAGCA GTTGTGAGG AACACATCT ATGAAGTCAT 1620
 GGTCTTGGCC ATGGACAATG GAAGCCCTCC CACCACTGGC ACGGGAACCC TTCTGCTAAC 1680
 ACTGATTGAT GTCAATGACC ATGGCCAGT CCCTGAGCCC CGTCAGATCA CCATCTGCAA 1740
 CCAAAGCCCT GTGCGCCAGG TGCTGAACAT CACGGACAAG GACCTGTCTC CCCACACCTC 1800
 CCCTTTCCAG GCCAGCTCA CAGATGACTC AGACATCTAC TGGACGGCAG AGGTCAACGA 1860
 GGAAGGTGAC ACAGTGGTCT TGTCCCTGAA GAAGTTCCCT AAGCAGGATA CATATGACGT 1920
 GCACCTTTCT CTGTCTGACC ATGGCAACAA AGAGCAGCTG ACGGTGATCA GGGCCACTGT 1980
 GTGCGACTGC CATGGCCATG TCGAAACCTG CCCTGGACCC TGGAAAGGAG GTTTCATCCT 2040
 CCCTGTGCTG GGGGCTGTCC TGGCTCTGCT GTTCTCCTG CTGGTGTCTG TTTTGTGGT 2100
 GAGAAAGAAG CGGAAGATCA AGGAGCCCTC CTAATCCCA GAAGATGACA CCCGTGACAA 2160
 CGTCTTCTAC TATGGCGAAG AGGGGGGTGG CGAAGAGGAC CAGGACTATG ACATCACCCA 2220
 GGTCCACCGA GGTCTGGAGG CCAGGCGGGA GGTGGTTCTC CGCAATGACG TGGCACCAAC 2280
 CATCATCCCG ACACCCATGT ACCGTCTCTG GCCAGCCAAC CAGATGAAA TCGGCAACTT 2340
 TATAATTGAG AACCTGAAGG CGGCTAACAC AGACCCCA GCCCCGCCCT ACGACACCTT 2400
 CTGGTGTTC GACTATGAGG GCAGCGGCTC CGACGCGCG TCCCTGAGCT CCCTCACCTC 2460
 TCCGCTCTCC GACCAAGACC AAGATTACGA TTATCTGAAC GAGTGGGGCA GCGCTTCAA 2520
 GAAGCTGGCA GACATGTACG GTGGCGGGGA GGACGACTAG GCGGCTCTGC TGCAGGGCTG 2580
 GGGACCAAC GTCAGGCCAC AGAGCATCTC CAAGGGGTCT CAGTTCCCCC TTCAGCTGAG 2640
 GACTTCGGAG CTGTTCAGGA AGTGGCCGTA GCAACTTGGC GGAGACAGGC TATGAGTCTG 2700
 ACGTTAGAGT GGTGTCTTCC TTAGCCTTTC AGGATGGAGG AATGTGGGCA GTTGTACTTC 2760
 AGCACTGAAA ACCTCTCCAC CTGGGCCAGG GTTGCCTCAG AGGCCAAGT TCCAGAAGCC 2820
 TCTTACCTGC CGTAAATGTC TCAACCTGT GTCTGGGCC TGGGCTGTCT GTGACTGACC 2880
 TACAGTGGAC TTTCTCTCTG GAATGAAGCC TTCTTAGGCC TCCTGGTGCA ACTTAATTTT 2940

TTTTTTTAAAT GCTATCTTCA AAACGTTAGA GAAAGTTCTT CAAAAGTGCA GCCCAGAGCT 3000
 GCTGGGCCCA CTGGCCGTCC TGCATTTCTG GTTTCAGAC CCCAATGCCT CCCATTCGGA 3060
 TGGATCTCTG CGTTTTTATA CTGAGTGTGC CCTTATTTT TATTTTCCT 3120
 GTTGGTGTGC TATAGATGAA GGGTGAAGAC AATCGTGTAT ATGTACTAGA ACTTTTTTAT 3180
 TAAAGAACT TTTCCAGAA AAAAA

Seq ID NO: 539 Protein sequence
 Protein Accession #: NP_001784.2

1 11 21 31 41 51
 MGLPRGPLAS LLLLQVCWLQ CAASEPCRAV FREAEVTLEA GGAEQEPGQA LGKVFMGCPG 60
 QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIFPSKR ILRRHKRDWV VAPISVPENG 120
 KGPFPQRLNQ LKSNKDRDTK IFYSITGPGA DSPPEGVFAV EKETGWLLLN KPLDREBIAK 180
 YELFGHAVSE NGASVEDPMN ISIIITDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT 240
 DEDDAIYTYN GVVAYSIHSQ EFKDPHDLMP TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300
 TMDMDGGSTT TAVAVVEILD ANDNAPMFDQ QKYEAHVFN AVGHEVQRLT VTDLDAPNSP 360
 AWRATYILMG GDDGDHFTIT THPESNQIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL 420
 PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIFTGEPVC VYTAEDPDKE NQKISYRILR 480
 DPAGNLAMP DSGQVTAVGT LDREDEQFVR NNIEYVMVLA MDNGSPPTTG TGTLLLTLD 540
 VNDHGEVPEP RQITCNQSP VRQVLNITDK DLSPTSPFQ AQLTDDSDIY WTAEVNEEGD 600
 TVVLSLKKFL KQDITYDVHLS LSDHGNKEQL TVIRATVCD C HGHVETCPGP WKGGFILPVL 660
 GLVLLALLFL LVLLLLVRRK RKIKEPLLLP EDDTRDNVYF YGEEGGGEED QDYDITQLHR 720
 GLEARPEVVL RNDVAPTIIP TPMYRPRPAN PDEIGNFIE NLKAANTDPT APPYDTLLVF 780
 DYEGSGSDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKKLA DMYGGGEDD

Seq ID NO: 540 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..672

1 11 21 31 41 51
 ATGAGGCTCC AAAGACCCCG ACAGGCCCCG GCGGGTGGGA GCGCGCGGCC CCGGGGCGGG 60
 CGGGGCTCCC CCTACCGGCC AGACCCGGGG AGAGCGCGCG GGAGGCTGCG AAGGTTCCAG 120
 AAGGGCGGGG AGGGGGCGCG GCGCGCTGAC CCTCCCTGGG CACCGCTGGG GACGATGGCG 180
 CTGCTCGCCT TGCTCTGTGT CGTGGCCCTA CCGCGGGTGT GGACAGACGC CAACCTGACT 240
 GCGAGACAAC GAGATCCAGA GGAATCCAG CGAACGACG AGGGTGACAA TAGAGTGTGG 300
 TGTCTATGTT GTGAGAGAGA AAACACTTTC GAGTGCCAGA ACCCAAGGAG GTGCAATAGG 360
 ACAGAGCCAT ACTGCGTTAT AGCGGCCGTG AAAATATTTC CACGTTTTTT CATGGTTGCG 420
 AAGCAGTGCT CGCTGGTTTG TGCAGCGATG GAGAGACCCA AGCCAGAGGA GAAGCGGTTT 480
 CTCCTGGAAG AGCCCATGCC CTCTTTTAC CTCAGTGTGT GTAAAATTTC CTACTGCAAT 540
 TTAGAGGGGC CACCTATCAA CTCATCAGTG TTCAAAGAAT ATGCTGGGAG CATGGGTGAG 600
 AGCTGTGGTG GGTGTGGCT GGCATCCTC CTGCTGCTGG CCTCCATTGC AGCCGGCCTC 660
 AGCCTGTCTT GA

Seq ID NO: 541 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MRLQRPRQAP AGRRRAPRGG RGSPYRPDPG RGARRLRRFQ KGGEGAPRAD PPWAPLGTMA 60
 LLALLLVVAL PRVWTDANLT ARQRDPEDSQ RTDEGDNRVW CHVCEERNTF ECQNPERRCKW 120
 TEPYCVIAAV KIFPRFFMVA KQCSAGCAAM ERPKPEEKRF LLEEMPFFFY LKCKKIRYCN 180
 LEGPPINSSV FKEYAGSMGE SCGGLWLAIL LLLASIAAGL SLS

Seq ID NO: 542 DNA sequence
 Nucleic Acid Accession #: XM_035292.2
 Coding sequence: 53..1576

1 11 21 31 41 51
 GCTCGCTGGG CCGCGGCTCC CGGGTGTCCC AGGCCCGGCC GGTGCGCAGA GCATGGCGGG 60
 TCGGGGCCCG AAGCGGCGCG CGCTAGCGGC GCCCGCGGCC GAGGAGAAGG AAGAGGCGCG 120
 GGAGAAGATG CTGGCCGCCA AGAGCGCGGA CGGCTCGGCG CCGGCAGGCG AGGGCGAGGG 180
 CGTGACCCCTG CAGCGGAACA TCACGCTGCT CAACGCGCTG GCCATCATCG TGGGGACCAT 240
 TATCGGCTCG GGCATCTTCG TGACGCCAC GGGCGTGCTC AAGGAGGCAG GCTCGCCGGG 300
 GCTGGCGCTG GTGGTGTGGG CGCGTGCCTG CGTCTTCTCC ATCGTGGGCG CGCTCTGCTA 360
 CGCGGAGCTC GGCACCAACA TCTCCAAATC GGGCGGCGAC TACGCTTACA TGCTGGAGGT 420
 CTACGGCTCG CTGCCCCTCT TCCTCAAGCT CTGGATCGAG CTGCTCATCA TCCGGCCTTC 480
 ATCGCAGTAC ATCGTGGCCC TGGTCTTCGC CACCTACCTG CTCAAGCCGC TCTTCCCCAC 540
 CTGCCCGGTG CCCGAGGAGG CAGCCAAGCT CGTGGCCTGC CTCTGCGTGC TGCTGCTCAC 600
 GGCCGTGAAC TGCTACAGCG TGAAGGCCG CACCCGGGTC CAGGATGCCT TTGCCGCGC 660
 CAAGCTCCTG GCCCTGGCCC TGATCATCTT GCTGGGCTTC GTCCAGATCG GAAAGGGTGA 720
 TGTGTCCAAT CTAGATCCCA ACTTCTCATT TGAAGGCACC AAACCTGGATG TGGGGAACAT 780
 TGTGCTGGCA TTATACAGCG GCCTCTTTGC CTATGGAGGA TGAATTTACT TGAATTTCTG 840
 CACAGAGGAA ATGATCAACC CCTACAGAAA CCTGCCCTCG GCCATCATCA TCTCCCTGCC 900
 CATCTGTAGC CTGGTGTAGC TGCTGACCAA CTGGCCTTAC TTCACCAACC TGTCCACGGA 960
 GCAGATGCTG TCGTCCGAGG CCGTGGCCGT GGAATTCGGG AACTATCACC TGGGCGTCAT 1020
 GTCTCTGATC ATCCCGCTCT TCGTGGGCGT GTCTCTGCTT GGCTCCGTCA ATGGGTCCCT 1080
 GTTCAATATC CTTCAGCTCT TCTTCTGGG GTCCCGGGAA GGCCACCTGC CCTCCATCCT 1140
 CTCCATGATC CACCCACAGT TCTTCAACCC CGTGGCGTCC CTCGTGTTCA CGTGTGTGAT 1200
 GACGCTGCTC TACGCTTCTT CCAAGGACAT CTTCTCCGTC ATCAACTTCT TCAGCTTCTT 1260
 CAACTGGCTC TGCGTGGCCC TGGCCATCAT CGGCATGATC TGGCTGCGCC ACAGAAAGCC 1320
 TAGCTTTAGC CGGCCCATCA AGGTGAACCT GGCCCTGCCT GTGTTCTTCA TCCTGGCCTG 1380
 CCTCTTCTCG ATCGCCGTCT CTTCTGGGAA GACACCCGTC GAGTGTGGCA TCGGCTTCA 1440
 CATCATCCTC AGCGGGCTGC CCGTCTACTT CTTCGGGGTC TGGTGGAAAA ACAAGCCCAA 1500
 GTGGCTCCTC CAGGGCATCT TCTCCACGAC CGTCTGTGT CAGAAGCTCA TGCAGGTGTT 1560

CCCCCAGGAG ACATAGCCAG GAGGCCGAGT GGCTGCCGGA GGAGCATGC

Seq ID NO: 543 Protein sequence
Protein Accession #: XP_035292.2

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1      11      21      31      41      51
|      |      |      |      |      |
MAGAGPKRRA LAAPAAEEKE EAREKMLAAK SADGSAPAGE GEGVTIQRNI TLLNGVAIIV 60
GTIIIGSGIFV TPTGVLKEAG SPGLALVWVA ACQVFSIVGA LCYAEIQTII SKSGGDYAYM 120
10 LEVYGSPLPAF LKLWIELLII RPSSQYIVAL VFATYLLKPL FPTCPVPPEA AKLVACLCLVL 180
LLTAVNCYSV KAATRVQDAF AAKLLALAL IILLGFVQIG KGDVSNLDPN FSFEGTKLDV 240
GNIVLALYSG LFAYGWNYL NFVTEEMINP YRNLPLAIII SLPIVTLVYV LTNLAYFTTL 300
STEQMLSSSA VAVDFGNVHL GVMSWIIPVF VGLSCFSGVN GSLFTSSRLF FVGSREGHLP 360
15 SILSMIHPQL LTPVPSLVFT CVMTLIYAFS KDIFSVINFP SFFNWLCLVAL AIIGMIWLRH 420
RKPELERPIK VNLALFVFFI LACLFLIAVS FWKTPVECGI GFTIILSGLP VYFFGVWVKN 480
KPKWLLQGIF STTVLCQKLM QVVPQET

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Seq ID NO: 544 DNA sequence
Nucleic Acid Accession #: NM_005268.1
Coding sequence: 168..989

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1      11      21      31      41      51
|      |      |      |      |      |
TAAAAAGCAA AAGAATTCGC GGCCGCGTCG ACACGGGCTT CCCCAGAAAC CTTCCCCGCT 60
TCTGATATG AAATTCAGC TGCTTGCTGA GTCTTATGCG CGGCTGCTGG GAGCCAGGAG 120
25 AGCCCTGAGG AGTAGTCACT CAGTAGCAGC TGACGCGTGG GTCCACCATG AACTGGAGTA 180
TCTTTGAGGG ACTCCTGAGT GGGGTCAACA AGTACTCCAC AGCCTTTGGG CGCATCTGGC 240
TGCTCTCTGT CTTCATCTTC CGCGTCTGCG TGTACTCTGT GACGGCCGAG CGTGTGTGGA 300
GTGATGACCA CAAGGACTTC GACTGCAATA CTCGCCAGCC CGGCTGCTCC AACGTCTGCT 360
30 TTGATGAGTT CTTCCTGTG TCCCATGTGC GCCTCTGGGC CCTGCAGCTT ATCCTGGTGA 420
CATGCCCTCT ACTGCTCGTG GTCATGCACG TGGCTTACCG GGAGGTTTCA GAGAAGAGGC 480
ACCGAGAAGC CATCGGGGAG AACAGTGGGC GCCTCTACCT GAACCCCGGC AAGAAGCGGG 540
GTGGGCTCTG GTGGACATAT GTCTGCAGCC TAGTGTTCAG GCGGAGCGTG GACATCGCCT 600
TTCTCTATGT GTTCCACTCA TTCTACCCCA AATATATCCT CCCTCCTGTG GTCAAGTGCC 660
35 ACGCAGATCC ATGTCCCAAT ATAGTGGACT GCTTCATCTC CAGGCCCTCA GAGAAGAACA 720
TTTTCACCTT CTTCATGGTG GCCACAGCTG CCATCTGCAT CTGTCTCAAC CTCGTGGAGC 780
TCATCTACCT GGTGAGCAAG AGATGCCACG AGTGCCTGGC AGCAAGGAAA GCTCAAGCCA 840
TGTGCACAGG TCATCACCCC CACGGTACCA CCTCTTCTCT CAAACAAGAC GACCTCCTTT 900
CGGGTGACCT CATCTTTCTG GGCTCAGACA GTCATCTCTC TCTCTTACCA GACCGCCCCC 960
40 GAGACCATGT GAAGAAAACC ATCTTGTGAG GGGCTGCCTG GACTGTGCTG GCAGGTTGGG 1020
CCTGATGGG GAGGCTCTAG CATCTCTCAT AGGTGCAACC TGAGAGTGGG GGAGCTAAGC 1080
CATGAGGTAG GGGCAGGCAA GAGAGAGGAT TCAGACGCTC TGGGAGCCAG TTCCTAGTCC 1140
TCAACTCCAG CCACCTGCCC CAGCTCGACG GCACTGGGCC AGTTCCCCCT CTGCTCTGCA 1200
45 GCTCGGTTTC CTTTCTAGA ATGGAAATAG TGAGGGCCAA TGC

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Seq ID NO: 545 Protein sequence
Protein Accession #: NP_005259.1

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1      11      21      31      41      51
|      |      |      |      |      |
MNWSIFEGLL SGVKNYSTAF GRIWLSLVFI FRVLVYLVT A ERVWSDHDKD FDCNTRQPGC 60
SNVCFDEFFP VSHVRLWALQ LILVTCPSLL VVMHVAYREV QEKRHREAHG ENSGRLYLNP 120
50 GKRRGGLWMT YVCSLVFKAS VDIAPLYVFH SFYPKYILPP VVKCHADPCP NIVDCFISKP 180
SEKNIFTLFM VATAAICILL NLVELIYLV S KRCHECLAAR KQAMCTGHH PHGTTSSCKQ 240
55 DBLLSGDLIF LGSDSHPPLL PDRPRDHVK TIL

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Seq ID NO: 546 DNA sequence
Nucleic Acid Accession #: NM_002391.1
Coding sequence: 26..457

```

1      11      21      31      41      51
|      |      |      |      |      |
CGGGCGAAGC AGCGCGGGCA GCGAGATGCA GCACCGAGGC TTCCTCCTCC TCACCCTCCT 60
CGCCCTGCTG GCGCTCACCT CCGCGGTGCG CAAAAAGAAA GATAAGGTGA AGAAGGGCGG 120
65 CCGGGGAGC GAGTGCCTG AGTGGGCTG GGGGCCCTGC ACCCCAGCA GCAAGGATTG 180
CGGCGTGGGT TTCCGCGAGG GCACCTGCGG GCGCCAGACC CAGCGCATCC GGTGCAGGGT 240
GCCCTGCAAC TGAAGAAGG AGTTTGGAGC CGACTGCAAG TACAAGTTTG AGAACTGGGG 300
TGCGTGTGAT GGGGGCACAG GCACCAAGT CCGCCAAGGC ACCCTGAAGA AGGCGCGCTA 360
CAATGCTCAG TGCCAGGAGA CCATCCGCGT CACCAAGCCC TGCAACCCCA AGACCAAGC 420
70 AAAGGCCAAA GCCAAGAAAG GGAAGGGAAG GGAAGGAGC CCAAGCCTGG ATGCCAAGGA 480
GCCCTGGTGT TCACATGGGG CCTGGCCACG CCTCCCTCT CCCAGGCCG AGATGTGACC 540
CACCAGTGCC TTCTGTCTGC TCGTTAGCTT TAATCAATCA TGCCCTGCCT TGTCCCTCTC 600
ACTCCCAGC CCCACCCCTA AGTGCCAAA GTGGGGAGG ACAAGGGATT CTGGGAAGCT 660
75 TGAGCCTCCC CCAAAGCAAT GTGAGTCCCA GAGCCCGCTT TTGTTCTTCC CCACAATTCC 720
ATTACTAAGA AACACATCAA ATAAACTGAC TTTTCCCCC CAATAAAGC TCTTCTTTT 780
TAATAT

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Seq ID NO: 547 Protein sequence
Protein Accession #: NP_002382.1

```

1      11      21      31      41      51
|      |      |      |      |      |
MQHRGFLLLT LLALLAL TSA VAKKDKVKK GPGSECAEW AWGPCTPSSK DCGVGFREGT 60
80 CGAQTQIRIC RVPCNWKKEF GADCKYKFEN WGACDGGTGT KVRQGTLLKA RYNAQCQETI 120
RVTKPCTPKT KAKAKAKKKG GKD

```

Seq ID NO: 548 DNA sequence

Nucleic Acid Accession #: NM_006783.1

Coding sequence: 1..786

```
5 1 11 21 31 41 51
| | | | |
ATGGATTGGG GGACGCTGCA CACTTTCATC GGGGGTGTCA ACAAACTCTC CACCAGCATC 60
GGGAAGGTGT GGATCACAGT CATCTTTAT TCCGAGTCA TGATCCTAGT GGTGGCTGCC 120
CAGGAAGTGT GGGGTGACGA GCAAGAGGAC TTCGTCTGCA ACACACTGCA ACCGGGATGC 180
AAAAATGTGT GCTATGACCA CTTTTCCTCG GTGTCCACA TCCGGCTGTG GGCCCTCCAG 240
10 CTGATCTTCG TCTCCACCCC AGCGCTGCTG GTGGCCATGC ATGTGGCCTA CTACAGGCAC 300
GAAACCACTC GCAAGTTCAG GCGAGGAGAG AAGAGGAATG ATTTCAAAGA CATAGAGGAC 360
ATTAAAAAGC ACAAGGTTTCG GATAGAGGGG TCGCTGTGTT GGACGTACAC CAGCAGCATC 420
TTTTTCCGAA TCATCTTTGA AGCAGCCTTT ATGTATGTGT TTTACTTCCT TTACAATGGG 480
15 TACCACCTGC CCTGGGTGTT GAAATGTGGG ATTGACCCTT GCCCAACCTT TGTGACTGTC 540
TTTATTTCTA GGCCAACAGA GAAGACCGTG TTTACCATTT TTATGATTTT TCGCTCTGTG 600
ATTTGCATGC TGCTTAACGT GGCAGAGTTG TGCTACCTGC TGCTGAAAGT GTGTTTTAGG 660
AGATCAAAGA GAGCAGAC GCAAAAAAAT CACCCCAATC ATGCCCTAAA GGAGAGTAAG 720
CAGAATGAAA TGAATGAGCT GATTTTCAGAT AGTGGTCAAA ATGCAATCAC AGGTTTCCCA 780
AGCTAA
```

Seq ID NO: 549 Protein sequence

Protein Accession #: NP_006774.1

```
25 1 11 21 31 41 51
| | | | |
MDWGTLTHTFI GGVNKHSTSI GKVWITVIFI FRVMILVVAA QEVWGDQED FVCNTLQPGC 60
KNVCYDHFPP VSHIRLWALQ LIFVSTPALL VAMHVAYYRH ETTRKFRRGE KRNDPKDIED 120
IKKKVRIEG SLWWTYTSI FRIIFEAFF MYVFYFLYNG YHLPWVLKCG IDPCPNLVDC 180
FISRPTEKTV FTIFMISASV ICMLLNVAEL CYLLKVCFR RSKRAQTQKN HPNHALKESK 240
30 QNEMNELISD SQQNAITGFP S
```

Seq ID NO: 550 DNA sequence

Nucleic Acid Accession #: NM_002571.1

Coding sequence: 99..587

```
35 1 11 21 31 41 51
| | | | |
CATCCCTCTG GCTCCAGAGC TCAGAGCCAC CCACAGCCGC AGCCATGCTG TGCCCTCTGC 60
TCACCTCTGG CGTGGCCCTG GTCTGTGGTG TCCCGGCCAT GGACATCCCC CAGACCAAGC 120
40 AGGACCTGGA GCTCCCAAAG TTGGCAGGGA CCTGGCACTC CATGGCCATG GCGACCAACA 180
ACATCTCCCT CATGGCGACA CTGAAGGCC CTTGAGGGT CCACATCACC TCACTGTTGC 240
CCACCCCGGA GGACAACCTG GAGATCGTTC TGCACAGATG GGAGAACAAC AGCTGTGTTG 300
AGAAGAAGGT CCTTGAGAG AAGACTGGGA ATCCAAAGAA GTTCAAGATC AACTATACGG 360
45 TGGCGAAGCA GGCCACGCTG CTCGATACTG ACTACGACAA TTCTCTGTTT CTCTGCCTAC 420
AGGACACCAC CACCCCATC CAGAGCATGA TGTGCCAGTA CCTGGCCAGA GTCCTGGTGG 480
AGGACGATGA GATCATGCAG GGATTTCATCA GGGCTTTCAG GCCCTGCC AGGCACCTAT 540
GGTACTTGCT GGACTTGAAA CAGATGGAAG AGCCGTGCCG TTTCTAGCTC ACCTCGCCT 600
50 CCAGGAAGAC CAGACTCCCA CCCTTCCACA CCTCCAGAGC AGTGGGACTT CCTCTGCC 660
TTTCAAAGAA TAACCACAGC TCAGAAGACG ATGACGTGTT CATCTGTGTC GCCATCCCCT 720
TCCTGCTGCA CACCTGCACC ATTGCCATGG GGAGGCTGCT CCCTGGGGGC AGAGTCTCTG 780
GCAGAGGTTA TTAATAAACC CTGGAGCAT G
```

Seq ID NO: 551 Protein sequence

Protein Accession #: NP_002562.1

```
55 1 11 21 31 41 51
| | | | |
MDIPQTKQDL ELPKLAGTWH SMAMATNNIS LMATLKAPLR VHITSLLPTE EDNLEIVLHR 60
WENNSCVERK VLGEKTGNPK KFKINYTVAN EATLLDTDYD NFLFLCLQDT TTPIQSMMQC 120
60 YLARVLVEDD EIMQGFIRAF RPLPRHLWYL LDLKQMBEPC RF
```

Seq ID NO: 552 DNA sequence

Nucleic Acid Accession #: NM_006500.1

Coding sequence: 27..1967

```
65 1 11 21 31 41 51
| | | | |
ACTTGCCTCT CGCCCTCCGG CCAAGCATGG GGCTTCCCAG GCTGGTCTGC GCCTTCTTGC 60
TCGCCGCTTG CTGCTGCTGT CCTCGGTCG CGGGTGTGCC CGGAGAGGCT GAGCAGCCTG 120
70 CGCCTGAGCT GGTGGAGGTG GAAGTGGGCA GCACAGCCCT TCTGAAGTGC GGCCCTCTCC 180
AGTCCCAAGG CAACCTCAGC CATGTGCACT GGTTTTCTGT CCACAAGGAG AAGCGGACGC 240
TCATCTTCCG TGTGCCCCAG GGCCAGGGCC AGAGCGAACC TGGGGAGTAC GAGCAGCGGC 300
TCAGCCTCCA GAGCAGAGGG GCTACTCTGG CCTGACTCA AGTCACCCCC CAAGACGAGC 360
75 GCATCTTCTT GTGCCAGGGC AAGCGCCCTC GGTCCAGGA GTACCGCATC CAGCTCCGCG 420
TCTACAAAGC TCCGGAGGAG CCAAACATCC AGGTCAACCC CCTGGGCATC CCTGTGAACA 480
GTAAGGAGCC TAGGAGGTC GTACTCTGTG TAGGGAGGAA CGGGTACCCC ATTCCTCAAG 540
80 TCATCTGGTA CAGAATGGC CGGCCCTCTGA AGGAGGAGAA GAACCGGGTC CACATTCACT 600
CGTCCCAGAC TGTGGAGTCG AGTGGTTTGT ACACCTTGCA GAGTATTCTG AAGGCACAGC 660
TGGTTAAAGA AGACAAAGAT GCCCAGTTTT ACTGTGAGCT CAACTACCGG CTGCCCAGTG 720
85 GGAACCATAT GAAGGAGTCA AGGGAAGTCA CCGTCCCTGT TTTCTACCCG ACAGAAAAAG 780
TGTGGCTGGA AGTGGAGGCT GTGGGAATGC TGAAGGAAGG GGACCGCGTG GAAATCAGGT 840
GTTTGGCTGA TGGCAACCTT CCACCACTC TCAGCATCAG CAAGCAGAAC CCGAGCAGCA 900
GGGAGGCAGA GGAAGAGACA ACCAACGACA ACGGGGTCCT GGTGCTGGAG CCTGCCCGGA 960
AGGAACACAT TGGGCGCTAT GAATGTCAAG CTGGAACCTT GGACACCATG ATATCGCTGC 1020
TGTGTGAACC ACAGGAACCT CTGGTGAAC TGTGTCTGTA CGTCCGAGTG AGTCCCGCAG 1080
CCCCTGAGAG ACAGGAAGGC AGCAGCTCTA CCCTGACCTG TGAGGCAGAG AGTAGCCAGG 1140
ACCTCGAGTT CAGTGGCTG AGAGAAGAGA CAGACCAAGT GCTGGAAGG GGGCCTGTGC 1200
```

Seq ID NO: 553 Protein sequence
Protein Accession #: NP_006491.1

Seq ID NO: 554 DNA sequence
Nucleic Acid Accession #: NM_003183.3
Coding sequence: 165..2639

395

	AATTGGGACA	TAATTTTGGG	GCAGAACATG	ATCCGGATGG	TCTAGCAGAA	TGTGCCCCGA	1440
	ATGAGGACCA	GGGAGGGAAA	TATGTCATGT	ATCCCATAGC	TGTGAGTGGC	GATCACGAGA	1500
	ACAAATAAGAT	GTTTTCAAAAC	TGCAGTAAAC	AATCAATCTA	TAAGACCATT	GAAAGTAAGG	1560
5	CCGAGGAGTG	TTTTCAAGAA	CGCAGCAATA	AAGTTTGTGG	GAACCTCGAGG	GTGGATGAAG	1620
	GAGAAGAGTG	TGATCCTGGC	ATCATGTATC	TGAACAACGA	CACCTGCTGC	AACAGCGACT	1680
	GCACGTTGAA	GGAAGGTGTC	CAGTGCAGTG	ACAGGAACAG	TCCTTGCTGT	AAAAACTGTC	1740
	AGTTTGAGAC	TGCCCAGAAAG	AAGTGCCAGG	AGGCGATTAA	TGCTACTTGC	AAAGGCGTGT	1800
	CCTACTGCAC	AGGTAATAGC	AGTGAGTGCC	CGCCTCCAGG	AAATGCTGAA	AATGACACTG	1860
	TTTGCTTGGA	TCCTGGCAAG	TGTAAGGATG	GGAAATGCAT	CCCTTCTGTC	GAGAGGGAAAC	1920
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	AGTTTTTAGC	AGACAACATC	GTTGGGTCTG	TCCTGGTTTT	CTCCTTGATA	TTTTGGATTG	2220
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Seq ID NO: 555 Protein sequence
Protein Accession #: NP_003174.2

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	PKVCGYLKVD	NEELLPKGLV	DREPPEELVH	RVKRRADPDF	MKNCTKLLVV	ADHRFYRYMG	240
	RGEESTTTNY	LIELIDRVDD	IYRNTSWDNA	GFKGYGIQIE	QIRILKSPQE	VKPGKEHYNM	300
	AKSYNPEEKD	ANDVKMLLEQ	FSFDIAEBAS	KVCLAHLFY	QDFDMGTLL	AYVGSPPRNS	360
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	SRVDEGEEDC	PIMILNNND	CCNSDCTLKE	GVQCSDRNSP	CKNCQFETA	QKKCQEAINA	540
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Nucleic Acid Accession #: NM_021832.1
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	CGGCCCCCAC	CAGAGACTCG	AGAAGCTTGA	TTCTTTGCTC	TCAGACTACG	ATATTCTCTC	300
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	GTACACTGTA	AAATGGCAGG	ACTTCTTCAC	TGGACACGTG	GTTGGTGAGC	CTGACTCTAG	540
	GGTTCTAGCC	CACATAAGAG	ATGATGATGT	TATAATCAGA	ATCAACACAG	ATGGGGCCGA	600
75	ATATAACATA	GAGCCACTTT	GGAGATTTGT	TAATGATACC	AAAGACAAAA	GAATGTTAGT	660
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 Protein Accession #: NP_068604.1

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 45 PKVCGYLVKLD NEELLEPKGLV DREPPEELVH RVKRRADDPD MKNTCKLLVV ADHRFYRYMG 240
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 TTCCACGTCC AGCTCAGCAA CCCTAAGTTT GGGGCCACC TGGGCCAGCC CCACTCCACC 3420
 ACCATCATCA TCAGGGAGCC AGATGAATCG GACCGGAGCT TCACGAGTCA GATGTTGTCA 3480
 TCACAGCCAC CCCCTCAGGG CGACCTGGGC GCCCGCAGA ACCCCAATGC TAAGGCCGCT 3540
 GGGTCCAGGA AGATCCATTT CAACTGGCTG CCCCTTCTG GCAAGCCAAT GGGGTACAGG 3600
 GTAAAGTACT GGATTCAGGG TGAATCCGAA TCCGAAGCCC ACCTGCTGCA CAGCAAGGTG 3660
 CCCTCAGTGG AGCTCACCAA CCTGTACCCG TATTGCGACT ATGAGATGAA GGTGTGCGCC 3720
 TACGGGGCTC AGGGCGAGGG ACCCTACAGC TCCCTGGTGT CCTGCCGCAC CCACCAGGAA 3780
 GTGCCACGCG AGCCAGGGCG TCTGGCCTTC AATGTCGTCT CCTCCACGGT GACCCAGCTG 3840
 AGCTGGGCTG AGCCGGCTGA GACCAACGGT GAGATCACAG CCTACGAGGT CTGCTATGGC 3900
 CTGGTCAACG ATGACAACCG ACCTATTGGG CCCATGAAGA AAGTGCTGGT TGACAACCCT 3960
 AAGAACCAGA TGCTGCTTAT TGAGAACCTT CGGGAGTCCC AGCCCTACCG CTACACGGTG 4020
 AAGGCGCGCA ACGGGGCCGG CTGGGGGCTT GAGCGGGAGG CCATCATCAA CCTGGCCACC 4080
 CAGCCCAAGA GGCCCATGTC CATCCCCATC ATCCCTGACA TCCCTATGCT GGACGCCAG 4140
 AGCGGGGAGG ACTACGACAG CTTCCTTATG TACAGCGATG ACCTTCTACG CTCTCCATCG 4200
 GGCAGCCAGA GGCCCGAGCT CTCCGATGAC ACTGAGCACC TGGTGAATGG CCGGATGGAC 4260
 TTTGCTCTCC CGGGCAGCAC CAATCCCTG CACAGGATGA CCACGACCAG TGCTGCTGCC 4320
 TATGGCACCC ACCTGAGCCC ACACGTGCCC CACCGCGTGC TAAGCACATC CTCCACCTC 4380
 ACACGGGACT ACAACTCACT GACCCGCTCA GAACACTCAC ACTCGACCAC ACTGCCGAGG 4440
 GACTACTCCA CACTCACTCT CGTCTCCTCC CACGACTCTC GCCTGACTGC TGGTGTGCCC 4500
 GACACGCCCA CCCGCTGGT GTTCTCTGCC CTGGGGCCCA CATCTCTCAG AGTGAGCTGG 4560
 CAGGAGCCGC GGTGCGAGCG GCCGTGTCAG GGCTACAGT TGGAGTACCA GCTGCTGAAC 4620
 GGCGGTGAGC TGCATCGGCT CAACATCCCC AACCTGCCCC AGACCTCGGT GGTGGTGGAA 4680
 GACCTCCTGC CCAACCACTC CTACGTGTTT CGCGTGCGGG CCCAGAGCCA GGAAGGCTGG 4740
 GGCCGAGAGC GTGAGGGTGT CATCACCATT GAATCCCAGG TGCAACCCGA GAGCCCACTG 4800
 TGTCCCTGTC CAGGCTCCGC CTTCACCTTG AGCACTCCCA GTGCCCCAGG CCCGCTGGTG 4860
 TTCCTGCCCC TGAGCCCACT CTGCTGTCAG CTGAGCTGGG AGCGGCCACG GAGGCCCAAT 4920
 GGGGATATCG TCGGCTACCT GGTGACCTGT GAGATGGGCC AAGGAGGAGG GCCAGCCACC 4980
 GCATTCGGGG TGGATGGAGA CAGCCCCGAG AGCCGGCTGA CCGTGCCGGG CCTCAGCGAG 5040
 AACGTGCCCT ACAAGTTCAA GGTGCAGGCC AGGACCACTG AGGGCTTCGG GCCAGAGCGC 5100
 GAGGGCATCA TCACCATAGA GTCCAGGAT GGAGGACCTT TCCCGCAGCT GGGCAGCGT 5160
 GCCGGGCTCT TCCAGCACCC GCTGCAAAAG GAGTACAGCA GCATCACCA CACCCACACC 5220
 AGCGCCACCG AGCCCTTCTT AGTGGATGGG CCGACCTTGG GGGCCAGCA CCTGGAGGCA 5280
 GGCGGCTCCC TCACCCGCA TGTGACCCAG GAGTTTGTGA GCCGACACT GACCACCAGC 5340
 GGAAACCTTA GCACCCACAT GGACCAACAG TTCTTCCAAA CTGAGCCGCA CCCTGCCCCA 5400
 CCCCAGCAT CTCCCATAG GCGTCTCTCC GACTCCTCTC CCGGAGCCTC CTCAGCTACT 5460
 CCATCTTGC ACCCTGGGG GCCCAGCCCA CCCGATGCA CAGAGCAGGG GCTAGGTGTC 5520
 TCCTGGGAGG CATGAAGGG GCAAGGTCCG TCCTCTGTGG GCCCAAACCT ATTTGTAACC 5580
 AAAGAGCTGG GAGCAGCACA AGGACCCAGC CTTTGTCTG CACTTAATAA ATGTTTTTGC 5640
 TACTG

Seq ID NO: 561 Protein sequence
 Protein Accession #: NP_000204.1

1 11 21 31 41 51
 MAGPRPSPWA RLLLAALISV SLSGTLANRC KKAPVKSCTE CVRVKDCAY CTDEMFRDRR 60
 CNTQAEALLAA GCQRRESIVM ESSFQITEET QIDTTLRRSQ MSPQGLRVRL RPGEERHFEL 120
 EVFEPLESPV DLYILMDFSN SMSDDLNLK KMGQNLARVL SOLTSDYTIG FGKFDVKVSV 180
 PQTDMRPEKL KEPWPNSDPP FSKFNVISLT EDVDEFRNKL QGERISGNLD APEGGFDAIL 240
 QTAVCTRIDG WRPDSTHLLV FSTESAFHYE ADGANVLGAI MSRNDERCHL DTTGTYTQYR 300
 TQDYPSPVPTL VRLAKHNI PIFAVTNYSY SYEKLHTYF PVSSLGVLQE DSSNIVELLE 360
 EAFNIRIRNL DIRALDSPRG LRTEVTSKMF QKTRTGSFHI RRGEVGIVQV QLRALHEVDG 420
 THVCQLPEDQ KGNHILKPSF SDGLKMDAGI ICDVCTCELQ KEVRSARCSF NGDFVCGQCV 480
 CSEGNWGGTC NCSTGSLSDI QPCLREGEDEK PCSGRGECQC GHCVCYGEGR YEGQFCEYDN 540
 FQCPRTSGFL CNDRCRCSMG QCVCEFGWTG PSCDCPLSNA TCIDSNNGIC NGRGHCECGR 600
 CHCHQQLSYT DTICEINYSA IHPGLCEDLR SCVQCQAWGT GEKKGRTECE CNFKVKMVDE 660
 LKRAEEVVVR CSFRDEDDDC TYSYTMEDG APGPNSTVLV HKKKDCPPGS FWLPLPLLL 720
 LLPLALLLLL LCWKYCACCK ACLALLPCCN RGHMVGFKEG HYMLRENMA SDHLDTPLMR 780
 SGNLKGDRDV RWKVTNNMQR PGFATHAASI NPTELVPYGL SLRLARLCTE NLLKPDTRC 840
 AQLRQVEVEN LNEVYRQISG VHKLQQTFR QPNAGKKQD HTIVDTVLMA PRSAKPALLK 900
 LTEKQVEQRA FHDLVKAPGV YTLTADQDAR GMVEFQEGVE LVDVRVPLFI RPEDDDEKQL 960
 LVEAIDVPAG TATLGRRLVN ITIIEQARD VVSFEQPEFS VSRGDQVARI PVIRRVLDGG 1020
 KSQVSYRTQD GTAQGNRDI PVEGELLFQP GEAWKELQVK LLELQEVDSL LRGRQVRRFH 1080
 VQLSNPKFGA HLGQPHSTTI IIRDPDELDR SFTSQMLSSQ PPPHGDLAGP QNPNAKAAGS 1140
 RKIHFNLWLP SGKPMGYRVK YWIQDSESE AHLDSKVPS VELTNLYPYC DYEMKVCAYG 1200
 AQGEGPYSSL VSCRTHQEV SEPGRALFNV VSSTVTQLSW AEPATNGEI TAYEVCYGLV 1260
 NDDNRPIGPM KVLVDNPNK RMLLENLRE SQPYRYTVKA RAGAGWGP ER EAIINLATQP 1320
 KRPMSPPIIP DIPIVDAQSG EDYDSFLMYS DDVLRSPSGS QRPSVSDTE HLVNGRMDFA 1380
 FPGSTNSLHR MTTTSAAYG THLSPHVPHR VLSTSTLTR DYNLSRSEH SHSTTLPRDY 1440
 STLTSSSHD SRLTAGVPDT PTRLVFSALG PTLRLVSWQE PRCEPLQGY SVEYQLLNGG 1500
 ELHRLNIPNP AQTSVVVEDL LPNHSYVFRV RAQSQEGWGR EREGVITIES QVHPQSPLCP 1560
 LPSAFTLST PSAGPLVFT ALSPDSLQLS WERPRRPNGD IVGYLVTCEM AQGGGPATAP 1620
 RVDGDSPEBR LTVPLGSENV PYKFKVQART TEGFGPEREG IITIESQDGG PFPQLGSRA 1680
 LFQHLPLQSEY SSITTTHTSA TEPFLVDGPT LGAQHLEAGG SLTRHVTQEF VSRTLTTSST 1740
 LSTHMDQQFF QT

Seq ID NO: 562 DNA sequence
 Nucleic Acid Accession #: NM_013332.1
 Coding sequence: 1..63

1 11 21 31 41 51
 | | | | |

GCACGAGGGC GCTTTTGTCT CCGGTGAGTT TTGTGGCGGG AAGCTTCTGC GCTGGTGCTT 60
 AGTAACCGAC TTTCTCCGG ACTCTGCAC GACCTGCTCC TACAGCCGCG GATCCACTCC 120
 CGGCTGTTC CCCGAGGGT CCAGAGGCTT TCCAGAAAGG GAAGGCAGCT CTGTTTCTCT 180
 GCACGAGGAGT AGGGTCCCTT CAGCCATGAA GCATGTGTTG AACCTCTACC TGTTAGGTGT 240
 GGTACTGAAC CTACTCTCCA TCTTCGTTAG AGTGATGGAG TCCCTAGAAG GCTTACTAGA 300
 GAGCCCATCG CCTGGGACCT CCTGGACCAC CAGAAGCCAA CTAGCCAACA CAGAGCCAC 360
 CAAGGGCCTT CCAGACCATC CATCCAGAAG CATGTGATAA GACCTCCTTC CATACTGGCC 420
 ATATTTTGGG ACACCTGACCT AGACATGTCC AGATGGGAGT CCCATTCTTA GCAGACAAAGC 480
 TGAGCACCGT TGTAAACAGA GAACTATTAC TAGGCCTTGA AGAACCTGTC TAACTGGATG 540
 CTCATTGCCT GGGCAAGGCC TGTTTAGGCC GGTTCGCGTG GCTCATGCCT GTAATCCTAG 600
 CACTTTGGGA GGCTGAGGTG GGTGGATCAC CTGAGGTCAG GAGTTCGAGA CCAGCCTCGC 660
 CAACATGGCG AAACCCCATC TCTACTAAAA ATACAAAAGT TAGCTGGGTG TGGTGGCAGA 720
 GGCCTGTAAT CCCAGTTCCT TGGGAGGCTG AGGCGGAGGA ATTGCTTGAA CCCGGGGACG 780
 GAGGTTGCAG TGAACCGAGA TCGCACTGCT GTACCCAGCC TGGGCCACAG TGCAAGACTC 840
 CATCTCAAAA AAAAAAAGAA AAGAAAAAGC CTGTTTAATG CACAGGTGTG AGTGGATTGC 900
 TTATGGCTAT GAGATAGGTT GATCTCGCCC TTACCCGGGG GTCTGGTGTA TGCTGTGCTT 960
 TCCTCAGCAG TATGGCTCTG ACATCTCTTA GATGTCCCAA CTTCAGCTGT TGGGAGATGG 1020
 TGATATTTTC AACCTACTT CCTAAACATC TGCTCTGGGT TCCTTTAGTC TTGAATGTCT 1080
 TATGCTCAAT TATTTGGTGT TGAGCCTCTC TTCCACAAGA GCTCCTCCAT GTTTGGATAG 1140
 CAGTTGAAGA GGTGTGTGTG GTGGGCTGTT GGGAGTGAGG ATGGAGTGT CAGTGCCCAT 1200
 TTCTCATTTT ACATTTTAAA GTCGTTCTCT CAACATAGTG TGTATTGGTC TGAAGGGGGT 1260
 GGTGGGATGC CAAAGCCTGC TCAAGTTATG GACATTGTGG CCACCATGTG GCTTAAATGA 1320
 TTTTCTCTAA CTAATAAAGT GGAATATATA TTTCAAAAA AAAAAAAAAA AA

Seq ID NO: 563 Protein sequence
 Protein Accession #: NP_037464.1

1 11 21 31 41 51
 MKHVLNLYLL GVVLTLLSIF VRVMESLEGL LESPSPGTSW TTRSQLANTE PTKGLPDHPS 60
 RSM

Seq ID NO: 564 DNA sequence
 Nucleic Acid Accession #: NM_023915.1
 Coding sequence: 250..1326

1 11 21 31 41 51
 GGCACGAGGG TTTCTTTTTC ATGCTTTACC AGAAAAATCCA CTTCCTGCCC GACCTTAGTT 60
 TCAAAGCTTA TTCTTAATTA GAGACAAAGAA ACCTGTTTCA ACTTGAAGAC ACCGTATGAG 120
 GTGAATGGAC AGCCAGCCAC CACAATGAAA GAAATCAAAC CAGGAATAAC CTATGCTGAA 180
 CCCACGCTC AATCGTCCCC AAGTGTCTCC TGACACGCAT CTTTGCTTAC AGTGCAATCAC 240
 AACTGAAGAA TGGGGTTCAA CTTGACGCTT GCAAAATTAC CAAATAACGA GCTGCACGGC 300
 CAAGAGAGT ACAATTACAG CAACAGGAGC GACGGGCCAG GAAAGAACAC CACCTTCAC 360
 AATGAATTG ACACAATTGT CTGCGCGTG CTTTATCTCA TTATATTTGT GGCAAGCATC 420
 TTGCTGAATG GTTTAGCACT GTGGATCTTC TTCCACATTA GGAATAAAAC CAGCTTCATA 480
 TTCTATCTCA AAAACATAGT GGTTCGACAC CTCATAATGA CGCTGACATT TCCATTTTGA 540
 ATAGTCCATG ATGCAAGATT TGGACCTTGG TACTTCAAGT TTATCTCTG CAGATACACT 600
 TCAGTTTTGT TTTATGCAAA CATGTATACT TCCATCGTGT TCCTTGGGCT GATAAGCATT 660
 GATCGCTATC TGAAGGTGGT CAAGCCATTG GGGGACTCTC GGATGTACAG CATAACCTTC 720
 ACGAAGGTTT TATCTGTTTG TGTTTGGGTG ATCATGGCTG TTTTGTCTTT GCCAAACATC 780
 ATCCTGACAA ATGGTCAGCC AACAGAGGAC AATATCCATG ACTGCTCAA ACTTAAAAGT 840
 CCTTTGGGGG TCAAATGGCA TACGGCAGTC ACCTATGTGA ACAGCTGCTT GTTTGTGGCC 900
 GTGCTGGTGA TTCTGATCGG ATGTTACATA GCCATATCCA GGTACATCCA CAAATCCAGC 960
 AGGCAATTCA TAAGTCAGT AAGCCGAAAG CGAAAAACATA ACCAGAGCAT CAGGGTTGTT 1020
 GTGGCTGTGT TTTTACCTG CTTTCTACCA TATCACTTGT GCAGAATTCC TTTTACTTTT 1080
 AGTCACTTAG ACAGGCTTTT AGATGAATCT GCACAAAAA TCCTATATTA CTGCAAGAA 1140
 ATTACACTTT TCTTGTCTGC GTGTAATGTT TGCCCTGGATC CAATAATTGA CTTTTCATG 1200
 TGTAGGTCAT TTTCAGAGAG GCTGTTCAAA AAATCAAATA TCAGAACCAG GAGTGAAAGC 1260
 ATCAGATCAC TGCAAGGTGT GAGAAGATCG GAAAGTCGCA TATATTATGA TTACTACTGAT 1320
 GTGTAGGCTT TTTATTGTTT GTTGAATCG ATATGTACAA AGTGTAATAA AATGTTTCTT 1380
 TTCATTATCC TTAATAAAAA AA

Seq ID NO: 565 Protein sequence
 Protein Accession #: NP_076404

1 11 21 31 41 51
 MGFNLTAKL PNNELHQES HNSGNRSDGP GKNTTLHNEF DTIVLPVLYL IIFVASILLN 60
 GLAVWIFPHI RNKTSFIFYL KNIVVADLIM TLTFPFRIVH DAGFGPWYFK FILCRYTSVL 120
 FYANMYTSIV FLGLISIDRY LKVVKPFPGDS RMYSTFTKV LSVCVWVIMA VLSLPIIILT 180
 NGQPTEDNIH DCSKLKSPLG VKWHTAVTYV NSCLFVAVLV ILIGCYIAIS RYIHKSSRQF 240
 ISQSSRRKRK NQSIRVVVAV FFTCFLPYHL CRIPFTFSLH DRLLDESAQK ILYYCKEITL 300
 FLSACNVCLD PIIFYFMCRS FSRRLFKKSN IRTRESIRS LQSVRRSEVR IYYDITDV

Seq ID NO: 566 DNA sequence
 Nucleic Acid Accession #: NM_005365.1
 Coding sequence: 1..948

1 11 21 31 41 51
 ATGTCCTCTG AGCAGAGGAG TCCGCACTGC AAGCCTGATG AAGACCTTGA AGCCCAAGGA 60
 GAGGACTTGG GCCTGATGGG TGCACAGGAA CCCACAGGCG AGGAGGAGGA GACTACCTCC 120
 TCCTCTGACA GCAAGGAGGA GGAGGTGTCT GCTGCTGGGT CATCAAGTCC TCCCAGAGT 180
 CCTCAGGAG GCGCTTCCTC CTCCATTTCG GTCTACTACA CTTTATGGAG CCAATTCGAT 240
 GAGGGCTCCA GCAGTCAAGA AGAGGAAGAG CCAAGCTCCT CGGTGAGACC AGCTCAGCTG 300
 GAGTTCATGT TCCAAGAAGC ACTGAAATTG AAGGTGGCTG AGTTGGTTCA TTTCTGCTC 360

CACAAATATC GAGTCAAGGA GCCGGTCACA AAGGCAGAAA TGCTGGAGAG CGTCATCAAA 420
 AATTACAAGC GCTACTTTCC TGTGATCTTC GGCAAAGCCT CCGAGTTCAT GCAGGTGATC 480
 TTTGGCACTG ATGTGAAGGA GGTGGACCCC GCCGGCCACT CCTACATCCT TGTCACTGCT 540
 CTTGGCCTCT CGTGCAGATG CATGCTGGGT GATGGTCATA GCATGCCCAA GGCCGCCCTC 600
 CTGATCATTT TCCCTGGGTG GATCCTAACC AAAGACAACT GCGCCCTTGA AGAGGTTATC 660
 TGGGAAGCGT TGAGTGTGAT GGGGGTGTAT GTTGGGAAGG AGCACATGTT CTACGGGGAG 720
 CCCAGGAAGC TGCTCACCCA AGATTGGGTG CAGGAAAACCT ACCTGGAGTA CCGGCAGGTG 780
 CCCGGCAGTG ATCCTGCGCA CTACGAGTTC CTGTGGGGTT CCAAGGCCCA CGCTGAAACC 840
 AGCTATGAGA AGGTCAATAA TTATTGGTC ATGCTCAATG CAAGAGAGCC CATCTGCTAC 900
 CCATCCCTTT ATGAAGAGGT TTTGGGAGAG GAGCAAGAGG GAGTCTGA

Seq ID NO: 567 Protein sequence
 Protein Accession #: NP_005356.1

1 11 21 31 41 51
 MSLEQRSPHC KPDEDLAQQ EDLGLMGAQE PTGEEETTS SSSKEEEVS AAGSSPPQS 60
 PQGGASSIS VYITLWSQFD EGSSSQEEEE PSSVDPAQL EFMFQALKL KVAELVHLL 120
 HKYRVKEPVT KAEMLESVIF NYKRYFPVIF GKASEFMQVI FGTDVKEVDP AGHSYILVTA 180
 LGLSCDSMLG DGHSMFKAAL LIIVLGVILT KDNCAPEEVI WEALSVMGVY VGKHEMFYGE 240
 PRKLLTQDWV QENYLEYRQV PGSDPAHYEF LWGSKAHAET SYEKVINILV MLNAREPICY 300
 PSLYEVLGE EQEGV

Seq ID NO: 568 DNA sequence
 Nucleic Acid Accession #: NM_014400
 Coding sequence: 86..1126

1 11 21 31 41 51
 GGTTACTCAT CCTGGGCTCA GGTAAAGAGG CCGGAGCTCG GAGGCGGCAC ACCCAGGGGG 60
 GACGCCAAGG GAGCAGGACG GAGCCATGGA CCCC GCCAGG AAAGCAGGTG CCCAGGCCAT 120
 GATCTGGACT GCAGGCTGGC TGCTGCTGCT GCTGCTTCGC GGAGGAGCGC AGGCCCTGGA 180
 GTGCTACAGC TGCCTGCAGA AAGCAGATGA CGGATGCTCC CGAACAAGA TGAAGACAGT 240
 GAAGTGCGCG CCGGGCGTGG ACGTCTGCAC CGAGGCCGTG GGGGCGGTGG AGACCATCCA 300
 CGGACAAATC TCGCTGGCAG TGCSGGGTTG CGGTTGCGGA CTCCCCGCCA AGAATGACCG 360
 CGGCCCTGAT CTTACCGGGC TTCTGGOGTT CATCCAGCTG CAGCAATGCG CTCAGGATCG 420
 CTGCAACGCC AAGCTCAACC TCACCTCGCG GCGGCTCGAC CCGGCAGGTA ATGAGAGTGC 480
 ATACCCGCCC AACGCGGTGG AGTGCTACAG CTGTGTGGGC CTGAGCCGGG AGCGGTGCCA 540
 GGGTACATCG CCGCCGGTGG TGAGCTGCTA CAACGCCAGC GATCATGTCT ACAAGGGCTG 600
 CTTGACCGCG AACGTCAACT TGACGGCAGC TAATGTGACT GTGTCTTGC CTGTCCGGGG 660
 CTGTGTCCAG GATGAATTCT GCACTCGGGA TGGAGTAACA GGCCCAAGGT TCACGCTCAG 720
 TGGCTCCTGT TGCCAGGGGT CCCGCTGTAA CTCTGACCTC CGCAACAAGA CCTACTTCTC 780
 CCCTCGAATC CCACCCCTTG TCCGGCTGCC CCCACGACTG TGGCTCTAAC 840
 CACATCTGTC ACCACTTCTA CCTCGGCCCC AGTGAGACCC ACATCCACCA CCAAAACCAT 900
 GCCAGCGGCA ACCAGTCAGA CTCGAGACA GGGAGTAGAA CACGAGGCCT CCCGGGATGA 960
 GGAGCCAGG TTAGCTGGAG GCGCCGCTGG CCACCAGGAC CGCAGCAATT CAGGGCAGTA 1020
 TCCTGCAAAA GGGGGGCCCC AGCAGCCCCA TAATAAAGGC TGTGTGGCTC CCACAGCTGG 1080
 ATTGGCAGCC CTTCTGTTGG CCGTGGCTGC TGGTGTCTTA CTGTGAGCTT CTCACCTGG 1140
 AAATTTCCCT CTCACCTACT TCTCTGGCCC TGGGTACCCC TCTTCTCATC ACTTCTCTGT 1200
 CCCACCACTG GACTGGGCTG GCCCAGCCCC TGTTTTTCCT ACATTCCTCA GTATCCCTAG 1260
 CTTCTGCTGC GCTGTTTGGG GGCTTTGGGA AATAAAATAC CGTTGTATAT ATTCTGGCAG 1320
 GGGTGTCTA GCTTTTGTAG GACAGCTCCT GTATCCTTCT CATCCTTGTC TCTCCGCTTG 1380
 TCCTCTTGTG ATGTTAGGAC AGAGTGAGAG AAGTCAGCTG TCACGGGGAA GGTGAGAGAG 1440
 AGGATGCTAA GCTTCTACT CACTTCTTCC TAGCCAGCCT GGACTTTGGA GCGTGGGGTG 1500
 GGTGGGACAA TGGCTCCCCA CTCTAAGCAC TGCCCTCCCT ACTCCCCGCA TCTTTGGGGA 1560
 ATCGGTTCCC CATATGTCTT CCTTACTAGA CTGTGAGCTC CTCGAGGGCA GGGACCGTGC 1620
 CTTATGTCTG TGTGTGATCA GTTCTGGCA CATAAATGCC TCAATAAAGA TTTAATTACT 1680
 TTGTATAGTG AAAAAAA

Seq ID NO: 569 Protein sequence
 Protein Accession #: NP_055215

1 11 21 31 41 51
 MDPARKAGAQ AMIWTAGWLL LLLLRGAQA LECYSCVQKA DDGCSFNKMK TVKCAPGVVDV 60
 CTEAVGAVET IHGQFSLAVX GCGSGLPGKN DRGLDLHGLL AFIQLQQCAQ DRCNAKLNLT 120
 SRALDPAGNE SAYPPNGVEC YSCVGLSREA CQGTSPPVVS CYNASDHVYK GCFDGNVILT 180
 AANVTVSLPV RGCVDDEFCT RDGVTGPFFT LSGSCCQSSR CNSDLRNKTY FSPRIPLVR 240
 LPPPEPTTVA STTSVTSTIS APVRPTSTTK PMPAPTSQTF RQGVHEASR DEEPRLTGGA 300
 AGHQDRSNSG QYPAKGPPQ PHNKGCVAPT AGLAALLLAV AAGVLL

Seq ID NO: 570 DNA sequence
 Nucleic Acid Accession #: NM_005329.1
 Coding sequence: 1..1662

1 11 21 31 41 51
 ATGCCGGTGC AGCTGACGAC AGCCCTGCGT GTGGTGGGCA CCAGCCTGTT TGCCCTGGCA 60
 GTGCTGGGTG GCATCCTGCG AGCCTATGTG ACGGGCTACC AGTTCATCCA CACGGAAAAG 120
 CACTACCTGT CCTTGGGCTT GTACGGCGCC ATCCTGGGCC TGCACTGTCT CATTGAGAGC 180
 CTTTTTGCTT TCCTGGAGCA CCGGCGCATG CGACGTGCGG GCCAGGCCCT GAAGCTGCCC 240
 TCCCCGCGCG GGGGCTCGGT GGCAGTGTGC ATTGCCGCGT ACCAGGAGGA CCCTGACTAC 300
 TTGCGCAAGT GCCTGCGCTC GGCCAGCGCG ATCTCCTTCC CTGACCTCAA GGTGGTCATG 360
 GTGGTGGATG GCAACCGCCA GGAGGACGCC TACATGCTGG ACATCTTCCA CGAGGTGCTG 420
 GGGCGCACCG AGCAGGCCGG CTTCTTTGTG TGGCGCAGCA ACTTCCATGA GGCAGGCGAG 480
 GGTGAGACGG AGGCCAGCCT GCAGGAGGGC ATGGACCGTG TGCGGGATGT GGTGCGGGCC 540
 AGCACCTTCT CGTGATCATG GCAGAGTGAG GGAGGCAAGC GCGAGGTCTAT GTACACGGCC 600

TCAAGGCC TCGGGGATTC GGTGGACTAC ATCCAGGTGT GCGACTCTGA CACTGTGCTG 660
 GATCCAGCCT GCACCATCGA GATGCTTCGA GTCTGGAGG AGGATCCCCA AGTAGGGGGA 720
 GTCCGGGGAG ATGTCCAGAT CCTCAACAAG TACGACTCAT GGATTTCCTT CCTGAGCAGC 780
 GTGGGGTACT GGATGGCCTT CAACGTGGAG CGGGCCTGCC AGTCCCTACTT TGGCTGTGTG 840
 CAGTGTATTA GTGGGCCCTT GGGCATGTAC CGCAACAGCC TCCTCCAGCA GTTCTCGGAG 900
 GACTGGTACC ATCAGAAGTT CCTAGGCAGC AAGTGCAGCT TCGGGGATGA CCGGCACCTC 960
 ACCAACCCAG TCCTGAGCCT TGGCTACCGA ACTAAGTATA CCGCGCGCTC CAAGTGCCTC 1020
 ACAGAGACCC CCACTAAGTA CCTCCGGTGG CTCAACCAGC AAACCCGCTG GAGCAAGTCT 1080
 TACTTCCGGG AGTGGCTCTA CAACTCTCTG TGGTTCCATA AGCACCACCT CTGGATGACC 1140
 TACGAGTCAG TGGTCACGGG TTTCTTCCCC TTCTTCTCTA TTGCCACGGT TATACAGCTT 1200
 TTCTACCGGG GCCGCATCTG GAACATTCTC CTCTTCTTGC TGACGGTGA GCTGGTGGGC 1260
 ATTATCAAGG CCACCTACGC CTGCTTCCCT CGGGGCAATG CAGAGATGAT CTTTATGTCC 1320
 CTCTACTCCC TCCTCTATAT GTCCAGCCTT CTGCCGGCCA AGATCTTTGC CATTGCTACC 1380
 ATCAACAAT CTGGCTGGGG CACCTCTGGC CGAAAAACCA TTGTGGTGAA CTTTATTGGC 1440
 CTCATTCTCT GTTCCATCTG GGTGGCAGTT CTCTGGGAG GGCTGGCCTA CACAGCTTAT 1500
 TGCCAGGACC TGTTCAGTGA GACAGAGCTA GCCTTCCTTG TCTCTGGGGC TATACGTAT 1560
 GGCTGCTACT GGTGGCCCTT CCTCATGCTA TATCTGGCCA TCATCGCCCG GCGATGTGGG 1620
 AAGAAGCCGG AGCAGTACAG CTTGGCTTTT GCTGAGGTGT GA

Seq ID NO: 571 Protein sequence
 Protein Accession #: NP_005320.1

1 11 21 31 41 51
 MPVQLTTALR VVGTSLFALA VLGGILAAVY TGYQFIHTEK HYLSFGLYGA ILGLHLLIQS 60
 LFAFLEHRRM RRAGQALKLP SPRRGSVALC IAAYQEDPDY LRKCLRSAQR ISFPDLKVVM 120
 VVDGNRQEDA YMLDIFHEVL GGTGQAGFFV WRSNFHEAGE GETEASLQEG MDRVRDVVRA 180
 STFSICIMQKW GKGREVMYTA FKALGDSVDY IQVCDSDTVL DPACTIEMLR VLEEDPQVGG 240
 VGGDVQILNK YDSWISFLSS VRYWMAFNVE RACQSYFGCV QCISGPLGMY RNSLLQQFLE 300
 DWYHQKFLGS KCSFGDDRHL TNRVLSLGYR TKYTARSKCL TETPTKYLRW LNQQTRWSKS 360
 YFRFWLYNSL WFPHKHLWMT YESVVTGFFP FFLIATVIQL FYRGRIWNIL LFLBLTVQLVG 420
 IIKATYACFL RGNAEIMFMS LYSLLYMSSL LPAKIFAIAI INKSGWGTSG RKTIVVNFIG 480
 LIPVSIWVAV LLGLLAYTAY QDLFSETEL AFLVSGAILY GCVWVALIML YLAI IARRCG 540
 KKPEQYSLAF AEV

Seq ID NO: 572 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 148-7095

1 11 21 31 41 51
 CACACATACG CACGCACGAT CTCACCTCGA TCTATACACT GGAGGATTAA AACAAACAAA 60
 CAAAAAAAC ATTTCTCTCG CTCCCCTCC CTCTCCACTC TGAGAAGCAG AGGAGCCGCA 120
 CGGGCAGGGG CCGCAGACCG TCTGGAAATG CGAATCCATA AGCGTTTCCT CGCTTGCAAT 180
 CAGCTCCTCT GTGTTTGCCG CCTGGATTGG GCTAATGGAT ACTACAGACA ACAGAGAAAA 240
 CTTGTGTAAG AGATTGGCTG GTCCTATACA GGAGCACTGA ATCAAAAAA TTGGGGAAAG 300
 AAATATCCAA CATGTAATAG CCCAAAAA TCTCTATCA ATATTGATGA AGATCTTACA 360
 CAAGTAAATG TGAATCTTAA GAACTTAAA TTTCAGGGTT GGGATAAAAC ATCATTGGAA 420
 AACACATTCA TTCATAACAC TGGGAAAAA GTGGAAATTA ATCTCACTAA TGACTACCGT 480
 GTCAGCGGAG GAGTTTCAGA AATGGTGT TT AAAGCAAGCA AGATAACTTT TCACTGGGGA 540
 AAATGCAATA TGTATCTGTA TGGATCAGAG CATAGTTTAG AAGGACAAAA ATTTCCACTT 600
 GAGATGCAAA TCTACTGCTT TGATGCGGAC CGATTTTCAA GTTTTGAGGA AGCAGTCAAA 660
 GGAAAAAGGA AGTTAAGAGC TTTATCCATT TTGTTGAGG TTGGGACAGA AGAAAAATTG 720
 GATTTCAAAG CGATTATTGA TGGAGTCGAA AGTGTAGTC GTTTTGGGAA GCAGGCTGCT 780
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	GATTCTGTGG	GTGTAACCTA	TCAGGGTTCC	TTATTAGCG	GCCCTAGCCA	TATACCAATA	3060
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	GGTGATGGGG	AAATGGTCTGG	AGCCTCTTCT	GATAGTGAAT	TTCTTTTACC	TGACACAGAT	3180
	GGGCTGACAG	CCCTTAAACAT	TTCTTCACTT	GTTTCTGTAG	CTGAATTAC	ATATACAACA	3240
10	TCTGTGTTTG	GTGATGATAA	TAAGGCGCTT	TCTAAAAGTG	AAATAATATA	TGGAAATGAG	3300
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	CCCAACATGT	ATGATAATGT	AAATAAGTTG	AATGCGTCTT	TACAAGAAAC	CTCTGTTTCC	3420
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	GACACCTTGC	TTAAACCTGT	TCTTCCAGCT	GTGCCAGTG	ATCCAATATT	GGTTGAAACC	3780
	CCCAAGTTG	ATAAAATTAG	TTCTACAATG	TTGCATCTCA	TTGTATCAAA	TTCTGCTTCA	3840
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	CCAATCTCAT	ACTCACTATC	TGAGAATTCT	GAAGAAGATA	ATAGAGTCAC	AAGTGATATC	4620
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	TCCCAAAAGC	ACAATGATGG	AAAAGAGGAA	AATGACATTC	AGACTGGTAG	TGCTCTGCTT	4740
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	GGGCAAGGTA	CCTCAGATAG	CCTTAATGAG	AATGAGACTT	CCACAGATTT	CAGTTTTCGA	4860
	GACACTAATG	AAAAAGATGC	TGATGGGATC	CTGGCAGCAG	GTGACTCAGA	AATAACTCCT	4920
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	TCAGAGGCAG	AGGCCAGTAA	TAGTAGCCAT	GAGTCTCGTA	TTGGTCTAGC	TGAGGGGTTG	5040
40	GAATCCGAGA	AGAAGGCAGT	TATACCCCTT	GTGATCGTGT	CAGCCCTGAC	TTTTATCTGT	5100
	CTAGTGGTTC	TTGTTGGGTAT	TCTCATCTAC	TGGAGGAAAT	GCTTCCAGAC	TGCACACTTT	5160
	TACTTAGAGG	ACAGTACATC	CCCTAGAGTT	ATATCCACAC	CTCCAAACACC	TATCTTTCCA	5220
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45	CATGCAAGTA	GTGGGTTTAC	TGAAGAATTT	GAGACACTGA	AAGAGTTTAA	CCAGGAAGTG	5340
	CAGAGCTGTA	CTGTGTACTT	AGGTATTACA	GCAGACAGCT	CCAACCAACC	AGACAACAAG	5400
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55	CTGACCTTTG	TAGAAAGGCC	AGCCTATGCC	AAGCGCCATG	CAGTGGGGCC	TGTTGTGCTC	5940
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	CAGATTCAAC	ACGAAGGAAC	TGTCAACATA	TTTGGCTTCT	TAAACACAT	CCGTTTCAAA	6060
	AGAAATTTAT	TGGTACAAAC	TGAGGAGCAA	TATGTCTTCA	TTCATGTATC	ACTGGTTGAG	6120
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60	CAGTCAAAATA	TACAGCAGAG	TGACTATTCT	GCAGCCCTAA	AGCAATGCAA	CAGGGAAGAG	6300
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	TTTATCATTA	CCCAGCACCC	TCTCCTTCAT	ACCATCAAGG	ATTCTTGGAG	GATGATATGG	6480
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65	TTTGTTTACT	GGCCAAATAA	AGATGAGCCT	ATAAATTGTG	AGAGCTTTAA	GGTCACTCTT	6600
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	TTAGAAGCTA	CACAGGATGA	TTATGTACTT	GAAGTGAGGC	ACTTTCAGTG	TCCTAAATGG	6720
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	GCTGCCAATA	GGGATGGGCC	TATGATTGTT	CATGATGAGC	ATGGAGGAGT	GACGGCAGGA	6840
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Seq ID NO: 573 Protein sequence:
Protein Accession #: Bos sequence

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	ILFEVGTEN	LDFKAIIDGV	ESVSRFGKQA	ALDPFILLNL	LPNSTDKYII	YNGSLTSPPC	240
	TDTVDWIVFK	DTVSISESQL	AVFCEVLTMQ	QSGYVMLMDY	LQNNFREQQY	KFSRQVFSSY	300
	TGKEEIEHAV	CSSEPNVQA	DPENYTSLLV	TWERPRVVD	TMIEKFAVLY	QQLDGEDQTK	360
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	RSPTRGSEFS	GKGDVPNTSL	NSTSQPVTKL	ATEKDISLTS	QTVTELPPHT	VEGTSASLND	540
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20	TEVTPHAFPT	SSRQDLVST	VNVVYSQTTQ	PVYNGETPLQ	PSYSSEVFPL	VTPLLLDNQI	780
	LNTTPAASSS	DSALHATPVF	PSVDVSFESI	LSSYDGAPLL	PFSSASFSSS	LFRHLHTVSQ	840
	ILPQVTSATE	SDKVPLHASL	PVAGDGLLE	PSLAQYSDVL	STTHAASETL	EFSGESGVLY	900
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	SLFSGPSHIP	IPKSSLLTPT	ASLLQPTHAL	SGDGEWSGAS	SDSEFLLPDT	DGLTALNISS	1020
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35	HESRIGLAEG	LESEKKAVIP	LVIVSALTFFI	CLVVLVGLI	YWRKCFQTAH	FYLEDSTSPR	1680
	VISTPPTPIF	PISDDVGAIP	IKHPKPHVAD	LHASSGPTTE	FETLKEFYQE	VQSCVLDLGI	1740
	TADSSNHDPN	KHKRNRYNIV	AYDHSRVKLA	QLAEKDGKLT	DYINANYVDG	YNRPKAYIAA	1800
	QGPKLKSTAE	FWRMIWHEVN	EVIVMITNLV	EKGRKCDQY	WPADGSEEG	NFLVTQKSVQ	1860
	VLAYYTVRNF	TLRNTKIKKG	SQKGRPSGRV	VTQVHYTQWP	DMGVPEYSLP	VLTFRVKAAY	1920
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	QYVFIHDTLV	BAILSKETE	LDSHIHAYVN	ALLIPGPAGK	TKLEKQFQLL	SQSNIQQSDY	2040
	SAALKQCNRE	KNRTSSSIPV	ERSRVGISSL	SGEGTDYINA	SYIMGYVQSN	EFIITQHPLL	2100
	HTIKDFWRMI	WDHNAQLVVM	IPDQGNMAED	EFVYVWPKDE	PINCESFKVT	LMAEHKKCLS	2160
	NEEKLIQDF	ILEATQDDYV	LEVHRFQCPK	WPNPDSPIK	TFELISVIKE	EAANRDGPFI	2220
45	VHDEHGGVTA	GTFCALTTL	HQLEKENSVD	VYQVAKMINL	MRPGVFADIE	QYQFLYKVI	2280
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Seq ID NO: 574 DNA sequence
Nucleic Acid Accession #: Bos sequence
Coding sequence: 148-4518

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	CTTGTTGAAG	AGATTGCTG	GTCCTATACA	GGAGCACTGA	ATCAAAAAAA	TTGGGGAAAG	300
	AAATATCCAA	CATGTAATAG	CCCCAAACAA	TCTCCTATCA	ATATTGATGA	AGATCTTACA	360
60	CAAGTAAATG	TGAATCTTAA	GAACCTTAAA	TTTCAGGGTT	GGGATAAAAC	ATCATTGGAA	420
	AACACATTCA	TTCATAACAC	TGGGAAAACA	GTGGAAATTA	ATCTCACTAA	TGACTACCGT	480
	GTCAGCGGAG	GAGTTTCCAG	AATGGTGTTT	AAAGCAAGCA	AGATAACTTT	TCACTGGGGA	540
	AAATGCAATA	TGTCATCTGA	TGGATCAGAG	CATAGTTTAG	AAGACAAAAA	ATTTCCACTT	600
	GAGATGCAAA	TCTACTGCTT	TGATGCGGAC	CGATTTTCAA	GTTTGTAGGA	AGCAGTCAAA	660
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70	TCTGGTTATG	TCTAGCTGAT	GGACTACTTA	CAAAACAATT	TTCCAGAGCA	ACAGTACAAG	1020
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	ACAGAAAAG	ATATTTCTCT	GACTTCTCAG	ACTGTGACTG	AACTGCCACC	TCACACTGTG	1740
	GAAGGTACTT	CAGCCTCTTT	AAATGATGGC	TCTAAAACCT	TTCTTAGATC	TCCACATATG	1800
	AACTGTGCG	GGACTGCAGA	ATCCTTAAAT	ACAGTTTCTA	TAACAGAATA	TGAGGAGGAG	1860
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	GAAAACCCAG	AGACAATAAC	ATATGATGTC	CTTATACCAG	AATCTGCTAG	AAATGCTTCC	2040
	GAAGATTCAA	CTTCATCAG	TTCAAGAGAA	TCATAAAGG	ATCCTTCTAT	GGAGGGAAT	2100

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5	CATTATTCTA	CCTTTGCCTA	CTTCCCAACT	GAGGTAACAC	CTCATGCTTT	TACCCCATCC	2340
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10	TTTTACTTAG	AGGACAGTAC	ATCCCTTAGA	GTTATATCCA	CACCTCCAAC	ACCTATCTTT	2640
	CCAATTTTCA	ATGATGTCTG	AGCAATTTCA	ATAAAGCACT	TTCCAAAGCA	TGTTGCAGAT	2700
	TTACATGCAA	GTAGTGGGTT	TACTGAAGAA	TTTGAGACAC	TGAAAGAGTT	TTACCAGGAA	2760
	GTGCAGAGCT	GTACTGTTGA	CTTAGGTATT	ACAGCAGACA	GCTCCAACCA	CCCAGACAAC	2820
	AAGCACAAGA	ATCGATACAT	AAATATCGTT	GCCTATGATC	ATAGCAGGGT	TAAGCTAGCA	2880
15	CAGCTTGCTG	AAAAGGATGG	CAAACTGACT	GATTATATCA	ATGCCAATTA	TGTTGATGGC	2940
	TACAACAGAC	CAAAAGCTTA	TATTGCTGCC	CAAGGCCCCAC	TGAAATCCAC	AGCTGAAGAT	3000
	TTCTGGAGAA	TGATATGGGA	ACATAATGTG	GAACTTATTT	TCATGATAAC	AAACCTCGTG	3060
	GAGAAAGGAA	GGAGAAAATG	TGATCAGTAC	TGGCTTGCCG	ATGGGAGTGA	GGAGTACGGG	3120
	AACTTTCTGG	TCACTCAGAA	GAGTGTGCAA	TGCTTGCCT	ATTATACTGT	GAGGAATTTT	3180
20	ACTCTAAGAA	ACACAAAATA	AAAAAAGGGC	TCCAGAAAAG	GAAGACCCAG	TGGACGTGTG	3240
	GTACACAGAT	ATCACTACAC	GCAGTGGCCT	GACATGGGAG	TACCAGAGTA	CTCCCTGCCA	3300
	GTGCTGACCT	TTGTGAGAAA	GGCAGCCTAT	GCCAAGCGCC	ATGCAGTGGG	GCCTGTTGTC	3360
	GTCCACTGCA	GTGCTGGAGT	TGGAAGAACA	GGCACATATA	TTGTGCTAGA	CAGTATGTTG	3420
	CAGCAGATTC	AACACGAAGG	AACGTGCAAC	ATATTTGGCT	TCTTAAACAA	CATCCGTTCA	3480
25	CAAAGAAATT	ATTTGGTACA	AACGTGAGGAG	CAATATGTCT	TCATTCATGA	TACACTGGTT	3540
	GAGGCCATAC	TTAGTAAAGA	AACGTGAGGTG	CTGGACAGTC	ATATTCATGC	CTATGTTAAT	3600
	GCACCTCTCA	TTCTTGAGCC	AGCAGGCCAA	ACAAAGCTAG	AGAAACAATT	CCAGCTCCTG	3660
	AGCCAGTCAA	ATATACAGCA	GAGTGACTAT	TCTGCAGCCC	TAAAGCAATG	CAACAGGGAA	3720
	AAGAATCGAA	CTCTTCTTAT	CATCCCTGTG	GAAAGATCAA	GGGTTGGCAT	TTTATCCCTG	3780
30	AGTGGAGAAG	GCACAGACTA	CATCAATGCC	TCCTATATCA	TGGGCTATTA	CCAGAGCAAT	3840
	GAATTCATCA	TTACCCAGCA	CCCTCTCCTT	CATACCATCA	AGGATTTCTG	GAGGATGATA	3900
	TGGGACCATA	ATGCCCAACT	GGTGGTTATG	ATTCTGTATG	GCCAAAACAT	GGCAGAAGAT	3960
	GAATTTGTTT	ACTGGCCAAA	TAAAGATGAG	CCTATAAATT	GTGAGAGCTT	TAAGGTCACT	4020
	CTTATGGCTG	AAGAACACAA	ATGCTATCTT	AATGAGGAAA	AACCTTATAAT	TCAGGACTTT	4080
35	ATCTTAGAAG	CTACACAGGA	TGATTATGTA	CTTGAAGTGA	GGCACTTTCA	GTGTCCTAAA	4140
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	GAAGCTGCCA	ATAGGGATGG	GCCTATGATT	GTTTATGATG	AGCATGGAGG	AGTGACGGCA	4260
	GGAACTTTCT	GTGCTCTGAC	AACCTTATG	CACCAACTAG	AAAAAGAAAA	TTCCGTGGAT	4320
	GTTTACCAGG	TAGCCAAGAT	GATCAATCTG	ATGAGGCCAG	GAGTCTTTGC	TGACATTGAG	4380
40	CAGTATCAGT	TCTCTACAAA	AGTGATCTCT	AGCCTTGTGA	GCACAAAGCA	GGAAGAGAAT	4440
	CCATCCACCT	CTCTGGACAG	TAATGGTGCA	GCATTGCTCT	ATGGAATAT	AGCTGAGAGC	4500
	TTAGAGTCTT	TAGTTTAAAC	CAGAAAGGGG	TGGGGGGACT	CACATCTGAG	CATTGTTTTC	4560
	CTCTTCTTAA	AATTAGGCAG	GAAATCAGT	CTAGTTCTGT	TATCTGTTGA	TTTCCCATCA	4620
	CCTGACAGTA	ACTTTTCAAT	CATAGGATTC	TGCCGCCAAA	TTTATATCAT	TAACAATGTG	4680
45	TGCTTTTGTG	CAAGACTTGT	AATTACTTAA	TTATGTTTGA	ACTAAAATGA	TTGAATTTTA	4740
	CAGTATTTCT	AAGAATGGAA	TTGTGGTATT	TTTTTCTGTA	TTGATTTTAA	CAGAAAATTT	4800
	CAATTTATAG	AGGTTAGGAA	TTCCAAACTA	CAGAAAATGT	TTGTTTTTAG	TGTCAAATTT	4860
	TTAGCTGTAT	TTAGTACAA	TATCAGGTTT	GCTAGAAATA	TAACTTTATA	TACAGTAGCC	4920
	TGTAATAATA	ACACTCTTCC	ATATGATATT	CAACATTTTA	CAACTGCAGT	ATTACACCTA	4980
50	AGTAGAAATA	ATCTGTTACT	TATGTAAAT	ACTGCCCTAG	TGCTCTCCATG	GACCAAAATTT	5040
	ATATTTATAA	TTGTAGATTT	TTATATTTTA	CTACTGAGTC	AAGTTTCTTA	GTTCTGTGTA	5100
	ATTGTTTAGT	TTAATGACGT	AGTTCATTAG	CTGCTCTTAC	TCTACCAGTT	TTCTGACATT	5160
	GTATTTGTGT	ACCTAAGTGA	TTAATCTTGT	TTCAGCATGT	AATTTTAACT	TTTGTGGAAA	5220
	ATAGAAATAC	CTTCAATTTG	AAAGAAAGTT	TTATGAGAAT	AACACCTTAC	CAACATTTGT	5280
55	TCAATGGTTT	TTTATCCAAG	GAATTGCAAA	AATAAATATA	AATATTGCCA	TTAAAAAAA	5340
	AAAAAATAAA	AAAAAATAAA	AAAAAATA				

Seq ID NO: 575 Protein sequence:
Protein Accession #: Eos sequence

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65	QSPINIDEDL	TQVNVNLLKL	KFQGWDKTSL	ENTFIHNTGK	TVEINLTNDY	RVSGGVSEMV	120
	EKASKITFHW	GKCNMSSDGS	EHSLEGQKFP	LEMQIYCFDA	DRFSSFEEAV	KGKGLRLALS	180
	ILFEVGTEN	LDFKAIIDGV	BSVSRFGKQA	ALDPFILLNL	LPNSTDKYI	YNGSLTSPPC	240
	TDTVDWIVFK	DTVSISESQL	AVFCEVLTMQ	QSGYVMLMDY	LQNNFREQQY	KFSRQVFSSY	300
	TGKEEIHFAV	CSSEPEVQQA	DPENYTSLLV	TWERPRVVDY	TMIEKFAVLY	QQLDGEDQTK	360
70	HEFLTGDYQD	LGAILNNLLP	NMSYVLQIVA	ICTNGLYGYK	SDQLIVDMPT	DNPELDLFFE	420
	LIGTEEIIKE	EEEGKDIEEG	AIVNPGRDSA	TNQIRKKEFQ	ISTTTHYNRI	GTKYNEAKTN	480
	RSPTRGSEFS	KGKDVNPNTSL	NSTSQPVTKL	ATEKDISLTS	QTVTELPPhT	VEGTSASLND	540
	GSKTVLRSPH	MNLGGTAESL	NTVSITEYEE	ESLLTSFKLD	TGAEDSSGSS	PATSAIPFIS	600
	ENISQGYIFS	SENPETITYD	VLIPESARNA	SEDSTSSGSE	ESLKDPSMEG	NVWFPSSTDI	660
75	TAQPDVSGSR	ESFLQNTYTE	IRVDESEKTT	KSFSAGPVMS	QGPSVTDLEM	PHYSTFAYFP	720
	TEVTPHAFTP	SSRQDLVST	VNVVYSQTTQ	PVYNAEASNS	SHESRIGLAE	GLESEKKAVI	780
	PLVIVSALT	ICLVVLVGLL	IYWRKCFQTA	HFYLEDTSP	RVISTPPTPI	FPISDDVGAI	840
	PIKHFPHKVA	DLHASSGSTE	EFETLKEFYQ	EVQSCVTDLG	ITADSSNHPD	NKHKNRYINI	900
	VAYDHSRVKL	AQLAEKDGKL	TDYINANYVD	GYNRPKAYIA	AQGPLKSTAE	DFWRMIWEHN	960
80	VEVIMITNL	VEKGRRKCDQ	YWPADGSEBY	GNFLVTQKSV	QVLAYYTVRN	FTLRNTKIKK	1020
	GSQKGRPSGR	VVTQYHYTQW	PDMGVPEYSL	PVLTFVRKAA	YAKRHAHVGP	VVHCSAGVGR	1080
	TGTYIVLDSM	LQQIQHEGTV	NIFGLFKHIR	SQRNXLVQTE	BQYVFIHDTL	VEAILSKETE	1140
	VLDSHIHAYV	NALLIPGPAG	KTKLEKQFQL	LSQSNIQQSD	YSAALKQCNR	EKNRTSSIIP	1200
	VERSRVGISS	LSGBGTDYIN	ASYIMGYYS	NEFIITQHPL	LHTIKDFWRM	IWDHNAQLVV	1260
85	MIPDQNMMAE	DEFVYWPNDK	BPINCESFKV	TLMAEEHKCL	SNEEKLIQD	FILEATQDDY	1320
	VLEVRHFQCP	KWPNFQSPIS	KTFELISVIK	EEAANRDGPM	IVHDEHGGVT	AGTFCALTTL	1380
	MHOLEKENS	DVYQVAKMIN	LMRPGVFADI	BQYQFLYKVI	LSLVSTRQEE	NPSTSLDSNG	1440
	AALPDGNIAE	SLESLEV					

Seq ID NO: 576 DNA sequence
Nucleic Acid Accession #: EOS sequence
Coding sequence: 148-4494

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10	CAAAAAAACC	ATTTCCTTCG	CTCCCCCTCC	CTCTCCACTC	TGAGAAGCAG	AGGAGCCGCA	120
	CGGCGAGGGG	CCGCAGACCG	TCTGGAAATG	CGAATCCTAA	AGCGTTTCCT	CGCTTGCAAT	180
	CAGCTCCTCT	GTGTTTGCCG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240
	CTTGTTGAAG	AGATTGGCTG	GTCCTATACA	GGAGCACTGA	ATCAAAAAAA	TTGGGGAAAG	300
	AAATATCCAA	CATGTAATAG	CCCAAAACAA	TCTCCTATCA	ATATTGATGA	AGATCTTACA	360
15	CAAGTAAATG	TGAATCTTAA	GAACTTAA	TTTCAGGGTT	GGGATAAAAC	ATCATTGGAA	420
	AACACATTCA	TTCAATAACAC	TGGGAAAACA	GTGGAAATTA	ATCTCACTAA	TGACTACCGT	480
	GTACGCGGAG	GAGTTTCAGA	AATGGTGT	AAAGCAAGCA	AGATAACTTT	TCACTGGGGA	540
	AAATGCAATA	TGTCATCTGA	TGGATCAGAG	CATAGTTTAG	AAGGACAAAA	ATTCCACTT	600
	GAGATGCAAA	TCTACTGCTT	TGATGCAGAC	CGATTTTCAA	GTTTGGAGGA	AGCAGTCAAA	660
20	GGAAAAGGGA	AGTTAAGAGC	TTTATCCATT	TTGTTTGAGG	TTGGGACAGA	AGAAAAATTTG	720
	GATTTCAAG	CGATTATTTA	TGGAGTCGAA	AGTGTAGTCT	GTTTGGGAA	GCAGGCTGCT	780
	TTAGATCCAT	TCATACTGTT	GAACTTCTG	CCAAACTCAA	CTGACAAGTA	TTACATTAC	840
	AATGGCTCAT	TGACATCTCC	TCCCTGCACA	GACACAGTTG	ACTGGATTGT	TTTTAAAGAT	900
	ACAGTTAGCA	TCTCTGAAG	CCAGTTGGCT	GTTTTTTG	AAGTTCTTAC	AATGCAACAA	960
25	TCTGGTTATG	TCATGCTGAT	GGATCTACTA	CAAAACAATT	TTCCAGAGCA	ACAGTACAAG	1020
	TTCTCTAGAC	AGGTGTTTTC	CTCATACACT	GGAAAGGAAG	AGATTCTATGA	AGCAGTTTGT	1080
	AGTTTCAGAAC	CAGAAAATGT	TCAGGCTGAC	CCAGAGAATT	ATACCAGCCT	TCTTGTAC	1140
	TGGGAAGAGC	CTCCAGTCGT	TTATGTATAC	ATGATTGAGA	AGTTTGCAGT	TTTGTACCAG	1200
	CAGTTGGATG	GAGAGGACCA	AACCAAGCAT	GAATTTTGA	CAGATGGCTA	TCAAGACTTG	1260
30	GGTGCTATTG	TCATAATTT	GCTACCCAAT	ATGAGTTATG	TTCTTCAGAT	AGTAGCCATA	1320
	TGCACTAATG	GCTTATATGG	AAAATACAGC	GACCAACTGA	TTGTGACAT	GCCTACTGAT	1380
	AATCCTGAAC	TTGATCTTTT	CCCTGAATTA	ATTGGAAC	AAGAAATAAT	CAAGGAGGAG	1440
	GAAGAGGGAA	AAGACATTGA	AGAAGGCGCT	ATTGTGAATC	CTGGTAGAGA	CAGTGCTACA	1500
	AACCAATCA	GGAAAAGGA	ACCCAGATT	TCTACCACAA	CACACTACAA	TCCGATAGGG	1560
35	ACGAAATACA	ATGAAGCCAA	GACTAACCGA	TCCCAACAA	GAGGAAGTGA	ATTCTCTGGA	1620
	AAGGGTGATG	TTCCCAATAC	ATCTTTAAAT	TCCACTTCCC	AACCAAGTCA	TAAATTAGCC	1680
	ACAGAAAAAG	ATATTTCTTT	GACTTCTCAG	ACTGTGACTG	AACCTGCCAC	TCACACTGTG	1740
	GAAGTACTTT	CAGCTCTTT	AAATGATGGC	TCTAAACTG	TTCTTAGATC	TCCACATATG	1800
	AACTTGTGCG	GGACTGCAGA	ATCCTTAAAT	ACAGTTTCTA	TAACAGAATA	TGAGGAGGAG	1860
40	AGTTTATTTA	CCATTTTCAA	GCTTGATACT	GGAGCTGAAG	ATTCTTCAGG	CTCCAGTCCC	1920
	GCAACTTCTG	CTATCTTCTG	AACATATCCC	AAGGGTATAT	ATTTCTCTCC		1980
	GAAAACCCAG	AGACAATAAC	ATATGATGTC	CTTATACCAG	AATCTGCTAG	AAATGCTTCC	2040
	GAAGATTCAA	CTTCATCAGG	TTCAGAAGAA	TCACTAAAGG	ATCCTTCTAT	GGAGGGAAT	2100
45	GTGTGGTTTC	CTAGCTCTAC	AGACATAACA	GCACAGCCCG	ATGTTGGATC	AGGCAGAGAG	2160
	AGCTTTCTCC	AGACTAATTA	CACGTGAGATA	CGTGTGATG	AATCTGAGAA	GACAAACCAAG	2220
	TCTTTTCTG	CAGGCCAGT	GATGTCACAG	GGTCCCTCAG	TTACAGATCT	GGAAATGCCA	2280
	CATTATTCTA	CCTTTGCCTA	CTTCCCAACT	GAGGTAACAC	CTCATGCTTT	TACCCCATCC	2340
	TCCAGACAAC	AGGATTGGGT	CTCCACGGTC	AACGTGGTAT	ACTGCAGAC	AACCCCAACCG	2400
50	GTATACAATG	AGGCGAGTAA	TAGTAGCCAT	GAGTCTCGTA	TTGGTCTAGC	TGAGGGGTTG	2460
	GAATCCGAGA	AGAAGGCAGT	TATACCCCTT	GTGATCTGTG	CAGCCCTGAC	TTTATCTGT	2520
	CTAGTGGTTC	TTGTGGGTAT	TCTCATCTAC	TGGAGGAAAT	GCTTCCAGAC	TGCACACTTT	2580
	TACTTAGAGG	ACAGTACATC	CCCTAGAGTT	ATATCCACAC	CTCCAAACACC	TATCTTTCCA	2640
	ATTTTCAGATG	ATGTGCGAGT	AAATCCAATA	AAGCACTTTC	CAAAGCATGT	TGCAGATTTA	2700
55	CATGCAAGTA	TGTGGTTTAC	TGAAGAATT	GAGGAAGTGC	AGAGCTGTAC	TGTTGACTTA	2760
	GGTATTACAG	CAGACAGCTC	CAACCACCCA	GACAACAAGC	ACAAGAATCG	ATACATAAAT	2820
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	CTGACTGATT	ATATCAATGC	CAATTATGTT	GATGGCTACA	ACAGACCAAA	AGCTTATATT	2940
	GCTGCCCAAG	GCCCACTGAA	ATCCACAGCT	GAAGATTTCT	GGAGAATGAT	ATGGGAACAT	3000
60	AATGTGGAAG	TTATTGTCTA	GATAACAAAC	CTCGTGGAGA	AAGGAAGGAG	AAATGTGAT	3060
	CAGTACTGGC	CTGCCGATGG	GAGTGAGGAG	TACGGGAAC	TTCTGGTCA	TCAGAAGAGT	3120
	GTGCAAGTGC	TTGCTTATTA	TACTGTGAGG	AATTTTACTC	TAAGAAACAC	AAAAATAAAA	3180
	AAGGGCTCCC	AGAAAGGAAG	ACCCAGTGA	CGTGTGGTCA	CACAGTATCA	CTACACGCAG	3240
	TGGCCTGACA	TGGGAGTACC	AGAGTACTCC	CTGCCAGTGC	TGACCTTTGT	GAGAAAGGCA	3300
65	GCCTATGCCA	AGCCCATATG	AGTGGGGCCT	GTTGTCGTCC	ACTGCAGTGC	TGGAGTTGGA	3360
	AGAACAGGCA	CATATATTGT	GCTAGACAGT	ATGTTGCAGC	AGATTCAACA	CGAAGGAACT	3420
	GTCACATAT	TTGGCTTCTT	AAACACATC	CGTTCAACAA	GAAATTATTT	GGTACAAACT	3480
	GAGGAGCAAT	ATGCTTTCAT	TCATGATACA	CTGGTTGAGG	CCATACTTAG	TAAAGAAACT	3540
70	GAGGTGCTGG	ACAGTCAAT	TCATGCCAT	GTTAATGCAC	TCCTCATTCC	TGGACCAGCA	3600
	GGCAAAACAA	AGCTAGAGAA	ACAATTCAG	CTCCTGAGCC	AGTCAAAAT	ACAGCAGAGT	3660
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	CCTGTGGA	GATCAAGGGT	TGGCATTTCA	TCCCTGAGTG	GAGAAGGCAC	AGACTACATC	3780
75	AATGCCTCCT	ATATCATGGG	CTATTACCAG	AGCAATGAAT	TCATCATTAC	CCAGCACCTT	3840
	CTCCTTCATA	CCATCAAGGA	TTTCTGGAGG	ATGATATGGG	ACCATAATGC	CCAACTGGTG	3900
	GTTATGATTC	CTGATGGCCA	AAACATGGCA	GAAGATGAAT	TTGTTTACTG	GCCAAATAAA	3960
	GATGAGCCTA	TAAATTGTGA	GAGCTTTAAG	GTCACTCTTA	TGGCTGAAGA	ACACAAATGT	4020
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	TATGTACTTG	AAGTGAGGCA	CTTTCAGTGT	CCTAAATGGC	CAAATCCAGA	TAGCCCATTT	4140
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	ATGATTGTTC	ATGATGAGCA	TGGAGGAGTG	ACGCGCAGAA	CTTCTGTGTC	TCTGACAACC	4260
	CTTATGACCC	AACTAGAAAA	AGAAAATTC	GTGGATGTTT	ACCAGGTAGC	CAAGATGATC	4320
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	ATCCTCAGCC	TTGTGAGCAC	AAGGCAGGAA	GAGAATCCAT	CCACCTCTCT	GGACAGTAAT	4440
85	GGTGACAGAT	TGCCTGATGG	AAATATAGCT	GAGAGCTTAG	AGTCTTTAGT	TTACACAGA	4500
	AAGGGGTGGG	GGGACTCACA	TCTGAGCATT	GTTTTCCTCT	TCCTAAATTT	AGGCAGGAAA	4560
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	GGATTCTGCC	GCCAAATTTA	TATCATTAAC	AATGTGTGCC	TTTTTGCAAG	ACTTGTAATT	4680
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	AAACTACAGA	AAATGTTTGT	TTTGTAGTGC	AAATTTTGTAG	CTGTATTGTG	AGCAATTATC	4860
	AGGTTTGTCTA	GAAATATAAC	TTTAAATACA	GTAGCCTGTA	AATAAAACAC	TCTTCCATAT	4920
	GATATTTCAAC	ATTTTACACA	TGCAGTATTC	ACCTAAAGTA	GAAATAATCT	GTTACTTTAT	4980
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5	ATTTTACTAC	TGAGTCAAGT	TTTCTAGTTC	TGTGTAATG	TTTAGTTTAA	TGACGTAGTT	5100
	CATTAGCTGG	TCTTACTCTA	CCAGTTTTCT	GACATTGTAT	TGTGTTACCT	AAGTCATTAA	5160
	CTTTGTTTCA	GCATGTAAT	TTAATCTTTG	TGGAAAAATAG	AAATACCTTC	ATTTTGAAAG	5220
	AAGTTTATAT	GAGAAATAAC	CCTTACCAAA	CATTGTTCAA	ATGGTTTTTA	TCCAAGGAAT	5280
10	TGCAAAAATA	AATATAAATA	TGCCATTAA	AAAAAATAAA	AAAAAATAAA	AAAAAATAAA	5340
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Seq ID NO: 577 Protein sequence:
Protein Accession #: EOS sequence

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20	FKASKITPHW	GKCNMSSDGS	EHSLEGGQKFP	LEMQIYCFDA	DRFSSFEEAV	KGKGKLRALS	180
	ILFEVGTBEN	LDFKAILDGV	ESVSRFGKQA	ALDPFILLNL	LPNSTDKYYI	YNGSLTSEPC	240
	TDTVDWIVFK	DTVSISESQL	AVFCEVLTMQ	QSGYVMLMDY	LQNNFREQQY	KFSRQVFSSY	300
	TGKEEIEHAV	CSSEPENVQA	DPENYTSLLV	TWERPRVVD	TMIEKFAVLY	QQLDGEDQTK	360
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	RSPTRGSEFS	GKGDVPNTSL	NSTSQPVTKL	ATEKDISLTS	QTVTELPHT	VEGTSASLND	540
	GSKTVLRSPH	MNLSCTAESL	NTVSITEYEE	ESLLTSFKLD	TGAEDSSGSS	PATSAIPFIS	600
	ENISQGYIFS	SENPETITYD	VLIPEASRNA	SEDSTSSGSE	ESLKDPSMEG	NVWFPSSTDI	660
	TAQPDVSGSR	BSFLTQNTYE	IRVDESEKTT	KSFSAGPVMS	QGPSVTDLME	PHYSTPAYFP	720
	TEVTPHATPT	SSRQQLDVST	VNVVYSQTTQ	PVYNEASNSS	HESRIGLAEG	LESEKKAVIP	780
30	LVIVSALTFI	CLVVLVGILI	YWRKCFQTAH	FYLEDDSTSPR	VISTPPTPIF	PISDDVGAIP	840
	IKHFPKHVAD	LHASSGFTFE	FEEVQSCTVD	LGITADSSNH	PDNKHKNRYI	NIVAYDHSRV	900
	KLAQLAEKDG	KLTDYINANY	VDGYNRPKAY	IAAQGPLKST	AEDFWRMIWE	HNVEYVIMIT	960
	NLVEKGRKRC	DQYWPADGSE	EYGNFLVTQK	SVQVLAYYTV	RNFTLRNTKI	KKGSQKGRPS	1020
35	GRVVTQYHYT	QWPDGMVPEY	SLPVLTFVRK	AAYAKRHAVG	PVVVHCASGV	GRTGTIYIVLD	1080
	SMLQQIQHEG	TVNIFGFLKH	IRSQRNYLVQ	TEEQYVFIHD	TLVEAILLSKE	TEVLDSHIHA	1140
	YVNALLIPGP	AGKTKLEKQF	QLLSQSNIQQ	SDYSAALKQC	NREKNRTSSI	IPVERSRVGI	1200
	SSLSGEGTDY	INASYIMGYI	QSNFIIITQH	PLLHTIKDFW	RMINDHNAQL	VVMIPDGQNM	1260
	AEDEFVYWFN	KDEPINCESF	KVTLMABEHK	CLSNEEKLI	QDFILEATQD	DYVLEVRHFQ	1320
40	CPKWPNDPSP	ISKTFELISV	IKEEAAANRDG	PMIVHDEHGG	VTAGTFCAIT	TLMHQLKEN	1380
	SVDVYQVAKM	INLMRPGVFA	DIEQYQFLYK	VILSLVSTRQ	EENPSTSLDS	NGAALPDGNI	1440
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Seq ID NO: 578 DNA sequence
Nucleic Acid Accession #: EOS sequence
Coding sequence: 501-4514

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	CAGCTCCTCT	GTGTTTGCCG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240
55	CTTGTTGAAG	AGATTGGCTG	GTCCTATACA	GGAGCACTGA	ATCAAAAAAT	TGGGGAAAGA	300
	AATATCCAAC	ATGTAATAGC	CCAAAACAAT	CTCCTATCAA	TATTGATGAA	GATCTTACAC	360
	AAGTAAATGT	GAATCTTAAG	AAACTTAAAT	TTCAGGGTTG	GGATAAAACA	TCATTGGAAA	420
	ACACATTCAT	TCATAACACT	GGGAAAACAG	TGGAAATTAA	TCTCACTAAT	GACTACCGTG	480
	TCAGCGGAGG	AGTTTCAGAA	ATGGTGTTTA	AAGCAAGCAA	GATAACTTTT	CACTGGGGAA	540
60	AATGCAATAT	GTGATCTGAT	GGATCAGAGC	ATAGTTTAGA	AGGACAAAAA	TTTCCACTGT	600
	AGATGCAAAAT	CTACTGCTTT	GATCGGGACC	GATTTTCAAG	TTTGTAGGAA	GCAGTCAAAG	660
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 Protein Accession #: EOS sequence

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Seq ID NO: 581 Protein sequence:
 Protein Accession #: EOS sequence

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Seq ID NO: 582 DNA sequence
 Nucleic Acid Accession #: NM_002851.1
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Seq ID NO: 583 Protein sequence
 Protein Accession #: NP_002842.1

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	AGGAAAAAGC	AGTAAAGCCA	GAGGAAGGGC	AGCTTGTGCA	GCTGGAAGAG	AAAGGGCAGG	2640
15	GTTCACTGCC	CTGGTCAGTA	TATGGTGTCT	ACATCCAGGC	TGCTGGGGGC	CCCTTGGCAT	2700
	TCCTGGTTAT	TATGGCCCTT	TTCATGCTGA	ATGTAGGCAG	CACCGCCTTC	AGCACCTGGT	2760
	GGTTGAGTTA	CTGGATCAAG	CAAGGAAGCG	GGAAACCCAC	TGTGACTCGA	GGGAACGAGA	2820
	CCTCGGTGAG	TGACAGCATG	AAGGACAATC	CTCATATGCA	GTACTATGCC	AGCATCTACG	2880
	CCCTCTCCAT	GGCAGTCACT	CTGATCCTGA	AAGCCATTCC	AGGAGTTGTC	TTTGTCAAGG	2940
20	GCACGCTCGG	AGCTTCCTCC	CGGCTGCATG	ACGAGCTTTT	CCGAAGGATC	CTTCGAAGCC	3000
	CTATGAAGTT	TTTTGACACG	ACCCCCACAG	GGAGGATTCT	CAACAGGTTT	TCCAAAGACA	3060
	TGGATGAAGT	TGACGTGCGG	CTGCGTTC	AGGCCGAGAT	GTTTCATCCAG	AACGTTATCC	3120
	TGGTGTCTCT	CTGTGTGGGA	ATGATCGCAG	GAGTCTTCCC	GTGGTTCCTT	GTGGCAGTGG	3180
	GGCCCCCTGT	CATCTCTTTT	TCAGTCCCTG	ACATTGTCTC	CAGGGTCTCT	ATTTCGGGAGC	3240
	TGAACGCTCT	GGACAATATC	ACGCAGTCAC	CTTTCCTCTC	CCACATCACG	TCCAGCATAC	3300
25	AGGGCCTTGC	CACCATCCAC	GCCTACAATA	AAGGGCAGGA	GTTTCTGCAC	AGATACCAGG	3360
	AGCTGCTGGA	TGACAACCAA	GCTCCTTTTT	TTTTGTTTAC	GTGTGCGATG	CGSTGGCTGG	3420
	CTGTGCGGCT	GGAGCTCATC	AGCATCGCCC	TCATCACCCAC	CACGGGGCTG	ATGATCGTTC	3480
	TTATGCACGG	CGAGATTCCC	CCAGCCTATG	CGGGTCTCGC	CATCTCTTAT	GCTGTCCAGT	3540
30	TAACGGGGCT	GTTCCAGTTT	ACGGTCAGAC	TGGCATCTGA	GACAGAAGCT	CGATTACCT	3600
	CGGTGGAGAG	GATCAATCAC	TACATTAAGA	CTCTGTCTCT	GGAAGCACCT	GCCAGAATTA	3660
	AGAACCAAGC	TCCCTCCCTC	GACTGGCCCC	AGGAGGGAGA	GGTGACCTTT	GAGAACGCAG	3720
	AGATGAGGTA	CCGAGAAAAC	CTCCCTCTTG	TCTTAAAGAA	AGTATCCCTC	ACGATCAAAAC	3780
	CTAAAGAGAA	GATTGGCATT	GTGGGGCGGA	CAGGATCAGG	GAAGTCCCTG	CTGGGGATGG	3840
35	CCCTCTTCCG	TCTGGTGGAG	TTATCTGGAG	GCTGCATCAA	GATTGATGGA	GTGAGAATCA	3900
	GTGATATTGG	CCTTGCCGAG	CTCCGAAGCA	AACTCTCTAT	CATTCTCTCA	GAGCGGCTGC	3960
	TGTTTCACTG	CAGTGTGAGA	TCAAATTTGG	ACCCCTTCAA	CCAGTACACT	GAAGACCAGA	4020
	TTTGGGATGC	CTGTGAGAGC	ACACACATGA	AAGAATGTAT	TGCTCAGCTA	CCTCTGAAAC	4080
	TTGAATCTGA	AGTGTGAGAG	AATSGGGATA	ACTTCTCAGT	GGGGGAACGG	CAGCTCTTGT	4140
40	GCATAGCTAG	AGCCCTGCTC	CGCCACTGTA	AGATTCTGAT	TTTAGATGAA	GCCACAGCTG	4200
	CCATGGACAC	AGAGACAGAC	TTATTGATTG	AAGAGACCAT	CCGAGAAGCA	TTTGACAGAT	4260
	GTACCATGCT	GACCATTGCC	CATCGCTGTC	ACACGGTTCT	AGGCTCCGAT	AGGATTATGG	4320
	TGCTGGCCCA	GGGACAGGTG	GTGGAGTTTG	ACACCCCATC	GGTCTTCTG	TCCAACGACA	4380
	GTTCGCCATT	CTATGCCATG	TTTGCTGCTG	CAGAGAACAA	GGTCGCTGTC	AAGGGCTGAC	4440
45	TCCTCCCTGT	TGACGAAGTC	TCTTTTCTTT	AGAGCATTGC	CATTCCCTGC	CTGGGGCGGG	4500
	CCCCTCATCG	GTCTCTCCTA	CCGAACCTT	GCCTTCTCG	ATTTTATCTT	TCGCACAGCA	4560
	GTTCGGGATT	GGCTTGTGTG	TTTCACTTTT	AGGGAGAGTC	ATATTTTGAT	TATTGTATTT	4620
	ATTCCATATT	CATGTAAACA	AAATTTAGTT	TTTGTCTTAA	ATTGCACTCT	AAAAGGTTCA	4680
	GGGAACCGTT	ATTATAATTG	TATCAGAGGC	CTATAATGAA	GCTTTATACG	TGTAGCTATA	4740
50	TCTATATATA	ATTCTGTACA	TAGCCTATAT	TTACAGTGAA	AATGTAAGCT	GTTTATTTTA	4800
	TATTAATAAT	AGCACTGTGC	TAATAACAGT	GCATATTCCT	TTCTATCATT	TTTGTACAGT	4860
	TTGCTGTACT	AGAGATCTGG	TTTTGCTATT	AGACTGTAGG	AAGAGTAGCA	TTTCATTCTT	4920
	CTCTAGCTGG	TGGTTTACAG	GTGCCAGGTT	TTCTGGGTGT	CCAAAGGAAG	ACGTGTGGCA	4980
	ATAGTGGGCC	CTCCGACAGC	CCCCCTGCCC	GCCTCCCCAC	AGCCGCTCCA	GGGGTGGCTG	5040
55	GAGACGGGTG	GGCGGCTGGA	GACCATGCAG	AGCGCCGTGA	GTTCTCAGGG	CTCCTGCCTT	5100
	CTGTCTGTGT	GTCACCTACT	GTTTCTGTCA	GGAGAGCAGC	GGGGCGAAGC	CCAGGCCCTT	5160
	TTTCACTCCC	TCCATCAAGA	ATGGGGATCA	CAGAGACATT	CCTCCGAGCC	GGGGAGTTTC	5220
	TTTCTGCTCT	TCTTCTTTTT	GCTGTGTGTT	CTAAACAAGA	ATCAGTCTAT	CCACAGAGAG	5280
	TCCCCTGCTC	TCAGGTTCTT	ATGGCTGGCC	ACTGCACAGA	GCTCTCCAGC	TCCAAGACCT	5340
60	GTGGGTTCCA	AGCCCTGGAG	CCAACTGCTG	CTTTTGTAGG	TGGCACTTTT	TCATTGTCCT	5400
	ATTCCACAC	CTCCACAGTT	CAGTGGCAGG	GCTCAGGATT	TCGTGGGTCT	GTTTTCCTTT	5460
	CTACCGCAG	TCGTGCGACA	GTCTCTCTCT	CTCTCTCCCC	TCAAAGTCTG	CAACTTTAAG	5520
	CAGCTCTTGC	TAATCAGTGT	CTCACACTGG	CGTAGAAGTT	TTTGTACTGT	AAAGAGACCT	5580
	ACCTCAGGTT	GCTGTGTGCT	GTGTGGTTTG	GTGTGTTCCC	GCAAAACCCC	TTTGTGCTGT	5640
65	GGGGCTGGTA	GCTCAGGTGG	GCGTGGTCC	TGCTGTCTATC	AGTTGAATGG	TCAGCGTTGC	5700
	ATGTGCTGAC	CAACTAGACA	TTCTGTGCCC	TTAGCATGTT	TGCTGAACAC	CTTGTGGAAG	5760
	CAAAAATCTG	AAAATGTGAA	TAAATATTAT	TTGGATTTTG	TAAAAAATAA	AAAAAATAA	5820

Seq ID NO: 585 Protein sequence
Protein Accession #: NP_005679.1

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	LDASHMSQLR	ILDEBHPKKG	YHHGLSALKP	IRTTSKHQHP	VDNAGLFSCM	TFSWLSLAR	120
	VAHKKGELSM	EDVWLSKSH	SSDVNCRRL	RLWQELNEV	GPDAASLRV	VWIFCRTRLI	180
	LSIVCLMITG	LAFSGPAPFM	VKHLLEYTQA	TESNLQYSL	LVLGLLLTEI	VRWSLALTW	240
	ALNYRTGVRL	RGAILTMAFK	KILKLKNIKE	KSLGELINIC	SNDGQRMFEA	AAVGSLLAGG	300
	PVVALILGMI	NVILIGPTGF	LGSAVFILFY	PAMMFASRLT	AYFRKRCVAA	TDERVQKMNE	360
80	VLTYIKFIKM	YAWVKAFSGS	VQKIREEERR	ILEKAGYFQG	ITVGVAPIVV	VIASVVTFSV	420
	HMTLGFDLTA	AQAFVTVTVF	NSMTFALKVT	PFSVKSLSSEA	SVAVDRFKSL	FLMEEVHMIK	480
	NKPASPHIKI	EMKNATLAWD	SSHSSIQNSP	KLTPKMKRDK	RASRGKKEKV	RQLQTEHQA	540
	VLAQKQHLL	LDSDERPSP	EEEGKHIHLG	HLRLQRTLHS	IDLEIQEGKL	VGICGSVSGS	600
	KTSLISAILG	QMTLLEGSIA	ISGTFAYVAQ	QAWILNATLR	DNILFGKEYD	EERYNSVLNS	660
85	CCLRPDLAFL	PSSDLTEIGE	RGANLGGGQR	QRISLARALY	SDRSIYILD	PLSALDAHV	720
	NHIFNSAIRK	HLKSKTVLFV	THQLQYLVD	DEVIFMKEGC	ITERGTHEEL	MNLNGDYATI	780
	FNNLLGETP	PVEINSKKET	SGSQKKSQDK	GPKTGSVKKE	KAVKPEEGQL	VQLBEKGQGS	840

VPWSVYGVYI QAAGGFLAFL VIMALFMLNV GSTAFSTWWL SYWIKQSGSN TTVTRGNETS 900
 VSDSMKDNPH MQYYASIAL SMAMVLILKA IRGVVFKGT LRASSRLHDE LFRRLRSPM 960
 KFDDTTPTR ILNRFSKMD EVDVRLPFQA EMFIQNVILV FFCVGMIAV FFWFLVAVGP 1020
 LVILFSLVLI VSRVLIRELK RLDNITQSPF LSHITSSIQG LATIHAYNKG QEFLLHRYQEL 1080
 LDDNQAPFL PTCAMRWLAV RDLISIALI TTGLMIVLM HGQIPPAYAG LAISYAVQLT 1140
 GLFQFTVRLA SETEARFTSV ERINHYIKTL SLEAPARIKN KAPSPDWPQE GEVTFENAEM 1200
 RYRENLPVLV KKVSTTIKPK EKIGIVGRTE SKKSSLGML FRLVELSGGC IKIDGVRISD 1260
 IGLADLRSLK SIIPQEPVLF SGTVRSNLDP FNQYTEDQIW DALERTHME CIAQLPLKLE 1320
 SEVMENGDNF SVGERQLLCI ARALLRHCKI LILDEATAAM DTETDLLIQE TIREAFADCT 1380
 MLTIAHRLHT VLGSDRIMVL AQGQVVEFDT PSVLLSNDSS RPYAMFAAAE NKVAVKG

Seq ID NO: 586 DNA sequence
 Nucleic Acid Accession #: NM_001327.1
 Coding sequence: 89..631

1 11 21 31 41 51
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 GACGGCGCAT GCTGTGGGCC CAGGAGGCCG TGGCATTCTT GATGGCCAG GGGGCAATGC 180
 TGGCGGCCCA GAGAGGGCGG GTGCCACGGG CGGCAGAGGT CCGCGGGGCA CAGGGGCAGC 240
 AAGGGCCTCG GGGCCGGGAG GAGGCGCCCC CGGGGCTCCG CATGGCGCGC CGGCTTCAGG 300
 GCTGAATGGA TGCTCGAGAT GCGGGGCCAG GGGGCGCGAG AGCCGCCTGC TTGAGTTCTA 360
 CCTCGCCATG CCTTTCGCGA CACCCATGGA AGCAGAGCTG GCCCGCAGGA CCCTGGCCCA 420
 GGATGCCCA CCGCTTCCCG TGCCAGGGGT GCTTCTGAAG GAGTTCATCT GTGCGGCAA 480
 CATACTGACT ATCCGACTGA CTGCTGCAGA CCACCGCCAA CTGCAGCTCT CCATCAGCTC 540
 CTGTCTCCAG CAGCTTTCCC TGTTGATGTG GATCAGCGAG TGCTTCTGTC CCGTGTCTTT 600
 GGCTCAGCTC CCCTCAGGGC AGAGGCGCTA AGCCAGCCCT GGCGCCCTT CCTAGGTCAT 660
 GCCTCTCTCC TAGGGAATG GTCCAGCAC GAGTGGCCAG TTCATTGTGG GGGCCTGATT 720
 GTTTGTCGCT GGAGGAGGAC GGCTTACATG TTTGTTCTG TAGAAAATAA AACTGAGCTA

Seq ID NO: 587 Protein sequence
 Protein Accession #: NP_001318.1

1 11 21 31 41 51
 MQAEGRGTTG STGDADGPGG PGIPDGPGGN AGGPGEAGAT GGRGPRGAGA ARASGPGGGA 60
 PRGPHGGAAS GLNGCCRCGA RGPESRLLEF YLAMPFATPM EAELARRSLA QDAPPLPVFG 120
 VLLKEFTVSG NILTIRLTA AHRQLQLSIS SCLQQLSLLM WITQCFLPVF LAQPPSGQRR

Seq ID NO: 588 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 52..459

1 11 21 31 41 51
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 GAAGGCCAGG GCACAGGGGG TCGACGGGC GATGCTGATG GCCCAGGAG CCCTGGCATT 120
 CCTGTATGGC CAGGGGGCAA TGCTGGCGGC CCAGGAGAGG CGGGTGCCAC GGGCGGCAGA 180
 GGTCCCCGGG GCGCAGGGGC AGCAAGGGCC TCGGGGCCGA GAGGAGGCGC CCGCGGGGT 240
 CCGCATGGGG GTGCCGCTTC TGCGCAGGAT GGAAGGTGCC CCTGCGGGGC CAGGAGGCCG 300
 GACAGCCGCG TGCTTCAGTT CCGACTGACT GCTGCAGACC ACCGCCAACT GCAGCTCTCC 360
 ATCAGCTCTT GTCTCCAGCA GCTTCCCTG TTGATGTGGA TCACGCACTG CTTTCTGCCC 420
 GTGTTTTTGG CTCAGGCTCC CTCAGGCGAG AGGCGCTAAG CCCAGCCTGG CGCCCTTCC 480
 TAGGTCATGC CTCCTCCCTC AGGGAATGTT CCCAGCACGA GTGGCCAGTT CATTTGTGGG 540
 GCCTGATTGT TTGTCGCTGG AGGAGGACGG CTTACATGTT TGTTCCTGTA GAAAATAAAG 600
 CTGAGCTA

Seq ID NO: 589 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MQAEGQGTGG STGDADGPGG PGIPDGPGGN AGGPGEAGAT GGRGPRGAGA ARASGPRGGA 60
 PRGPHGGAAS AQDGRCPGCA RRPDSRLQLF RLTAADHRQL QLSISSCLQQ LSLLMWITQC 120
 FLFPVLAQAP SQRR

Seq ID NO: 590 DNA sequence
 Nucleic Acid Accession #: NM_005562.1
 Coding sequence: 90..3671

1 11 21 31 41 51
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 AGACAGAGAC TGAGCGGGCC GGCACCGCCA TGCCCTGCGT CTGGCTGGGC TGCTGCCTCT 120
 GCTTCTCGCT CCTCTGCCC GCAGCCCGGG CCACCTCCAG GAGGGAAGTC TGTGATTGCA 180
 ATGGGAAGTC CAGGCAGTGT ATCTTTGATC GGGAACCTCA CAGACAACT GGTAAATGGAT 240
 TCCGCTGCCT CAACTGCAAT GACAACACTG ATGGCATTCA CTGCAGAAAG TGCAAGAAATG 300
 GCTTTTACCG GCACAGAGAA AGGGACCGCT GTTTGCCCTG CAATTGTAACT TCCAAAGGTT 360
 CTCTTAGTGC TCGATGTGAC AACTCTGGAC GGTGCAGCTG TAAACCAGGT GTGACAGGAG 420
 CCAGATGCGA CCGATGTCTG CCAGGCTTCC ACATGCTCAC GGATGCGGGG TGCACCCAAG 480
 ACCAGAGACT GCTAGACTCC AAGTGTGACT GTGACCCAGC TGGCATCGCA GGGCCCTGTG 540
 ACGCGGGCCG CTGTGTCTGC AAGCCAGCTG TTAAGTGGAG ACGCTGTGAT AGGTGTGAT 600
 CAGGTTACTA TAATCTGGAT GGGGGGAACC CTGAGGGCTG TACCCAGTGT TTCTGCTATG 660
 GGCAATCAGC CAGCTGCGCG AGCTCTGCGA AATACAGTGT CCATAAGATC ACCTCTACCT 720
 TTCATCAAGA TGTGTATGCG TGAAGGCTG TCCAACGAAA TGGGTCTCTC GCAAGACTCC 780
 AATGGTCACA GGCATCAAA GATGTGTTTA GCTCAGCCCA ACGACTAGAC CCTGTCTATT 840

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 5 TGAGTTACTT TGAGTATCGA AGTTACTGCG GGAATCTCAC AGCCTCCGC ATCCGAGCTA 1140
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 15 TGAGGCCTTG TCAGCCCTGT CAATGCAACA ACAATGTGGA CCCAGTGCC TCTGGGAATT 1680
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 20 AGGCCCTGAT TTCAAAGGCT CAGGGTGGTG ATGGAGTAGT ACCTGATACA GAGCTGGAAG 2040
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 25 CAGAAAGTGA AGCTTCCCTG GGAACACTA ACATTCTGCT CTCAGACCAC TACGTGGGGC 2340
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 30 CTGTGGTGCA AGGGCTTGTG GAAAAATTGG AGAAAACCAA GTCCCTGGCC CAGCAGTTGA 2580
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 40 CCGGGGAGGC CCTGGAATAT TCCAGTGAGA TTGAACAGGA GATTGGGAGT CTGAACCTTG 3180
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 45 AGCCTCTCAG TGTAGATGAA GAGGGGCTGG TCTTACTGGA GCAGAAGCTT TCCCGAGCCA 3480
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 70 CATGGGGGCA CTTGAGTTTT GGCAAGGCTG ACAGAGCTCT GGGTTGTGCA CATTCTTTTG 4980
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 TAACACCAGT GGGAAATGCT GGAGGAACCA GAGGCACTTC CACCTTGGCT GGGAAAGACTA 5100
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 CAATTGTTAG ATGCC

Seq ID NO: 591 Protein sequence
 Protein Accession #: NP_005553.1

1 11 21 31 41 51
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 HMLTDAGCTQ DQRLLDKSCD CDPAGIAGPC DAGRCVCKPA VTGERCDRCR SGYYNLDDGN 180
 PEGCTQCFCY GHSASCRSSA EYSVHKITST FHQDVGWKA VQRNGSPAKL QWSQRHQDVF 240
 85 SSAQRLLDPVY FVAPAKFLGN QQVSYGQSLF FDRVDRGGR HPSAHDVILE GAGLRITAPL 300
 MRLGKTLPCG LTKTYTFRLL EHPSNNWSPQ LSYFEYRRL RLNLALRIRA TYGEYSTGYI 360
 DNVTLISARP VSGAPAPWVE QCICPVGYKG QFCQDCASGY KRDSARLPGF GTCIPNCQCG 420
 GGACDPDTGD CYSGDENPDI ECADCPIGFY NDPHDPRSK PCPCHNGFSC SVMPEETEYV 480

CNNPCPGVVG ARCELADGY FGDPFGEHGP VRPCQPCQCN NNVDPSASGN CDRLTGRCLK 540
 CIHNTAGIYC DQCKAGYFGD PLAPNPADKC RACNCNPMGS BPVGCSDGT CVCKPGFGGP 600
 NCEHGAFSCP ACYNQVKIQM DQFMQQLQRM EALISKAQGG DGVVPDTELE GRMQQAEQAL 660
 QDILRDAQIS EGASRSLGLQ LAKVRSQENS YQSRLLDDLM TVERVRLGSG YQNVRRVDTH 720
 RLITQMQLSL AESEASLGNT NIPASDHYVG PNGFKSLAQE ATRLAESHVE SASNMEQLTR 780
 ETEDYSKQAL SLVRKALHEG VSGSGSPDGP AVVQGLVEKL ETKSLAQQL TREATQABIE 840
 ADRSYQHSIR LLDVSRRLQG VSDQSFQVEE AKRIKQKADS LSTLVTRHMD EFKRTQKNLG 900
 NWKEBAQQLL QNGKSGREKS DQLLSRANLA KSRAQEALSM GNATFYEVES ILKNLREFDL 960
 QVDNRKAEE EAMKRLSYIS QKVSDASDKT QQAERALGSA AADAQRAKNG AGEALEISSE 1020
 IEQEIGSLNL EANVTADGAL AMEKGLASLK SEMREVEGEL ERKELEFDTN MDAVQMVITE 1080
 AQKVDTRAKN AGVTIQDTLN TLDGLHLMD QPLSVDEEGL VLEQKLSRA KTQINSQRLP 1140
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Seq ID NO: 592 DNA sequence
 Nucleic Acid Accession #: AF101051.1
 Coding sequence: 221.856

1 11 21 31 41 51
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 GCGGGGCCCA GCCACCTTCG GGAGTCCGGG TTGCCACCTT GCAAACCTCT CGCCTTCTGC 180
 ACCTGCCACC CCTGAGCCAG CGCGGGCGCC CGAGCGAGTC ATGGCCAAACG CGGGGCTGCA 240
 25 GCTGTGTGGG TCTATCTCG CCTTCTGGG ATGGATCGGC GCCATCGTCA GCACTGCCCT 300
 GCCCCAGTGG AGGATTACT CCTATGCCGG CGACAACATC GTGACCGCCC AGGCCATGTA 360
 CGAGGGGCTG TGGATGTCTT GCGTGTCCGA GAGCACCGGG CAGATCCAGT GCAAAGTCTT 420
 TGACTCCTTG CTGAATCTGA CGAGCACATT GCAAGCAACC CGTGCCTTGA TGGTGGTTGG 480
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 CTTGGAAGAC GATGAGGTGC AGAAGATGAG GATGGCTGTC ATTGGGGGTG CGATATTTCT 600
 30 TCTTGCAGST CTGGCTATTT TAGTTGCCAC AGCATGGTAT GGCAATAGAA TCGTTCAAGA 660
 ATTCTATGAC CCTATGACCC CAGTCAATGC CAGGTACGAA TTTGGTCAGG CTCTCTTCC 720
 TGGCTGGGCT GCTGCTTCT TCTGCCCTCT GGGAGGTGCC CTACTTTGCT GTTCTGTCTC 780
 CCGAAAAACA ACCTCTTACC CAACACCAAG GCCCTATCCA AAACCTGCAC CTTCAGCGG 840
 35 GAAAGACTAC GTGTGACACA GAGGCAAAAG GAGAAAAATCA TGTGAAACA AACCGAAAAAT 900
 GGACATTGAG ATACTATCAT TAACATTAGG ACCTTAGAAT TTTGGGTATT GTAATCTGAA 960
 GTATGGTATT ACAAACAAA CAACACCAACA AAAAAACCAT GTGTTAAAT ACTCAGTGCT 1020
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 TTGTATTACT GCTTCCCAT T GAGTAATCAT ACTCAATGG GGAAGGGGT GCTCCTTAAA 1140
 40 TATATATAGA TATGATATA TACATGTTT TCTATTAAAA ATAGACAGTA AAATACTATT 1200
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 TTTGCTTTGA AAATATTGTT CCAATTGAGT AGCTGCATGC TGTTCGCCCA GGTGTTGTAA 1740
 50 CACAACCTTTA TTGATTGAAT TTTTAAGCTA CTATTTCATA GTTTTATATC CCCCTAAACT 1800
 ACCTTTTTGT TCCCATCTCC TTAATTGTAT TGTTTTCCCA AGTGTAAATTA TCATGCGTTT 1860
 TATATCTTCC TAATAAGGTG TGGTCTGTGT GTCTGAACAA AGTGCTAGAC TTTCTGGAGT 1920
 GATAATCTGG TGACAAATAT TCTCTCTGTA GCTGTAAGCA AGTCACTTAA TCTTTCTACC 1980
 TCTTTTCTCT ATCTGCCAAA TTGAGATAAT GATACTTAAC CAGTTAGAAG AGGTAGTGTC 2040
 55 AATATTAAAT AGTTTATATT ACTCTCATTC TTTGAACATG AACTATGCCT ATGTAGTGTC 2100
 TTTATTGTCT CAGCTGGCTG AGACACTGAA GAAGTCACTG AACAAACCTT ACACACGTAC 2160
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 70 TTTTGAATCA TAATAACTCA TAAGGTGCTA TCTGTTTCAAT GATGCCCTCA GAGCTCTTGC 3000
 TGTTAGCTGG CAGCTGACGC TGCTAGGATA GTTAGTTTGG AAATGGTACT TCATAATAAA 3060
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 75 ACAAAAAAAT TTTATGGCCC AAAATGACCA ACGAAATTGT TACAATAGAA TTTATCCAAT 3300
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 TTATAATGGG AATTTGTATA AAGCATTACT CTTTTCAAT AAATTGTTTT TTAATTTAAA 3420
 AAAAGGAAAA AAAAAA AAA

Seq ID NO: 593 Protein sequence
 Protein Accession #: AAD16433.1

1 11 21 31 41 51
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 85 MANAGLQLLG FILAFLGWIG AIVSTALPQW RIYSYAGDNI VTAQAMYEGL WMSCVSQSTG 60
 QIQCKVFDL LNLSSLTQAT RALMVVGILL GVIAIFVATV GMKCMKLED DEVQKMRMAV 120
 IGGAIFFLLG LAILVATAWY GNRIVQEFYD PMTPVNARYE FGQALFTGWA AASLCLLGGA 180
 LLCCSCPRKT TSYPTPRPYP KPAESSGKDY V

Seq ID NO: 594 DNA sequence
Nucleic Acid Accession #: NM_006180.1
Coding sequence: 352..2820

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10	TGCCCCGGCG	GCCGGGCCAT	GCAGCGACGG	CCGCCGCGGA	GCTCCGAGCA	GCGGTAGCGC	120
	CCCCCTGTAA	AGCGGTTTCG	TATGCGGGGA	CCACTGTGAA	CCCTGCCGCC	TGCCGGAACA	180
	CTCTTCGCTC	CGGACCAAGT	CAGCCTCTGA	TAAGCTGGAC	TGGGCACGCC	CGCAACAAGC	240
	ACCGAGGAGT	TAAGAGAGCC	GCAAGCGCAG	GGAAGGCCTC	CCCGCACGGG	TGGGGGAAAG	300
	CGGCCGGTGC	AGCGCGGGGA	CAGGCACCTG	GGCTGGCACT	GGCTGCTAGG	GATGTCGTCC	360
15	TGGATAAGGT	GGCATGGACC	CGCCATGGCG	CGGCTCTGGG	GCTTCTGCTG	GCTGGTTGTG	420
	GGCTTCTGGA	GGGCCGCTTT	CGCCTGTCCC	ACGTCTGTGA	AATGCAGTGC	CTCTCGGATC	480
	TGGTGCAGCG	ACCCTTCTCC	TGGCATCGTG	GCATTTCGGA	GATTGGAGCC	TAACAGTGTA	540
	GATCCTGAGA	ACATCACCGA	AATTTTCATC	GCAAAACCAG	AAAGGTTAGA	AATCATCAAC	600
	GAAGATGATG	TTGAAGCTTA	TGTGGGACTG	AGAAATCTGA	CAATTGTGGA	TTCTGGATTA	660
20	AAATTGTGGG	CTCATAAAGC	ATTTCTGAAA	AACAGCAACC	TGCAGCACAT	CAATTTTACC	720
	CGAAACAAAC	TGACGAGTTT	GTCTAGGAAA	CATTTCCGTC	ACCTTGACTT	GTCTGAACTG	780
	ATCTTGGTGG	GCAATCCAT	TACATGCTCC	TGTGACATTA	TGTGGATCAA	GACTCTCCAA	840
	GAGGCTAAAT	CCAGTCCAGA	CACCTCAGGAT	TTGTACTGCC	TGAATGAAAG	CAGCAAGAAT	900
	ATTCCTCTGG	CAAACTTGCA	GATACCCAAT	TGTGGTTTGC	CATCTGCAAA	TCTGGCCGCA	960
25	CCTAACTCTA	CTGTGGAGGA	AGGAAAGTCT	ATCACATTAT	CTGTAGTGTG	GGCAGGTGAT	1020
	CCGGTTCCTA	ATATGTATTG	GGATGTTGGT	AACCTGGTTT	CCAAACATAT	GAATGAAACA	1080
	AGCCACACAC	AGGGCTCCTT	AAGGATAACT	AACATTTTCT	CCGATGACAG	TGGGAAGCAG	1140
	ATCTCTTGTG	TGGCGGAAAA	TCTTGTAGGA	GAAGATCAAG	ATTCTGTCAA	CCTCACTGTG	1200
	CATTTTGCAC	CAACTATCAC	ATTTCTCGAA	TCTCCAACCT	CAGACCACCA	CTGGTGCAAT	1260
30	CCATTCACCT	TGAAAGGCGA	CCCCAAACCA	CGCCTTCAGT	GGTCTATAAA	CGGGGCAATA	1320
	TTGAATGAGT	CCAAATACAT	CTGTACTAAA	ATACATGTTA	CCAATCACAC	GGAGTACCAC	1380
	GGCTCGCTCC	AGCTGGATAA	TCCCACCTAC	ATGAACAATG	GGGACTACAC	TCTAATAGCC	1440
	AAGAATGAGT	ATGGGAAGGA	TGAGAAACAG	ATTTCTGCTC	ACTTCATGGG	CTGGCCTGGA	1500
	ATTGACGATG	GTGCAAAACC	AAATTATCCT	GATGTAATTT	ATGAAGATTA	TGGAAGTACA	1560
35	GCGAATGACA	TGCGGGACAC	CACGAACAGA	AGTAATGAAA	TCCCTTCCAC	AGACGTCACT	1620
	GATAAAACCG	CTCGGGAACA	TCTCTCGGTC	TATGCTGTGG	TGGTGATTGC	GTCTCTGGTG	1680
	GGATTTTGCC	TTTTGTGTAAT	GCTGTTTCTG	CTTAAGTTGG	CAAGACACTC	CAAGTTTGGC	1740
	ATGAAAGGCC	CAGCCTCCGT	TATCAGCAAT	GATGATGACT	CTGCCAGCCC	ACTCCATCAC	1800
	ATCTCCAATG	GGAGTAACAC	TCCATCTTCT	TGCGAAGGTG	GCCCAGATGC	TGTCAATTAT	1860
40	GGAAATGACCA	AGATCCCTGT	CATTGAAAAA	CCCCAGTACT	TTGGCATCAC	CAACAGTCAG	1920
	CTCAAGCCAG	ACACATTTGT	TCAGCACATC	AAGCGACATA	ACATTGTTCT	GAAAAGGGAG	1980
	CTAGGCGAAG	GAGCCTTTGG	AAAAGTGTTC	CTAGCTGAAT	GCTATAACCT	CTGTCTCTAG	2040
	CAGGACAAGA	TCTTGGTGGC	AGTGAAGACC	CTGAAGGATG	CCAGTGACAA	TGCACGCAAG	2100
45	GACTTCCACG	GTGCGGACCA	GCTCCTGACC	AACCTCCAGC	ATGAGCACAT	CGTCAAGTTC	2160
	TATGGCGTCT	CGGTGGAGGG	CGACCCCTCT	ATCATGGTCT	TTGAGTACAT	GAAGCATGGG	2220
	GACCTCAACA	AGTTCCTCAG	GGCACACGGC	CCTGATGCCG	TGCTGATGGC	TGAGGGCAAC	2280
	CCGCCACACG	AACTGACGCA	GTGCGAGATG	CTGCATATAG	CCCAGCAGAT	CGCCGCGGGC	2340
	ATGGTCTACC	TGGCGTCCCA	GCACTTCGTG	CACCGCGATT	TGGCCACCAG	GAAGTGCCTG	2400
50	GTGCGGGAGA	ACTTGTCTGG	GAAAATCGGG	GACTTTGGGA	TGTCCCGGGA	CGTGTACAGC	2460
	ACTGACTACT	ACAGGGTCCG	TGGCCACACA	ATGCTGCCCA	TTGCTGGGAT	GCCTCCAGAG	2520
	AGCATCATGT	ACAGGAAATT	CACGACGGAA	AGCGACGTCT	GGAGCCTGGG	GGTCTGTGTT	2580
	TGGGAGATTT	TCACCTATGG	CAAAACAGCC	TGGTACCAGC	TGTCAAACAA	TGAGGTGATA	2640
	GAGTGTATCA	CTCAGGGCCG	AGTCCTGCGA	CGACCCCGCA	CGTGCCCCCA	GGAGGTGTAT	2700
55	GAGCTGATGC	TGGGGTGTCT	GCAGCGAGAG	CCCCACATGA	GGAAGAACAT	CAAGGGCATC	2760
	CATACCTCTC	TTCAGAACTT	GGCCAAGGCA	TCTCCGCTCT	ACCTGGACAT	TCTAGGCTAG	2820
	GGCCCTTTTC	CCCAGACCGA	TCCTTCCCAA	CGTACTCCTC	AGACGGGCTG	AGAGGATGAA	2880
	CATCTTTTAA	CTGCCGCTGG	AGGCCACCAA	GCTGCTCTCC	TTCACTCTGA	CAGTATTAAAC	2940
	ATCAAAGACT	CCGAGAAGCT	CTCGAGGGAA	GCAGTGTGTA	CTTCTTCATC	CATAGACACA	3000
60	GTATTGACTT	CTTTTGGGCA	TTATCTCTTT	CTCTCTTTCC	ATCTCCCTTG	GTTGTTCTCT	3060
	TTTCTTTTTC	TAAATTTTCT	TTTTTCTCTT	TTTTTTCGTC	TTCCCTGCTT	CACGATTCTT	3120
	ACCCTTTTCT	TTGAATCAAT	CTGGCTTCTG	CATTACTATT	AACTCTGCAT	AGACAAAGGC	3180
	CTTAAACAAAC	GTAATTTGTT	ATATCAGCAG	ACACTCCAGT	TTGCCACCA	CAACTAACAA	3240
	TGCCTTGTGG	TATTCCTGCC	TTTGATGTGG	ATGAAAAAAA	GGGAAAAACA	ATATTTCAC	3300
65	TAAACTTTGT	CACCTTCTGCT	GTACAGATAT	CGAGAGTTTC	TATGGATTCA	CTTCTATTTA	3360
	TTTATTATTA	TTACTGTTCT	TATTGTTTTT	GGATGGCTTA	AGCCTGTGTA	TAAAAAAGAA	3420
	AACCTGTGTT	CAATCTGTGA	AGCCTTTATC	TATGGGAGAT	TAAACCAGA	GAGAAAGAAG	3480
	ATTTATTATG	AACCGCAATA	TGGGAGGAAC	AAAGACAACC	ACTGGGATCA	GCTGGTGTCA	3540
	GTCCCTACTT	AGGAAATACT	CAGCAACTGT	TAGCTGGGAA	GAATGTATT	GGCACCTTCC	3600
70	CCTGAGGACC	TTTCTGAGGA	GTAAAAAGAC	TACTGGCCTC	TGTGCCATGG	ATGATTCTTT	3660
	TCCCATCACC	AGAAATGATA	GCGTGCAGTA	GAGAGCAAAG	ATGGCTTT		

Seq ID NO: 595 Protein sequence
Protein Accession #: NP_006171.1

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	NFTRNKLTS	SRKHFRHL	SELILVGNPF	TCSCDIMWIK	TLQEAQSSPD	TQDLYCLNES	180
80	SKNIPLANLQ	IPNCGLPAN	LAAPNLVVEE	GKSITLSCSV	AGDPVPMNYW	DVGNLVSKHM	240
	NETSHTQGS	RITNISDDSD	GKQISCAVEN	LVGEDQDSVN	LTVHFAPTIT	FLESPTSDDH	300
	WCIPFTVKGN	PKPALQWFYN	GAILNESKYI	CTKIHVNTHT	EVHGCLQLDN	PTHMNNGDYT	360
	LIAKNEYGKD	EKQISAHFMG	WPGIDDGANP	NYPDVIYEDY	GTAANDIGDT	TNRSNEIPST	420
	DVTDKGTREH	LSVYAVVVIA	SVVGFCLLMV	LFLKLARHS	KFGMKGPASV	ISNDDDSASP	480
85	LHHISNGSNT	PSSSEGGPDA	VIIGMTKIPV	IENPQYFGIT	NSQLKPDFTV	QHIKRNHIVL	540
	KRELGEFAGF	KVFLAEYCYN	CPEQDKILVA	VKTLDASDN	ARKDFHREAE	LLTNLQHEHI	600
	VKPYGVCEVG	DPLIMVFPEY	KHGDNLKFLR	AHGFDAVLMA	EGNPPELTQ	SQMLHIAQOI	660
	AAGMVYLASQ	HFVHRDLATR	NCLVGENLLV	KIGDFGMSRD	VYSTDYRYRV	GHTMLPIRWM	720

PPESIMYRKF TTESDVSWSLG VVLWEIFTYG KQPWYQLSNN EVIECITQGR VLQRPRTCPQ 780
 EVELMLGCW QREPHMRKNI KGIHTLLQNL AKASPVYLDI LG

Seq ID NO: 596 DNA sequence
 Nucleic Acid Accession #: AF410899
 Coding sequence: 483..2999

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	TGCATACCGG	ACCCCATTC	GCATCTAACA	AGGAATCTGC	GCCCCAGAGA	GTCCCGGACG 180
	CCGCCGGTGG	GTGCCCGGCG	CGCCGGGCCA	TGCAGCGACG	GCCGCCGCGG	AGCTCCGAGC 240
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	CTGCCGGAAC	ACTCTTCGCT	CCGGACCAGC	TCAGCCTCTG	ATAAGCTTGA	CTCGGCACGC 360
	CGCAACAAG	CACCGAGGAG	TAAAGAGAGC	CGCAAGCGCA	GGGAAGGCCT	CCCCGCACGG 420
	GTGGGGGAAA	GCGGCCGGTG	CAGCGCGGGG	ACAGGCACTC	GGGCTGGCAC	TGGCTGCTAG 480
	GGATGTCTGC	CTGGATAAGG	TGGCATGGAC	CCGCCATGGC	GCGGCTCTGG	GGCTTCTGCT 540
20	GGCTGTTTGT	CGGCTTCTGG	AGGGCCGCTT	TCGCCTGTCC	CACGTCCTGC	AAATGCAGTG 600
	CCTCTCGGAT	CTGGTGCAGC	GACCCTTCTC	CTGGCATCGT	GGCATTTCCG	AGATTGGAGC 660
	CTAACAGTGT	AGATCTCTGAG	AACATCACCG	AAATTTTCAT	CGCAAACCCAG	AAAAGGTTAG 720
	AAATCATCAA	CGAAGATGAT	GTTGAAGCTT	ATGTGGGACT	GAGAAATCTG	ACAATGTGG 780
	ATTCTGGATT	AAAAATTGTG	GCTCATAAAG	CATTTCTGAA	AAACAGCAAC	CTGCAGCACA 840
25	TCAATTTTAC	CCGAAACAAA	CTGACGAGTT	TGCTTAGGAA	ACATTTCCGT	CACCTTGACT 900
	TGCTGAACCT	GATCCTGGTG	GGCAATCCAT	TTACATGCTC	CTGTGACATT	ATGTGGATCA 960
	AGACTCTCCA	AGAGGCTAAA	TCCAGTCCAG	ACACTCAGGA	TTGTACTGTC	CTGAATGAAA 1020
	GCAGCAAGAA	TATTCGCCCTG	GCAAACTCTG	AGATAACCCAA	TTGTGGTTTG	CCATCTGCAA 1080
	ATCTGGCCGC	ACCTAACCTC	ACTGTGGAGG	AAGGAAAGTC	TATCACAATTA	TCCGTAGTAG 1140
	TGCGAGGTGA	TCCGGTTCCT	AATATGTATT	GGGATGTTGG	TAACTGTGTT	TCCAAACATA 1200
30	TGAATGAAAC	AAGCCACACA	CAGGGCTCCT	TAAGGATAAC	TAACATTTCA	TCCGATGACA 1260
	GTGGGAAGCA	GATCTCTTGT	GTGGCGGAAA	ATCTTGTAGG	AGAAGATCAA	GATTCTGTCA 1320
	ACCTCACTGT	GCATTTTGCA	CCAACATATCA	CATTTCTCGA	ATCTCCAACC	TCAGACCACC 1380
	ACTGGTGCAT	TCCATTCACT	GTGAAAGGCA	ACCCCAAACC	AGCGCTTCAG	TGGTTCTATA 1440
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	CGGAGTACCA	GAGCTGCCCT	CAGCTGGATA	ATCCCACTCA	CATGAACAAT	GGGGACTACA 1560
	CTCTAATAGC	CAAGAATGAG	TATGGGAAGG	ATGAGAAACA	GATTTCTGCT	CACCTTCATG 1620
	GCTGGCCTGG	AATTGACGAT	GGTGCAAAACC	CAAATTATCC	TGATGTAATT	TATGAAGATT 1680
	ATGGAAGTGC	AGCGAATGAC	ATCGGGGACA	CCACGAACAG	AAGTAATGAA	ATCCCTTCCA 1740
40	CAGACGCTAC	TGATAAAACC	GGTCGGGAAC	ATCTCTCGGT	CTATGCTGTG	GTGGTGATTG 1800
	GCTCTGTGGT	GGGATTTTGC	CTTTTGGTAA	TGCTGTTTCT	GCTTAAGTTG	GCAAGACACT 1860
	CCAAGTTTGG	CATGAAGAT	TTCTCATGGT	TTGGATTTGG	GAAAGTAAAA	TCAAGACAAG 1920
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45	TCTCCAATGG	GAGTAACACT	CCATCTTCTT	CGGAAGGTGG	CCCAGATGCT	GTCAATTATTG 2040
	GAATGACCAA	GATCCCTGTC	ATTGAAAATC	CCCAGTACTT	TGGCATCACC	AACAGTCAGC 2100
	TCAAGCCAGA	CACATTGTGT	CAGCACATCA	AGCGACATAA	CATTGTTCTG	AAAAGGGAGC 2160
	TAGGCGAAGG	AGCCTTTGGA	AAAGTGTTC	TAGCTGAATG	CTATAACCTC	TGTCCTGAGC 2220
	AGGACAAGAT	CTTGGTGGCA	GTGAAGACCC	TGAAGGATGC	CAGTGACAAT	GCACGCAAGG 2280
	ACTTCCACCG	TCAGGCGCAG	CTCCTGACCA	ACCTCCAGCA	TGAGCACATC	GTCAAGTTCT 2340
50	ATGGCGTCTG	CGTGGAGGGC	GACCCCTCA	TCATGCTCTT	TGAGTACATG	AAGCATGGGG 2400
	ACCTCAACAA	GTTCTCAGG	GCACACGGCC	CTGATGCCGT	GCTGATGGCT	GAGGGCAACC 2460
	CGCCACCGGA	ACTGACGACG	TCGCAGATGC	TGCATATAGC	CCAGCAGATC	GCCGCGGGCA 2520
	TGGTCTACCT	GCGCTCCCAG	CACCTTCGTG	ACCGCGATTT	GGCCACCAGG	AACTGCCTGG 2580
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55	CTGACTACTA	CAGGGTCCGT	GGCCACACAA	TGCTGCCCAT	TCGCTGGATG	CCTCCAGAGA 2700
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	GGGAGATTTT	CACCTATGGC	AAACAGCCCT	GGTACCAGCT	GTCAACAAT	GAGGTGATAG 2820
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60	ATACCCTCCT	TCAGAACTTG	GCCAAGGCAT	CTCCGGTCTA	CCTGGACATT	CTAGGCTAGG 3000
	GCCTTTTCC	CGAGACCGAT	CCTTCCCAAC	GTACTCCTCA	GACGGGCTGA	GAGGATGAAC 3060
	ATCTTTTAA	TGCCGTGGGA	GGCCACCAAG	CTGCTCTCCT	TCACTCTGAC	AGTATTAACA 3120
	TCAAAGACTC	CGAGAAGCTC	TCGAGGGAAG	CAGTGTGTAC	TTCTTATATC	ATAGACACAG 3180
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	TTAACAAACG	TAATTTGTGA	TATCAGCAGA	CACTCCAGTT	TGCCCACCAC	AACTAACAAAT 3420
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	AAACTTTGTC	ACTTCTGCTG	TACAGATATC	GAGAGTTTCT	ATGGATTAC	TTCTATTTAT 3540
70	TTATTATTAT	TACTGTCTCT	ATTGTTTTTG	GATGGCTTAA	GCCTGTGTAT	AAAAAGAGAA 3600
	ACTTGTGTTC	AATCTGTGAA	GCCTTTATCT	ATGGGAGATT	AAAACCAGAG	AGAAAGAAGA 3660
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	TCCTTACTTA	GGAATACTC	AGCAACTGTT	AGCTGGGAAG	AATGTATTTC	GCACCTTCCC 3780
	CTGAGGACCT	TTCTGAGGAG	TAAAAAGACT	ACTGGCCTCT	GTGCCATGGA	TGATTCTTTT 3840
75	CCCATCACCA	GAAATGATAG	CGTGCAGTAG	AGAGCAAAGA	TGCTTCCGT	GAGACACAAG 3900
	ATGGCGCATA	GTGTGCTCGG	ACACAGTTTT	GTCTTCTGAT	GTGTGATGTA	TAGCACTGGT 3960
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Seq ID NO: 597 Protein sequence
 Protein Accession #: AAL67965.1

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	NFTRNKLTS	SRKHFRHL	SELILVGNPF	TCSCDIMWIK	TLQEAQSSPD	TQDLYCLNES 180
	SKNIPLANLQ	IPNCGLP	LANPLNLTVEE	GKSITLSCSV	AGDPVPNMWY	DVGNLVSKHM 240

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 WCIPTFTVKN PKPALQWFFN GAILNESKYI CTKIHVNTHT EYHGCLQLDN PTHMNMGDYT 360
 FLAKNEYGKD EKQISAHFMG WPGIDDGANP NYPDVIYEDY GTAANDIGDT TNRSNEIPST 420
 DVTDKTGRH LSVYAVVVIA SVVGFCLLVM LFLKLARHS KFGMKDFSWF GFGKVKSRQG 480
 5 VGPASVISND DSDASPLHHI SNGSNTPSSS EGGPDVAVIIG MTKIPVIENP QYFGITNSQL 540
 KPDTFVQHIK RHNIVLKLREL GEGAFGKVF L AECYNLCPEQ DKILVAVKTL KDAASDNARKD 600
 FHREAEELLN LQHEHIVKFY GVCVEGDPLI MVFEYMKHGD LNKFLRAHGP DAVLMAEGNP 660
 PTELTSQSLM HIAQQIAAGM VYLASQHFVH RDLATRNCLV GENLLVKIGD FGMSRDVYST 720
 10 DYRVVGHTM LPIRWMPPE S IMYRKFTTES DVWSLGVVLW EIFTYKQPW YQLSNNEVIE 780
 CITQGRVLQR PRTCPQEVYE LMLGCWQREP HMRKNIKGIH TLLQNLAKAS PVYLDILG

Seq ID NO: 598 DNA sequence
 Nucleic Acid Accession #: AB052906
 Coding sequence: 74..814

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 20 GCTCCTGCTG TCCGCTGTGT CCGGGCTGG GCGAGCCGAC CCTCACTCTC TTGTCTATGA 180
 CATCACCGTC ATCCCTAAGT TCAGACCTGG ACCACGGTGG TGTGCGGTTT AAGGCCAGGT 240
 GGATGAAAAG ACTTTTCTTC ACTATGACTG TGGCAACAAG ACAGTACAC CTGTGAGTCC 300
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 GGTGGTGGAC ATACTTACAG AGCAACTGCG TGACATTCAG CTGGAGAAT ACACACCCAA 420
 25 GGAACCCCTC ACCCTGCAGG CCAGGATGTC TTGTGAGCAG AAAGCTGAAG GACACAGCAG 480
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 CTCTTTGATG GGCATGGACA GCACCTGGA GCCAAGTGCA GGAGCACCCAC TCGCCATGTC 720
 30 CTCAGGCACA ACCCACTCA GGGCCACAGC CACCACCCTC ATCCTTTGCT GCCTCCTCAT 780
 CATCCTCCCC TGCTTCTATC TCCCTGGCAT CTGAGGAGAG TCCTTTAGAG TGACAGGTTA 840
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 GTACTTCTTT GAATGATGAT CTCTTTCTTG CAAATGATAT TGTGAGTAAA ATAATCACGT 1200
 TAGACTTCAG ACCTCTGGGG ATTCTTCCG TGTCTGAAA GAGAATTTT AAATATTTA 1260
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Seq ID NO: 599 Protein sequence
 Protein Accession #: BAB61048.1

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 50 LQARMSCEQK AEGHSGGSQW FSEFGQIFLL FDSEKRMWTT VHPGARKMKE KWENDKVVAM 180
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Seq ID NO: 600 DNA sequence
 Nucleic Acid Accession #: NM_001898.1
 Coding sequence: 57..482

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 CCCAGTATCT GAGTACCTTG CTGCTCCTGC TGGCCACCCT AGCTGTGGCC CTGGCCCTGA 120
 60 GCCCCAAGGA GGAGGATAGG ATAATCCCGG GTGGCATCTA TAACGCAGAC CTCAATGATG 180
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 65 ATTACTTCTT CGACGTAGAG GTGGGCGGCA CCATATGTAC CAAGTCCCAG CCCAACTTGG 360
 ACACCTGTGC CTTCATGAA CAGCCAGAAC TGCAGAAGAA ACAGTTGTGC TCTTTGAGA 420
 TCTACGAAGT TCCCTGGGAG AACAGAAGGT CCCTGGTGAA ATCCAGGTGT CAAGAATCCT 480
 AGGGATCTGT GCCAGGCCAT TCGCACCAGC CACCACCAC TCCCACCCC TGTAGTGCTC 540
 CCACCCCTGG ACTGGTGGCC CCCACCTGCG GGGAGGCCTC CCCATGTGCC TGCGCCAAGA 600
 70 GACAGACAGA GAAGGCTGCA GGAGTCTTT GTTGCTCAGC AGGGCGCTCT GGCCTCCCTC 660
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Seq ID NO: 601 Protein sequence
 Protein Accession #: NP_001889.1

1 11 21 31 41 51
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 80 EIVEVPWENR RSLVKSRCQE S

Seq ID NO: 602 DNA sequence
 Nucleic Acid Accession #: NM_003976.2
 Coding sequence: 299..961

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GGGTGGCAGG CCGGTCCCCC ACAAAGATA ACTCATCTCT TAATTTGCAA GCTGCCTCAA 240
CAGGAGGGTG GGGGAACAGC TCAACAATGG CTGATGGGCG CTCTGGTGT TGATAGAGAT 300
GGAACCTGGA CTGGAGGGCC TCTCCACGCT GTCCCACTGC CCCTGGCCTA GCGGCGAGCC 360
TGCCCTGTGG CCCACCTTGG CCGCTCTGGC TCTGCTGAGC AGCGTCGCG AGGCCCTCCCT 420
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AGGGCTCGCT CCAGGGCTTT GCAGACTGGA CCTTACCGG TGCTCTTCC TGCTGGGAC 1020
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AGGCCCTACG CCGTGGGTGA TGGATATCAT CCCCAGAAC GTGAAGGGAC AACTGACTAG 1140
CAGCCCCCAG GCCTCACCCT TCGGATCCCG AGCCTAAAAG ACACCAAGAGA CCTCAGCTAT 1200
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CCCTCCTCTG ATGAACACTA CAGTGGCTGA GGCATCAGCC CCGCGCCAG CCCTGTAGGG 1320
ACAGCATTTG AAGGACACAT ATTGCAGTTG CTTGGTTGAA AGTGCTGTGT CTGGAAGTGG 1380
CCTGTACTCA CTCATGGGAG CTGGCCCC

Seq ID NO: 603 Protein sequence
Protein Accession #: NP_003967.1

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PAGHLPGGRT ARWCSSRRARR PPPQPSRPAP PPPAPPSALP RGGRAARAGG PGSRARAAGA 120
RGCRRLRSQLV PVRALGLGHR SDELVRFRFC SGSCRRARSP HDLSLASLLG AGALRPPPGS 180
RPVSPQCCRP TRYEAVSFMD VNSTWRTVDR LSATACGCLG

Seq ID NO: 604 DNA sequence
Nucleic Acid Accession #: NM_057091.1
Coding sequence: 783..1445

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CGCGTGTCTA CAAACTCAAC TCCCGGTTTC CGTGCCTCTC CACCGCTCGA GTTCTCTACT 240
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CGGGGAGGGG GCGCTCCGAG CCCCACCCCG GGATCTGGTG ACGCTGGGGC TGGAAATTGA 420
CACCGGACGG CTGCGGCGCG GGGCAGGAGG CTGCTGAGGG ATGGAGTTGG GCCCGGCCCG 480
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TCAACAGGAG GGTGGGGGAA CAGCTCAACA ATGGCTGATG GCGCTCCTG GTGTTGATAG 780
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GGCCGCGCGC GCAGCCTTCT CCGCCCGCGC CCGCCCGCGC TGCAACCCCA TCTGCTCTTC 1080
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CGCGGGGCTG CCGCTTGCCT TCGCAGCTGG TGCCGGTGGC CGCGCTCGGC CTGGGGCCAC 1200
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CACACGACCT CAGCCTGGCC AGCCTACTGG GCGCCGGGGC CTGCGACCG CCCCCGGGCT 1320
CCCGGGCCGT CAGCCAGCCC TGCTGCCGAC CCACGCGCTA CGAAGCGGTC TCCTTCATGG 1380
ACGTCAACAG CACCTGGAGA ACCGTGGACC GCCTCTCCGC CACCGCTGCG GGCTGCCTGG 1440
GCTGAGGGCT CGCTCCAGG CTCTGACAGC TGGACCTTA CCGGTGGCTC TTCTGCTCTG 1500
GGACCTCTCC GCAGAGTCCC ACTAGCCAGC GGCTCAGCC AGGGACGAAG GCCTCAAAGC 1560
TGAGAGGCCC CTACCGGTGG GTGATGGATA TCATCCCCGA ACAGGTGAAG GGACAACTGA 1620
CTAGCAGCCC CAGAGCCCTC ACCCTGCGGA TCCCAGCCTA AAAGACACCA GAGACCTCAG 1680
CTATGGAGCC CTTCGAGACC ACTTCTCACA GACTCTGGCA CTGGCCAGGC CTGCAACCTG 1740
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Seq ID NO: 605 Protein sequence
Protein Accession #: NP_003967.1

80

1 11 21 31 41 51
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RGCRRLRSQLV PVRALGLGHR SDELVRFRFC SGSCRRARSP HDLSLASLLG AGALRPPPGS 180
RPVSPQCCRP TRYEAVSFMD VNSTWRTVDR LSATACGCLG

85

Seq ID NO: 606 DNA sequence
Nucleic Acid Accession #: NM_057160.1

Seq ID NO: 607 Protein sequence
Protein Accession #: NP_476501.1

Seq ID NO: 608 DNA sequence
Nucleic Acid Accession #: NM_057090.1
Coding sequence: 29..715

Seq ID NO: 609 Protein sequence
Protein Accession #: NP_476431.1

Seq ID NO: 610 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1746

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CTCAACACGC	ACATCACTGA	ACTCAATGAG	TCCCGTGTCC	TCAATATCTC	AGCCCTCATC	240
GCCCTCTAGG	TTGAGAAGAA	TGAGCTGTGC	CGCATCAGCG	CTGGGGCTCT	CCGAACACTG	300
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TTCCAGGGCC	TGGACAGCCT	TGAGTCTCTC	CTTCTGTCCA	GTAACCAGCT	GTTGCAGATC	420
CAGCGGGCCC	ACTTCTCCCA	GTGCAGCAGAC	CTCAAGGAGC	TGCAGTTGCA	CGGCAACACC	480
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	GGCAAGAAATA	GCCTCACCCA	CATCTCACCC	AGGGTCTTCC	AGCACCTGGG	CAATCTCCAG	600
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5	TTCCACAAAC	ACCACAACCT	CCAGAGACTC	TACCTGTCCA	ACAACCACAT	CTCCAGCTG	780
	CCACCAGCA	TCTTCATGCA	GCTGCCCCAG	CTCAACCGTC	TTACTCTCTT	TGGGAATTCC	840
	CTGAAGGAGC	TCTCTCTGGG	GATCTTCTGG	CCCATGCCCA	ACCTGCGGGA	GCTTTGGGCTC	900
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10	ACGGAGCTTC	GGGAGCTGTG	CCTCCACACC	AACGCACTGC	AGGACCTGGA	CGGGAATGTG	1080
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	TGTTGCTGCT	GCAAGAGAG	GAGCCAGGCT	GTCTGTATGC	AGATGAAAGC	ACCCAATGAG	1740
	TGTTAAAGAG	GACGGCTGGA	GCAGGGCTGG	GGAATGATGG	GACTGGAGGA	CCTGGGAATT	1800
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25	CGTGCCGGAC	CTTCCCTACA	TCAGGAAGAT	AGATCCAACT	GGCCATGGCA	AAAGCCCTGG	1980
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	CCCCAGCACA	GCAAGCTCAG	CCTTTTAGAG	AAGGATATTT	CCAACTGCA	AACTTTGCTT	2520
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50	TCCAGGGTTA	TTCTCTCTCT	CGAGTCACAG	TCACACGAAT	ACCTGCCTTC	TCTGGCTTTC	3480
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60	ACTATTGGTG	GACCTTGGAG	GACATGCACC	AAGGCTTGCC	AGAGCCAAAC	GGAGGTGAGC	4080
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	GAGGGCCACT	GTCTCTCAGT	GACACCAACC	AGGAGCACCC	TAGGTGAGGG	GTGAGGGCCC	4440
	GCCTTATGTA	ACCTCTTGCC	CTTCTCTTTC	TCCCATCAGA	GTGGTTGGAT	GGAGCCATTG	4500
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70	GGGCTGGAAT	GAGCCGGCTG	GTCCCCCAGA	AAGCTGGAGT	GGGGTACAGA	GTTCAAGTTT	4680
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80	GAACCTTCAA	ACTCAGGAAG	TTTGCAGAGA	GCAGACAGCT	AGAGATAACT	CGGGACCCAG	5340
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85	CTTCAATGCT	CTCTCAAAGC	TAGATCATGT	TTGCCCTGCT	TAGAGAATTA	CTGCAAAATCA	5640
	GCCCCAGTGC	TTGGCGATGC	ATTACAGAT	TTCTAGGCCC	TCAGGGTTTT	GTAGAGTGTG	5700
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Seq ID NO: 611 Protein sequence
Protein Accession #: BAB84587.1

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LNTHITELNE SFFLNISALI ALRIEKNELS RITPGAFRNL GSLRYLSLAN NKLQVLPIGL 120
10  FQGLDSLES LLSSNQLLQI QPAHFSQCSN LKELQLHGNH LEYIPDGAFF HLVLTKLNL 180
GKNSLTHISP RVFQHLGNLQ VLRLYENRLT DIPMGTFDGL VNLQELALQQ NQIGLLSPGL 240
PHNNHNLQRL YLSNNHISQL PPSIFMQLPQ LNRLTLFGNS LKELSLGIFG PMPNLRRLWL 300
YDNHISSLPD NVFSNLRQLQ VLILSRNQIS FISPGAFNGL TELRELSLHT NALQDLDDGNV 360
15  FRMLANLQNI SLQNNRLRQL PGNIFANVNG LMAIQLQNNQ LENLPLGIFD HLGKLCLELRL 420
YDNPNWRCDSD ILPLRNWLLI NQPRLGTDTV PVCFSFANVR GQSLIIINVN VAVPSVHVPE 480
VPSYPETPWY PDPSPYDPTT SVSSTTELT S PVEDYTDLT IQVTDDRSVW GMTQAQSGLA 540
IAAIVIGIIVA LACSLAACVG CCCCKKRSQA VLMQMKAPNE C

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Seq ID NO: 612 DNA sequence
Nucleic Acid Accession #: XM_098151
Coding sequence: 1..447

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1      11      21      31      41      51
|      |      |      |      |      |
ATGATGCATT TGCTCAATTC TCAGGGCTGG AATGAGCCGG CTGGTCCCCC AGAAAGCTGG 60
AGTGGGGTAC AGAGTTCAGT TTTCTCTCTT GTTTACAGCT CCTTGACAGT CCCACGCCCA 120
TCTGGAGTGG GAGCTGGGGAG TCAGTGTGGG AGAAGAAACA ACAAAGCCA ATTAGAACCA 180
CTATTTTTAA AAAGTGCTTA CTGTGCACAG ATACTCTTCA AGCACTGGAC GTGGATTCTC 240
TCTCTAGCCC TCAGCACCCC TGCGGTAGGA GTGCCGCCCT TACCCTCTTG TGATGGGGTA 300
30  CAGAGGCACT TGCTCTTCTG CATGGTGTTC AATAGGCTGG GAGTTTTATT TATCTCTTCA 360
AATTTGTAC  AAGAGCTCAT GGCCTTGTCT GGGCTTTCGT CATTAAACCA AAGGAAATGG 420
AAGCCATTCC CTGTTGCTC TCCTTAG

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Seq ID NO: 613 Protein sequence
Protein Accession #: XP_098151

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1      11      21      31      41      51
|      |      |      |      |      |
MMHLLNSQGW NEPAGPPESW SGVQSSVFLS VYSSLTVPRP SGVGAGSQCW RRNNKSQLEP 60
LFLKSAYCAQ ILFKHWTWLL SLALSTPAVG VPPLPTCDGV QRHLLEFCMVF NRGVLFISS 120
NFVQELMACL GLSSLNQRKW KFPFCCSP

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Seq ID NO: 614 DNA sequence
Nucleic Acid Accession #: NM_002658.1
Coding sequence: 77..1372

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CCCCGACCTC GCCACCATGA GAGCCCTGCT GGCGCGCCTG CTTCTCTGCG TCTTGGTCTG 120
GAGCGACTCC AAAGGCAGCA ATGAACCTTCA TCAAGTTCCA TCGAACTGTG ACTGTCTAAA 180
TGGAGGAACA TGTGTGTCCA ACAAGTACTT CTCCAACATT CACTGGTGCA ACTGCCCAAA 240
GAAATTCGGA GGGCAGCACT GTGAAATAGA TAAGTCAAAA ACCTGCTATG AGGGGAATGG 300
55  TCACITTTTAC CGAGGAAAGG CCAGCACTGA CACCATGGGC CGGCCCTGCC TGCCCTGGAA 360
CTCTGCCACT GTCCITTCAGC AAACGTACCA TGCCACAGA TCTGATGCTC TTCAGCTGGG 420
CTCTGGGAAA CATAATTACT GCAGGAACCC AGACAAACCG AGGCGACCTT GGTGCTATGT 480
GCAGGTGGGC CTAAAGCCGC TTGTCCAAGA GTGCATGGTG CATGACTGCG CAGATGGAAA 540
AAAGCCCTCC TCTCTCCAG AAGAAATAAA ATTTCAGTGT GGCCAAAAGA CTCTGAGGCC 600
CGCTTTAAG ATTATTGGGG GAGAATTAC CACCATCGAG AACCGCCCTT GGTTTGCGGC 660
CATCTACAGG AGGCACCGGG GGGGCTCTGT CACCTACGTG TGTGGAGGCA GCCTCATCAG 720
60  CCCTTGCTGG GTGATCAGCG CCACACACTG CTTCAATTGAT TACCCAAAAGA AGGAGGACTA 780
CATCGTCTAC CTGGGTGCGT CAAGGCTTAA CTCCAACAG CAAGGGGAGA TGAAGTTTGA 840
GGTGGAAAAC CTCATCCTAC ACAAGGACTA CAGCGCTGAC ACGCTTGCTC ACCACAACGA 900
CATTGCCTTG CTGAAGATCC GTTCCAAGGA GGGCAGGTGT GCGCAGCCAT CCCGACTAT 960
65  ACAGACCATC TGCCCTGCCCT CGATGTATAA CGATCCCCAG TTGGGCACAA GCTGTGAGAT 1020
CACTGGCTTT GGAAGAGAGA ATTCTACCGA CTATCTCTAT CCGGAGCAGC TGAAGATGAC 1080
TGTTGTGAAG CTGATTTCCT ACCGGGAGTG TCAGCAGCCC CACTACTACG GCTCTGAAGT 1140
CACCACCAAA ATGCTATGTG CTGCTGACCC CCAATGGAAA ACAGATTCTT GCCAGGGAGA 1200
70  CTCAGGGGGA CCCCTCGTCT GTTCCCTCCA AGGCCGATG ACTTTGACTG GAATTGTGAG 1260
CTGGGGCCGT GGATGTGCC TGAAGGACAA GCCAGGCGTC TACACGAGAG TCTCACACTT 1320
CTTACCCTGG ATCCGCGATC ACACCAAGGA AGAGAATGGC CTGGCCCTCT GAGGGTCCCC 1380
AGGGAGGAAA CGGGCACCA CCGCTTCTT GCTGGTTGTC ATTTTTCAG TAGAGTCATC 1440
TCCATCAGCT GTAAGAAGAG ACTGGGAAGA TAGGCTCTGC ACAGATGGAT TTGCCTGTGG 1500
75  CACCACCAGG GTGAACGACA ATAGCTTTAC CTTACGGAT AGGCCTGGGT GCTGGCTGCC 1560
CAGACCTCTC GGCCAGGATG GAGGGGTGGT CCTGACTCAA CATGTTACTG ACCAGCAACT 1620
TGTCTTTTTC TGGACTGAAG CTGCAAGGAG TTAAGAAAGG CAGGGCATCT CCTGTGCATG 1680
GGCTCGAAGG GAGAGCCAGC TCCCCGACC GGTGGGCATT TGTGAGGCC ATGGTTGAGA 1740
AATGAATAAT TTCCCAATTA GGAAGTGTA GCAGCTGAGG TCTCTTGAGG GAGCTTAGCC 1800
AATGTGGGAG CAGCGGTTTG GGGAGCAGAG AACTAAACGA CTTACGGGCA GGGCTCTGAT 1860
80  ATTCCATGAA TGTATCAGGA AATATATATG TGTGTGATG TTTGCACACT TGTGTGTGG 1920
GCTGTGAGTG TAAGTGTGAG TAAGAGCTGG TGTCTGATTG TTAAGTCTAA ATATTTCCTT 1980
AAACTGTGTG GACTGTGATG CCACACAGAG TGGTCTTTCT GGAGAGGTTA TAGGTCACTC 2040
CTGGGGCCCT TTGGGTCCCC CACGTGACAG TGCCCTGGGA TGTACTTATT CTGCAGCATG 2100
ACCTGTGACC AGCATGTGCT CAGTTTCACT TTCACATAGA TGTCCTTTC TTGGCCAGTT 2160
85  ATCCCTTCCT TTTAGCTAG TTAATCCAAT CCTACTGGG TGGGGTGAGG ACCACTCCTT 2220
ACACTGAATA TTTATATTTT ACTATTTTTA TTTATATTTT TGTAATTTTA AATAAAGTG 2280
ATCAATAAAA TGTGATTTTT CTGA

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Seq ID NO: 615 Protein sequence
Protein Accession #: NP_002649.1

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5      1      11      21      31      41      51
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HCEIDKSKTC YEGNGHFYRG KASTDTMGRP CLPWNSATVL QQTYHAHRSD ALQLGLGKHN 120
YCRNPDNRNR PWCVVQVGLK PLVQECMVHD CADGKKPSSP PEEELKFQCGQ KTLRPRFKII 180
10    GGEFTTIENQ PWFAAIYRRH RGGSVTVYCG GSLISPCWVI SATHCFIDYP KKEDYIYVLG 240
RSRLNSNTQG EMKFEVENLI LHKDYSADTL AHNDIALLLK IRSKEGRCAQ PSRTIQTICL 300
PSMYNDPQFG TSCEITGFGK ENSTDYLYPE QLKMTVVKLI SHRECQPHY YGSEVTTKML 360
CAADFPQWKT SCQDSDGGLP VCSLQGRMTL TGIVSWGRGC ALKDKPGVYT RVSHFLPWIR 420
SHTKEENGLA L

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Seq ID NO: 616 DNA sequence
Nucleic Acid Accession #: NM_024422.1
Coding sequence: 202..2907

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GCTCCGCGCG CGGCCCTCGC CCCGCGGAGC CCTCCTACCC CGGCCCGACG CTCGCCCGCG 180
25    GACCTGCCCC GAGCCCTCTC CATGGAGGCA GCCCGCCCTC CCGGCTCCTG GAACGGAGCC 240
CTCTGCCGCG TGCTCCTGCT GACCCTCGCG ATCTTAATAT TTGCCAGTGA TGCCTGCAAA 300
AATGTGACAT TACATGTTTC CTCCAACTA GATGCCGAGA AACTTGTGTG TAGAGTTAAC 360
CTGAAGAGAGT GCTTTACAGC TGCAAATCTA ATTCAATCAA GTGATCCTGA CTTCCAAATT 420
TTGAGGATG GTTCAGTCTA TACAACAAAT ACTATTCTAT TGTCTCTCGA GAAGAGAAGT 480
30    TTTACCATAT TACTTTCCAA CACTGAGAAC CAAGAAAAGA AGAAAATATT TGTCTTTTGT 540
GAGCATCAAA CAAAGGTCCT AAAGAAAAGA CATACTAAAG AAAAAGTTCT AAGGCGCGCC 600
AAGAGAAGAT GGGCTCCAAAT TCCTTGTTCG ATGCTAGAAA ACTCCTTGGG TCCTTTTCCA 660
CTTTTCTCTC AACAGGTTCA ATCTGACACG GCCCAAAACT ATACCATATA CTATTCCATA 720
AGAGGTCCTG GAGTTGACCA AGAACCTCGG AATTTATTTT ATGTGGAGAG AGACACTGGA 780
35    AACTTGTATT GTACTCGTCC TGTAGATCGT GAGCAGTATG AATCTTTTGA GATAATTGCC 840
TTTGCAACAA CTCAGATGCG GTATACTCCA GAACCTCCAC TGCCCTTAAT AATCAAAATA 900
GAGGATGAAA ATGATAACTA CCCAATTTT ACAGAAGAAA CTTTACTTTT TACAATTTT 960
GAAAATTGCA GAGTGGGCAC TACTGTGGGA CAAGTGTGTG CTACTGACAA AGATGAGCCT 1020
GACACGATGC ACACACGCGT GAAGTACTCC ATCATTTGGG AGGTGCCACC ATCACCACCC 1080
40    CTATTTTCTA TGCATCCAA CACAGGCGTG ATCACCACAA CATCATCTCA GCTAGACAGA 1140
GAGTTAATTG ACAAGTACCA GTTGAAAATA AAAGTACAAG ACATGGATGG TCAGTATTTT 1200
GGTCTACAGA CAACTTCAAC TTGTATCATT AACATTGATG ATGTAAATGA CCACTTGCCA 1260
ACATTTACTC GTACTTCTTA TGTGACATCA GTGGAAGAAA ATACAGTTGA TGTGGAATC 1320
TTACGAGTTA CTGTTGAGGA TAAGGACTTA GTGAATACTG CTAAGTGGAG AGCTAATTAT 1380
45    ACCATTTTAA AGGCAATGA AAATGGCAAT TTTAAATTTG TAACAGATGC CAAAACCAAT 1440
GAAGGAGTTC TTTGTGTAGT TAAGCCTTTG AATTATGAAG AAAAGCAACA GATGATCTTG 1500
CAAAATGGTG TAGTTAATGA AGCTCCATT TCCAGAGAGG CTAGTCCAAG ATCAGCCATG 1560
AGCAGAGCAA CAGTTACTGT TAATGTAGAA GATCAGGATG AGGGCCCTGA GTGTAAACCT 1620
CCAATACAGA CTGTTGCGAT GAAAGAAAAT GCAGAAGTGG GAACAAACAG CAATGGATAT 1680
50    AAAGCATATG ACCCAGAAAC AAGAAGTAGC AGTGGCATAA GGTATAAGAA ATTAAGTAT 1740
CCAACAGGGT GGGTCACCAT TGATGAAAAT ACAGGATCAA TCAAAGTTT CAGAAGCCTG 1800
GATAGAGAGG CAGAGACCAT CAAAATGGC ATATATAATA TTACAGTCTC TGCATCAGAC 1860
CAAGAGGGA GAACATGTAC GGGGACACTG GGCATTATAC TTCAAGACGT GAATGATAAC 1920
55    AGCCCATTTA TACCTAAAA GACAGTGATC ATCTGCAAA CCACCATGTC ATCTGCGGAG 1980
ATTGTTGCGG TTGATCCTGA TGAGCCTATC CATGGCCAC CCTTTGACTT TAGTCTGGAG 2040
AGTTCTACTT CAGAAGTACA GAGAATGTGG AGACTGAAAG CAATTAATGA TACAGCAGCA 2100
CGTCTTCTCT ATCAGAATGA TCCTCCATTG GGCTCATATG TAGTACCTAT AACAGTGAGA 2160
GATAGACTTG GCATGTCTAG TGTCACTTCA TTGGATGTTA CACTGTGTGA CTGCATTACC 2220
60    GAAAATGACT GCACACATCG TGTAGATCCA AGGATTGGCG GTGGAGGAGT ACAACTTGGA 2280
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CTGGTCTGTG GGGCTTCTGG GACGCTTAAA CAACCAAAAG TAATTCTCTG TGATTAGACC 2400
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AATGGCTTCA CAACCAAAAC TGTGGGCGCT TCTGCTCAGG GAGTTTGTGG CACCGTGGGA 2520
TCAGGAATCA AAAACGGAGG TCAGGAGACC ATCGAAATGG TGAAAGGAGG ACACCAAGCC 2580
65    TCGGAATCCT GCCGGGGGGC TGGCCACCAT CACACCCTGG ACTCCTGCAG GGGAGGACAC 2640
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CTTGGTGAAA AAGTGTATCT GTGTAATCAA GATGAAAATC ACAAGCATGC CCAAGACTAT 2760
GTCCTGACAT ATAATATGA AGGAAGAGGA TCGGTGGCTG GGTCTGTAGG TTGTTGCAGT 2820
GAACGACAAG AAGAAGATGG GCTTGAATTT TTGGATAATT TGGAGCCCAA ATTTAGGACA 2880
70    CTAGCAGAAG CATGCATGAA GAGATGAGTG TGTCTAATA AGTCTCTGAA AGCCAGTGGC 2940
TTTATGACTT TAAAAAATA TTACAAACCA AGAATTTTIT AAAGCAGAAG ATGCTATTTG 3000
TGGGGGTTTT TCTCTCATTA TTTGGATGGA ATCTCTTTGG TCAAATGCAC ATTTACAGAG 3060
AGACACTATA AACAAGTACA CAAATTTTTC AATTTTITACA TATTTTITAA TTACTTATCT 3120
75    TCTATCCAAG GAGGTCTACA GAGAAATTAA AGTCTGCCCT ATTTGTTACA TTTGGGTATA 3180
ATGACAACAG CCAATTTTATA GTGCAATAAA ATGTAATTAA TTCAAGTCTC TATTATAGAC 3240
TATTTGAAGC ACAACCTAAT GGAAAATTGT AGAGACCTTG CTTTAACTAT ATCTCCAGTT 3300
AATTAAGTGT TCATGTGGTG CTTGGAACCT GTTGTTTTCC TGAACATCTA AAGTGTGTAG 3360
ACTGCATTCT TGCTATTATT TTATTCTTGT AATGTGACCT TTTCACTGTG CAAAGGGAGA 3420
80    TTTCTAGCCA GGCATTGACT ATTACAATTT CATT

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Seq ID NO: 617 Protein sequence
Protein Accession #: NP_077740.1

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85      1      11      21      31      41      51
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ANLIHSSDPD FQILEDGSVY TTNITLLSSE KRSFTILLSN TENQEKKKIF VFLEHQTKVL 120

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KKRHTTEKVL RRAKRWRWPI PCSMLNSLGG PFPLFLQQVQ SDTAQNYTIY YSIRGPGVDQ 180
 EPRNLFYVER DTGNLYCTRP VDREQYESFE IIAFATTDPG YTPELPLPLI IKIEDENDNY 240
 PIFTEETTYF TIFENCRRVGT TVGQVCATDK DEPDTHMTRL KYSIIGQVPP SPTLFSMHPT 300
 TGVITTTSSQ LDRELIDKQY LKIKVQDMQG QYFGLQTTST CIINIDVDND HLPFTFRTSY 360
 VTSVENTVD VEILRVTVED KDLVNTANWR ANYTILKGNE NGNFKIVTDA KTNEGVLVGV 420
 KPLNYEEKQQ MILQIGVVNE APFSREASPR SAMSTATVTV NVEDQDEGPE CNPPIQTVRM 480
 KENAEVGTTS NGYKAYDPBT RSSSGIRYKK LTDPTGWVTI DENTGSIKVF RSLDREAETI 540
 KNGIYNITVL ASDQGGRTCT GTLGILQDV NDNSPFIKK TVIICKPTMS SAEIVAVDPD 600
 EPIHGPPFFD SLESSTSEVQ RMWRLKAIND TAARLSYQND PPFSGSYVVP1 TVRDRLGMSS 660
 VTSLDVTLCD CITENDCTHR VDPRIIGGGV QLGKWAILAI LLGIALLLFCI LFTLVCGASG 720
 TSKQPKVIPD DLAQGNLIVS NTEAPGDDKV YSANGFTTQT VGASAQGVCG TVGSGIKNGG 780
 QETIEMVKGK HQTSESCRGA GHHHTLDSRC GGHTEVDNCR YTYSEWHSFT QPRLGEKVYL 840
 CNQDENHKAH QDYVLTNYE GRGSVAGSVG CCSEREQEEDG LEFLDNLEPK FRTLAEACMK 900
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Seq ID NO: 618 DNA sequence
 Nucleic Acid Accession #: NM_004949.1
 Coding sequence: 202..2745

1 11 21 31 41 51
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 TTGGAGGATG GTTCAGTCTA TACAACAAAT ACTATTCTAT TGCTCTCGGA GAAGAGAAGT 480
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Seq ID NO: 619 Protein sequence
 Protein Accession #: NP_004940.1

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 KKRHTKEKVL RRAKRRWAPI PCSMLENSLG FFLFLQVQV SDTAQNYTIY YSIRGPGVDQ 180
 EPRNLFYVER DTGNLYCTRP VDREQYESFE IIAFATTPDG YTPELPLPLI IKIEDENDNY 240
 PIFTEETVTF TIFENCVRGT TVGQVCATDK DEPDTHMTRL KYSIIGQVPP SPTLFSMHPT 300
 TGVITTTSSQ LDRELIDKYQ LKIKVQMDG QYFGLQTTST CIINIDVDND HLPFTFRTSY 360
 VTSVEENTVD VEILRVTVED KDLVNTANWR ANYTILKONE NGNFKIVTDA KTNEGVLVCV 420
 KPLNYEEKQQ MILQIGVNE APFSREASPR SAMSTATVTV NVEDQDEGPE CNPPIQTVRM 480
 KENAEVGTTS NGYKAYDPET RSSSGIRYKK LTDPTGWVTI DENTGSIKVF RSLDREAETI 540
 KNGIYNTIVL ASDGGGTCT GTLGIILQDV NDNSPFIFPK TVIICKPTMS SAEIVAVDPD 600
 EPIHGPPPDF SLESSTSEVQ RMWRLKAIN TAARLSYQND PPGSYVVPV TVRDRLGMSS 660
 VTSLDVTLCD CITENDCTHR VDPRIIGGGV QLKGWAILAI LLGIALLFICI LFTLVCGASG 720
 TSKQPKVIPD DLAQONLIVS NTEAPGDDKV YSANGFTTQT VGASAQVCG TVGSGIKNGG 780
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Seq ID NO: 620 DNA sequence
 Nucleic Acid Accession #: NM_032545.1
 Coding sequence: 46..718

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 CGAGGGCTGG GGGCCGAGG AGCCGCTCCC TACTCTCCGG GCTTTCGGAG AGGGTGCCTC 300
 CGCGCGGCGG CGTGTCTGCA GGAACGCGCG TACTGCGTG CTGGGAGCT TCTGCGTGTG 360
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 CGTCTCCAG CGGAGCGGC GCCCTGCGG AAGCCCGGA CTTGGGCATC GCCTTTAATT 720
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 AAAAAA

Seq ID NO: 621 Protein sequence
 Protein Accession #: NP_115934.1

1 11 21 31 41 51
 | | | | |
 MTWRHHVRL FTVSLALQII NLGNSYQREK HNGGREEVTK VATQKHRQSP LNWTSSEHFE 60
 VTGSAEGWGP EEPLPYRAF GEGASARPRC CRNGGTCVLG SFCVCPAFT GRYCEHDQRR 120
 SECGALEHGA WTLRACHLCR CIFGALHCLP LQTPDRCDPK DFLASHAGP SAGGAPSLLL 180
 LLPCALLHRL LRPDAPAHPR SLVPSVLQRE RRPCGRPLG HRL

Seq ID NO: 622 DNA sequence
 Nucleic Acid Accession #: FGENESH predicted
 Coding sequence: 1..390

1 11 21 31 41 51
 | | | | |
 ATGAGGTTCA GTGTCTCAG CATGAGGACC GACTACCCCA GGAGTGTGCT GGCTCCTGCT 60
 TATGTGTGAG TCTGTCTCCT CCTCTTGTGT CCAAGGGAAG TCATCGCTCC CGCTGGCTCA 120
 GAACCATGGC TGTGCCAGGC GGCAACCAGG TGTGGAGACA AGATCTACAA CCCCTGGAG 180
 CAGTGTCTGT ACAATGACGC CATCGTGTCC CTGAGCGAGA CCCGCCAATG TGGTCCCCC 240
 TGCACCTTCT GGCCCTGCTT TGAGCTCTGC TGTCTTGATT CCTTTGGCCT CACAAACGAT 300
 TTTGTTGTGA AGCTGAAGGT TCAGGGGTGTG AATTCCCAGT GCCACTCATC TCCCATCTCC 360
 AGTAAATGTG AAAGAGGCGG GATATGTTAG

Seq ID NO: 623 Protein sequence
 Protein Accession #: FGENESH predicted

1 11 21 31 41 51
 | | | | |
 MRFSVSGMRT DYPRSVLAPA YVSVCLLLC PREVIAPAGS EPWLCQAPAP CGDKIYNPLE 60
 QCCYNDIAVS LSETRQCGPP CTFWPCFELC CLDSFGLTND FVVKLVQGV NSQCHSSPIS 120
 SKCERGRIC

Seq ID NO: 624 DNA sequence
 Nucleic Acid Accession #: M18728.1
 Coding sequence: 51..1085

1 11 21 31 41 51
 | | | | |
 GGAGCTCAAG CTCCTCTACA AAGAGGTGGA CAGAGAAGAC AGCAGAGACC ATGGGACCCC 60
 CCTCAGCCCC TCCCTGCAGA TTGCATGTCC CCTGGAAGGA GGTCTGCTC ACAGCCTCAC 120
 TTCTAACCTT CTGGAACCCA CCCACCACTG CCAAGCTCAC TATTGAATCC ACGCCATTCA 180
 ATGTGCGAGA GGGGAAGGAG GTTCTTCTAC TCGCCCAACA CCTGCCCCAG AATCGTATTG 240
 GTTACAGCTG GTACAAAGGC GAAAGAGTGG ATGGCAACAG TCTAATTGTA GGATATGTAA 300
 TAGGAACCTA ACAAGCTACC CCAGGGCCCG CATACAGTGG TCGAGAGACA ATATACCCCA 360
 ATGCATCCCT GCTGATCCAG AACGTCACCC AGAATGACAC AGGATTCTAT ACCCTACAAG 420
 TCATAAAGTC AGATCTTGTG AATGAAGAAG CAACCCGACA GTTCCATGTA TACCCGGAGC 480
 TGCCCAAGCC CTCCTCTTCC AGCAACAAC CCAACCCCGT GGAGGACAAG GATGCTGTGG 540
 CCTTCACCTG TGAACCTGAG GTTCAGAAAC CAACCTACCT GTGGTGGGTA AATGGTCAGA 600
 GCCTCCCGGT CAGTCCCAGG CTGCAGCTGT CCAATGGCAA CATGACCTC ACTCTACTCA 660

GCGTCAAAAG GAAAGATGCA GGATCCTATG AATGTGAAAT ACAGAACCCA GCGAGTGCCA 720
 ACCGCAGTGA CCCAGTCACC CTGAATGTCC TCTATGGCCC AGATGTCCCC ACCATTTCCTC 780
 CCTCAAAGGC CAATTACCGT CCAGGGGAAA ATCTGAACCT CTCCTGCCAC GCAGCCTCTA 840
 ACCCACTGTC ACAGTACTCT TGGTTTATCA ATGGGACGTT CCAGCAATCC ACACAAGAGC 900
 TCTTTATCCC CAACATCACT GTGAATAATA GCGGATCCTA TATGTGCCAA GCCCATAACT 960
 CAGCCACTGG CCTCAATAGG ACCACAGTCA CGATGATCAC AGTCTCTGGA AGTGCTCCTG 1020
 TCCTCTCAGC TGTGGCCACC GTCGGCATCA CGATTGGAGT GCTGGCCAGG GTGGCTCTGA 1080
 TATAGCAGCC CTGGTGTATT TTCGATATTT CAGGAAGACT GGCAGATTGG ACCAGACCTT 1140
 GAATTCCTCT AGCTCCTCCA ATCCCATTTT ATCCCATGGA ACCACTAAAA ACAAGGTCTG 1200
 CTCTGCTCCT GAAGCCCTAT ATGCTGGAGA TGGACAACTC AATGAAAATT TAAAGGGAAA 1260
 ACCCTCAGGC CTGAGGTGTG TGCCACTCAG AGACTTCACC TAACTAGAGA CAGTCAAACCT 1320
 GCAAACCATG GTGAGAAATT GACGACTTCA CACTATGGAC AGCTTTTCCC AAGATGTCAA 1380
 AACAAAGACT CTCATCATGA TAAGGCTCTT ACCCCCTTTT AATTGTCTCT TGCTTATGCC 1440
 TGCCTCTTTC GCTTGGCAGG ATGATGCTGT CATTAGTATT TCACAAGAAG TAGCTTCAGA 1500
 GGGTAACTTA ACAGAGTGTC AGATCTATCT TGTCAATCCC AACGTTTTTAC ATAAAAAAG 1560
 AGATCCTTTA GTGCACCCAG TGACTGACAT TAGCAGCATC TTTAACACAG CCGTGTGTTC 1620
 AAATGTACAG TGGTCTCTTT CAGAGTTGGA CTCTAGACT CACCTGTCTC CACTCCCTGT 1680
 TTTAATTCAA CCCAGCCATG CAATGCCAAA TAATAGAATT GCTCCCTACC AGCTGAACAG 1740
 GGAGGAGTCT GTGCAGTTTC TGACACTTGT TGTGAAACAT GGCTAAATAC AATGGGTATC 1800
 GCTGAGACTA AGTTGTAGAA ATTAACAAAT GTGCTGCTTG GTTAAATGCG CTACACTCAT 1860
 CTGACTCATT CTTTATTCTA TTTTAGTTGG TTTGTATCTT GCCTAAGGTG CGTAGTCCAA 1920
 CTCTTGGTAT TACCTCCTA ATAGTCATAC TAGTAGTCAT ACTCCCTGGT GTAGTGTATT 1980
 CTCTAAAGC TTTAAATGTC TGCAATGCAGC CAGCCATCAA ATAGTGAATG GTCTCTCTTT 2040
 GGCTGGAATT ACAAACTGCA GAGAAATGTG TCATCAGGAG AACATCATAA CCCATGAAGG 2100
 ATAAAGCCC CAAATGTTGG TAACTGATAA TAGCACTAAT GCTTTAAGAT TTGGTTCACAC 2160
 TCTCACCTAG GTGAGCGCAT TGAGCCAGTG GTGCTAAATG CTACATACTC CAACTGAAAT 2220
 GTTAAAGGAG AAGATAGATC CAATTAATAA AAATTAATAA CAATTTAAAA AAAAAAAGA 2280
 ACACAGGAGA TTCAGTCTA CTGAGTTAG CATAATACAG AAGTCCCTC TACTTTAACT 2340
 TTTACAAAAA AGTAACCTGA ACTAATCTGA TGTTAACCAA TGTATTTATT TCTGTGGTTC 2400
 TGTTCCTTGG TTCCAATTGG ACAAACCCA CTGTTCTTGT ATTGTATTGC CCAGGGGGAG 2460
 CTATCACTGT ACTGTAGAG TGGTGCTGCT TTAATTCATA AATCACAAT AAAAGCCAAT 2520
 TAGCTCTATA ACT

Seq ID NO: 625 Protein sequence
 Protein Accession #: AAA59907.1

1 11 21 31 41 51
 | | | | |
 MGPPSAPPCR LHVPEKEVLL TASLLTFWNP PTTAKLTIES TPFNVAEKKE VLLLAHNLPO 60
 NRIQSWYKYG ERVDGNLIV GYVIGTQQAT PGPAYSGRET IYPNASLLIQ NVTQNDTGFY 120
 TLQVIKSLDV NEEATGQFHV YPELKPSPIS SNNSNPVEDK DAVAFTEPE VQNTTYLWVW 180
 NGQSLFVSPR LQLSNGNMTL TLLSVKRNDG GSYECEIQNP ASANRSDPVT LNVLYGPDVP 240
 TISPSKANYR PGENLNLSCH AASNPPAQYS WFINGTFQQS TQELFIPNIT VNNSGSYMCQ 300
 AHNATGLNR TTVMTIVSG SAPVLSAVAT VGITIGVLAR VALI

Seq ID NO: 626 DNA sequence
 Nucleic Acid Accession #: M18728.1
 Coding sequence: 1355..1657

1 11 21 31 41 51
 | | | | |
 GGAGCTCAAG CTCTCTTACA AAGAGGTGGA CAGAGAAGAC AGCAGAGACC ATGGGACCCC 60
 CCTCAGCCCC TCCCTGCAGA TTGCATGTCC CCTGGAAGGA GGTCTGTCTC ACAGCCTCAC 120
 TTCTAACCTT CTGGAACCCA CCCACCACTG CCAAGCTCAC TATTGAATCC ACGCCATCTA 180
 ATGTGCGAGA GGGGAAGGAG GTTCTTCTAC TCGCCACAA CCTGCCCCAG AATCGTATTG 240
 GTTACAGCTG GTACAAAGGC GAAAGAGTGG ATGGCAACAG TCTAATTGTA GGATATGTAA 300
 TAGGAACCTA ACAAGCTACC CCAGGGCCCG CATACAGTGG TCGAGAGACA ATATACCCCA 360
 ATGCATCCCT GCTGATCCAG AACGTCACCC AGAATGACAC AGGATTCTAT ACCCTACAAG 420
 TCATAAAGTC AGATCTTGTG AATGAAGAAG CAACCGGACA GTTCCATGTA TACCCGGAGC 480
 TGCCCAAGCC CTCCATCTCC AGCAACAACCT CCAACCCCGT GGAGGACAAG GATGCTGTGG 540
 CCTTCACCTG TGAACCTGAG GTTCAGAAAC CAACCTACCT GTGGTGGGTA AATGGTCAGA 600
 GCCTCCCGGT CAGTCCCAGG CTGCAGCTGT CCAATGGCAA CATGACCCCTC ACTCTACTCA 660
 GCGTCAAAAG GAAAGATGCA GGATCCTATG AATGTGAAAT ACAGAACCCA GCGAGTGCCA 720
 ACCGCAGTGA CCCAGTCACC CTGAATGTCC TCTATGGCCC AGATGTCCCC ACCATTTCCTC 780
 CCTCAAAGGC CAATTACCGT CCAGGGGAAA ATCTGAACCT CTCCTGCCAC GCAGCCTCTA 840
 ACCCACTGTC ACAGTACTCT TGGTTTATCA ATGGGACGTT CCAGCAATCC ACACAAGAGC 900
 TCTTTATCCC CAACATCACT GTGAATAATA GCGGATCCTA TATGTGCCAA GCCCATAACT 960
 CAGCCACTGG CCTCAATAGG ACCACAGTCA CGATGATCAC AGTCTCTGGA AGTGCTCCTG 1020
 TCCTCTCAGC TGTGGCCACC GTCGGCATCA CGATTGGAGT GCTGGCCAGG GTGGCTCTGA 1080
 TATAGCAGCC CTGGTGTATT TTCGATATTT CAGGAAGACT GGCAGATTGG ACCAGACCTT 1140
 GAATTCCTCT AGCTCCTCCA ATCCCATTTT ATCCCATGGA ACCACTAAAA ACAAGGTCTG 1200
 CTCTGCTCCT GAAGCCCTAT ATGCTGGAGA TGGACAACTC AATGAAAATT TAAAGGGAAA 1260
 ACCCTCAGGC CTGAGGTGTG TGCCACTCAG AGACTTCACC TAACTAGAGA CAGTCAAACCT 1320
 GCAAACCATG GTGAGAAATT GACGACTTCA CACTATGGAC AGCTTTTCCC AAGATGTCAA 1380
 AACAAAGACT CTCATCATGA TAAGGCTCTT ACCCCCTTTT AATTGTCTCT TGCTTATGCC 1440
 TGCCTCTTTC GCTTGGCAGG ATGATGCTGT CATTAGTATT TCACAAGAAG TAGCTTCAGA 1500
 GGGTAACTTA ACAGAGTGTC AGATCTATCT TGTCAATCCC AACGTTTTAC ATAAAAAAG 1560
 AGATCCTTTA GTGCACCCAG TGACTGACAT TAGCAGCATC TTTAACACAG CCGTGTGTTC 1620
 AAATGTACAG TGGTCTCTTT CAGAGTTGGA CTCTAGACT CACCTGTCTC CACTCCCTGT 1680
 TTTAATTCAA CCCAGCCATG CAATGCCAAA TAATAGAATT GCTCCCTACC AGCTGAACAG 1740
 GGAGGAGTCT GTGCAGTTTC TGACACTTGT TGTGAAACAT GGCTAAATAC AATGGGTATC 1800
 GCTGAGACTA AGTTGTAGAA ATTAACAAAT GTGCTGCTTG GTTAAATGCG CTACACTCAT 1860
 CTGACTCATT CTTTATTCTA TTTTAGTTGG TTTGTATCTT GCCTAAGGTG CGTAGTCCAA 1920
 CTCTTGGTAT TACCTCCTA ATAGTCATAC TAGTAGTCAT ACTCCCTGGT GTAGTGTATT 1980
 CTCTAAAGC TTTAAATGTC TGCAATGCAGC CAGCCATCAA ATAGTGAATG GTCTCTCTTT 2040
 GGCTGGAATT ACAAACTGCA GAGAAATGTG TCATCAGGAG AACATCATAA CCCATGAAGG 2100
 ATAAAGCCC CAAATGTTGG TAACTGATAA TAGCACTAAT GCTTTAAGAT TTGGTTCACAC 2160

TCTCACCTAG GTGAGCGCAT TGAGCCAGTG GTGCTAAATG CTACATACTC CAACTGAAAT 2220
 GTTAAGGAAG AAGATAGATC CAATTAAAAA AAATTAAAAA CAAATTAAAAA AAAAAAAGA 2280
 ACACAGGAGA TTCCAGTCTA CTTGAGTTAG CATAATACAG AAGTCCCCTC TACTTTAACT 2340
 TTTACAAAAA AGTAACCTGA ACTAATCTGA TGTAAACCAA TGTATTTATT TCTGTGGTTC 2400
 TGTTCCTTG TTCCAATTG ACAAACCCA CTGTTCTTGT ATTGTATTGC CCAGGGGGAG 2460
 CTATCACTGT ACTTGTAGAG TGGTGCTGCT TTAATTCATA AATCACAAT AAAAGCCAAT 2520
 TAGCTCTATA ACT

Seq ID NO: 627 Protein sequence
 Protein Accession #: AAA59908.1

1 11 21 31 41 51
 MDSFSQDVKT RLLIMIRLLP PFNLSLLMPA SFAWQDDAVI SISQEVASEG NLTECQIYLV 60
 NPNVLHKIRD PLVHPVTDIS SIFNTAVCSN VQWSFSELDLF

Seq ID NO: 628 DNA sequence
 Nucleic Acid Accession #: M18728.1
 Coding sequence: 2370..2501

1 11 21 31 41 51
 GGAGCTCAAG CTCCTCTACA AAGAGGTGGA CAGAGAAGAC AGCAGAGACC ATGGGACCCC 60
 CCTCAGCCCC TCCCTGCAGA TTGCATGTCC CCTGGAAGGA GGTCTGTCTC ACAGCCTCAC 120
 TTCTAACCTT CTGAACCCA CCCACCACATG CCAAGCTCAC TATTGAATCC ACGCCATTCA 180
 ATGTCGCAGA GGGGAAGGAG GTTCTTCTAC TCGCCACAA CCTGCCCCAG AATCGTATTG 240
 GTTACAGCTG GTACAAAGGC GAAAGAGTGG ATGGCAACAG TCTAATTGTA GGATATGTAA 300
 TAGGAACCTA ACAAGCTACC CCAGGGCCCG CATAAGTGG TCGAGAGACA ATATACCCCA 360
 ATGCATCCCT GCTGATCCAG AACGTCACCC AGAATGACAC AGGATTCTAT ACCCTACAAG 420
 TCATAAAGTC AGATCTTGTG AATGAAGAAG CAACCGGACA GTTCCATGTA TACCCGGAGC 480
 TGCCCAAGCC CTCATCTTCC AGCAACAACCT CCAACCCCGT GGAGGACAAG GATGCTGTGG 540
 CCTTCACCTG TGAACCTGAG GTTCAGAAACA CAACCTACCT GTGGTGGGTA AATGGTCAGA 600
 GCCTCCCGGT CAGTCCCAGG CTGCAGCTGT CCAATGGCAA CATGACCCCTC ACTCTACTCA 660
 GCGTCAAAAG GAACGATGCA GGATCCTATG AATGTGAAAT ACAGAACCCA GCGAGTGCCA 720
 ACCGCAGTGA CCCAGTCACC CTGAATGTCC TCTATGGCCC AGATGTCCCC ACCATTTCCTC 780
 CCTCAAAAGC CAATTACCGT CCAGGGGAAA ATCTGAACCT CTCCTGCCAC GCAGCCTCTA 840
 ACCCACTGAC ACAGTACTCT TGGTTTATCA ATGGGACGTT CCAGCAATCC ACACAAGAGC 900
 TCTTTATCCC CAACATCACT GTGAATAATA GCGGATCCTA TATGTGCCAA GCCCATAACT 960
 CAGCCACTGG CCTCAATAGG ACCACAGTCA CGATGATCAC AGTCTCTGGA AGTGCTCCTG 1020
 TCCTCTCAGC TGTGGCCACC GTCGGCATCA CGATTGGAGT GCTGGCCAGG GTGGCTCTGA 1080
 TATAGCAGCC CTGGTGTATT TTCGATATTT CAGGAAGACT GGCAGATTGG ACCAGACCTT 1140
 GAATTCTTCT AGCTCCTCCA ATCCCATTAT ATCCCATTGA ACCACTAAAA ACAAGTCTG 1200
 CTCTGCTCCT AAGGCCCTAT ATGCTGGAGA TGGACAACCT AATGAAAATT TAAAGGGAAA 1260
 ACCCTCAGGC CTGAGGTGTG TGCCACTCAG AGACTTCACC TAACTAGAGA CAGTCAAACT 1320
 GCAAAACCATG GTGAGAAATT GACGACTTCA CACTATGGAC AGCTTTTCCC AAGATGTCAA 1380
 AACAAAGACT CTCATCATGA TAAGGCTCTT ACCCCCTTTT AATTGTCTCT TGCTTATGCC 1440
 TGCTCTTTTC GCTTGGCAGG ATGATGCTGT CATTAGTATT TCACAAGAAG TAGCTTCAGA 1500
 GGGTAACTTA ACAGAGTGTG AGATCTATCT TGTCAATCCC AACGTTTAC ATAAAAAAG 1560
 AGATCCTTTA GTGCACCCAG TGAATGACAT TAGCAGCATC TTTAACACAG CCGTGTGTTC 1620
 AAATGTACAG TGGTCTTTT CAGAGTTGGA CTTCTAGACT CACCTGTTCT CACTCCCTGT 1680
 TTTAATTCAA CCCAGCCATG CAATGCCAAA TAATAGAATT GCTCCCTACC AGCTGAACAG 1740
 GGAGGAGTCT GTGCACTTTC TGACACTTGT TGTGAAACAT GGCTAAATAC AATGGGTATC 1800
 GCTGAGACTA AGTTGTAGAA ATTAACAAAT GTGCTGCTTG GTTAAATGG CTACACTCAT 1860
 CTGACTCATT CTTTATTCTA TTTTAGTTGG TTTGTATCTT GCCTAAGGTG CGTAGTCCAA 1920
 CTCTTGGTAT TACCTCTCTA ATAGTCATAC TAGTAGTCAT ACTCCCTGGT GTAGTGTATT 1980
 CTCTAAAAGC TTTAAATGTC TGCAATGAGC CAGCCATCAA ATAGTGAATG GTCTCTCTTT 2040
 GGCTGGAATT ACAAACCTCA GAGAAATGTG TCATCAGGAG AACATCATAA CCCATGAAGG 2100
 ATAAAAGCCC CAAATGGTGG TAACTGATAA TAGCACTAAT GCTTTAAGAT TTGGTCACAC 2160
 TCTCACCTAG GTGAGCGCAT TGAGCCAGTG GTGCTAAATG CTACATACTC CAACTGAAAT 2220
 GTTAAGGAAG AAGATAGATC CAATTAAAAA AAATTAAAAA CAAATTAAAAA AAAAAAAGA 2280
 ACACAGGAGA TTCCAGTCTA CTTGAGTTAG CATAATACAG AAGTCCCCTC TACTTTAACT 2340
 TTTACAAAAA AGTAACCTGA ACTAATCTGA TGTAAACCAA TGTATTTATT TCTGTGGTTC 2400
 TGTTCCTTG TTCCAATTG ACAAACCCA CTGTTCTTGT ATTGTATTGC CCAGGGGGAG 2460
 CTATCACTGT ACTTGTAGAG TGGTGCTGCT TTAATTCATA AATCACAAT AAAAGCCAAT 2520
 TAGCTCTATA ACT

Seq ID NO: 629 Protein sequence
 Protein Accession #: AAA59909.1

1 11 21 31 41 51
 MLTNVFISVV LFPCSNLTKP TVLVLYCPGG AITVLVEWCC FNS

Seq ID NO: 630 DNA sequence
 Nucleic Acid Accession #: NM_016639.1
 Coding sequence: 40..429

1 11 21 31 41 51
 GCGGCGGGCG CAGACAGCGG CGGGCGCAGG ACGTGCCTA TGGCTCGGGG CTCGCTGCGC 60
 CGGTTGCTGC GGCTCTCTGT GCTGGGGCTC TGGCTGGCGT TGCTGCGCTC CGTGGCCGGG 120
 GAGCAAGCGC CAGGCACCGC CCCCTGCTCC CGCGGACGCT CCTGGAGCGC GGACCTGGAC 180
 AAGTGCATGG ACTGCGCGTC TTGCAGGGCG CGACCGCACA GCGACTTCTG CCTGGGCTGC 240
 GCTGAGCAC CTCTGCCCC CTTCGGGCTG CTTTGGCCCA TCCTTGGGGG CGCTCTGAGC 300
 CTGACCTTCG TGCTGGGGCT GCTTTCTGGC TTTTGGTCTT GGAGACGATG CCGCAGGAGA 360
 GAGAAGTTCA CCACCCCAT AGAGGAGACC GCGGAGAGG GCTGCCAGC TGTGGCGCTG 420

ATCCAGTGAC AATGTGCCCC CTGCCAGCG GGGCTCGCCC ACTCATCATT CATTCATCCA 480
 TTCTAGAGCC AGTCTCTGCC TCCCAGACGC GCGGGGAGCC AAGCTCCTCC AACACAAAG 540
 GGGGTGGGG GCGGTGAATC ACCTCTGAGG CCTGGGCCCA GGGTTCAGGG GAACCTTCCA 600
 AGGTGTCTGG TTGCCCTGCC TCTGGCTCCA GAACAGAAAG GGAGCCTCAC GCTGGCTCAC 660
 ACAAACAGC TGACACTGAC TAAGGAAGCTG CAGCATTTGC ACAGGGGAGG GGGGTGCCCT 720
 CCTTCCTTAG GACCTGGGG CCAGGCTGAC TTGGGGGGCA GACTTGACAC TAGGCCCCAC 780
 TCACCTCAGAT GTCCTGAAAT TCCACCACGG GGGTCACCCT GGGGGGTAG GGAGCTATT 840
 TTAACACTAG GGGCTGGCCC ACTAGGAGGG CTGGCCCTAA GATACAGACC CCCCACCTC 900
 CCCAAGCGG GGAGGAGATA TTTATTTTGG GGAGAGTTTG GAGGGGAGG AGAATTTATT 960
 AATAAAGAA TCTTTAATT TAAAAAATA AAAAAAATA

Seq ID NO: 631 Protein sequence
 Protein Accession #: NP_057723.1

1 11 21 31 41 51
 MARGSLRRLL RLLVLGLWLA LLRSVAGEQA PGTAPCSRGS SWSADLDKCM DCASCRARPH 60
 SDFCLGCAAA PPAPFRLWLP ILGGLSLTF VLGLLSGFLV WRRRCRRREKF TPIEETGGE 120
 GCPAVALIQ

Seq ID NO: 632 DNA sequence
 Nucleic Acid Accession #: NM_003816.1
 Coding sequence: 79..2538

1 11 21 31 41 51
 CGGCAGGGTT GGAAATGAT GGAAGAGGCG GAGGTGGAGG CGACCGAGTG CTGAGAGGAA 60
 CCTGCGGAAT CGGCCGAGAT GGGGTCTGGC GCGCGCTTTC CCTCGGGGAC CCTTCGTGTC 120
 CGGTGGTTGC TGTGTCTTGG CCTGGTGGGC CCAGTCTCTCG GTGCGGCGCG GCCAGGCTTT 180
 CAACAGACCT CACATCTTTC TTCTTATGAA ATTATACTC CTTGGAGATT AACTAGAGAA 240
 AGAAGAGAAAG CCCCTAGGCC CTATTCAAAA CAAGTATCTT ATGTTATTCA GGCTGAAGGA 300
 AAAGAGCATA TTATTCACCT GGAAAGGAAC AAAGACCTTT TGCCTGAAGA TTTTGTGGTT 360
 TATACCTACA ACAAGGAAGG GACTTTAATC ACTGACCATC CCAATATACA GAATCATTGT 420
 CATTATCGGG GCTATGTGGA GGGAGTTTCA AATTCATCCA TTGCTCTTAG CGACTGTTTT 480
 GGACTCAGAG GATTGCTGCA TTTAGAGAAAT GCGAGTTATG GGATTGAACC CCTGCAGAAC 540
 AGCTCTCATT TTGAGCAGAT CATTATCGA ATGGATGATG TCTACAAAGA GCCTCTGAAA 600
 TGTGGAGTTT CCAACAAGGA TATAGAGAAA GAAACTGCAA AGGATGAAGA GGAAGAGCCT 660
 CCCAGCATGA CTCAGCTACT TCGAAGAAGA AGAGCTGTCT TGCCACAGAC CCGGTATGTG 720
 GAGCTGTTCA TTGTCGTAGA CAAGGAAAGG TATGACATGA TGGGAAGAAA TCAGACTGCT 780
 GTGAGAGAAG AGATGATTCT CCTGGCAAAC TACTGGATA GTATGTATAT TATGTTAAAT 840
 ATTCGAATTT TGCTAGTTGG ACTGGAGATT TGGACCAATG GAAACCTGAT CAACATAGTT 900
 GGGGTGCTG GTGATGTGCT GGGGAACCTC GTGCAGTGGC GGGAAAGTT TCTTATCACA 960
 CGTCGGAGAC ATGACAGTGC ACAGCTAGTT CTAAAGAAAG GTTTTGGTGG AACTGCAGGA 1020
 ATGGCATTTC TGGGAACAGT GTGTTCAAGG AGCCACGCG GCGGGATTAA TGTGTTTGA 1080
 CAAATCACTG TGGAGACATT TGCTTCCATT GTTGCTCATG AATTGGGTCA TAATCTTGA 1140
 ATGAATCACG ATGATGGGAG AGATTGTTCC TGTGGAGCAA AGAGCTGCAT CATGAATTCA 1200
 GGAGCATCGG GTTCCAGAAA CTTTAGCAGT TGCAGTGAG AGGACTTTGA GAAGTTAACT 1260
 TTAATAAAG GAGGAACTCT CCTTCTTAAT ATTCCAAAGC CTGATGAAGC CTATAGTGCT 1320
 CCCTCCTGTG GTAATAAGTT GGTGACGCT GGGGAAGAGT GTGACTGTGG TACTCCAAAG 1380
 GAATGTGAAT TGGACCCCTG CTGCGAAGGA AGTACCTGTA AGCTTAAATC ATTTGCTGAG 1440
 TGTGCATATG GTGACTGTTG TAAAGACTGT CGGTTCCTTC CAGGAGGTAC TTTATGCCGA 1500
 GGAAAAACCA GTGAGTGTGA TGTTCAGAG TACTGCAATG GTTCTTCTCA GTTCTGTGAG 1560
 CCAGATGTTT TTATTCAGAA TGGATATCCT TGCCAGAAATA ACAAAGCCTA TTGCTACAAC 1620
 GGCATGTGCC AGTATTATGA TGCTCAATGT CAAGTCATCT TTGGCTCAAA AGCCAAAGCT 1680
 GCCCCCAAG ATGTTTCTAT TGAAGTGAAT TCTAAAGGTG ACAGATTGAG CAATTGTGCT 1740
 TTCTCTGGCA ATGATAACAA GAAGTGTGCC ACTGGGAATG CTTTGTGTGG AAAGCTTCAG 1800
 TGTGAGAAATG TACAAGAGAT ACCTGTATTT GGAATTGTGC CTGCTATTAT TCAAACGCT 1860
 AGTCGAGGCA CCAATGTTG GGGTGTGGAT TTCCAGCTAG GATCAGATGT TCCAGATCCT 1920
 GGGATGGTTA ACGAAGGCAC AAAATGTGGT GCTGGAAAGA TCTGTAGAAA CTTCCAGTGT 1980
 GTAGATGCTT CTGTTCTGAA TTATGACTGT GATGTTTACA AAAAGTGTCA TGGACATGG 2040
 GTATGTAATA CCAATAAGAA TTGTCACTGT GAAATGGCT GGGCTCCGCC AAATTGTGAG 2100
 ACTAAAGGAT ACGGAGGAAG TGTGGACAGT GGACCTACAT ACAATGAAAT GAATACTGCA 2160
 TTGAGGGACG GACTTCTGGT CTTCTCTTTC CTAATTGTTT CCCTTATTGT CTGTGCTATT 2220
 TTTATCTTCA TCAAGAGGGA TCAACTGTGG AGAAGCTACT TCAGAAAGAA GAGATCACA 2280
 ACATATGAGT CAGATGGCAA AAATCAAGCA AACCCTTCTA GACAGCCGGG GAGTGTTCCT 2340
 CGACATGTTT CTCAGTGAC ACCTCCAGGA GAAGTTCCTA TATATGCAAA CAGATTTGCA 2400
 GTACCAACCT ATGCAGCCAA GCAACCTCAG CAGTTCCTAT CAAGGCCACC TCCACCACA 2460
 CCGAAAGTAT CATCTCAGGG AAACCTTAAT CCTGCCCGTC CTGCTCCTGC ACCTCCTTTA 2520
 TATAGTTCCC TCACCTGATT TTTTAAACCT TCTTTTGGCA AATGTCTTCA GGGAACTGAG 2580
 CTAATACCTT TTTTTTTTCT TGATGTTTTC TTGAAAAGCC TTTCTGTGTC AACTATGAAT 2640
 GAAAACAAAA CACCACAAAA CAGACTTCAC TAACACAGAA AAACAGAAAC TGAGTGTGAG 2700
 AGTTGTGAAA TACAAGGAAA TGCAGTAAAG CCAGGGAATT TACAATAACA TTTCCGTTTC 2760
 CATCATGAA TAAGTCTTAT TCAGTCATCG GTGAGGTTAA TGCACATATC ATGGATTTTT 2820
 TGAACATGTT ATTGCAAGTA TTCTCAAATT AACTGTATTG GTGTAAGATT TTTGTCTTCA 2880
 AGTGTTTAAAG TGTATTCTG AATTTTCTAC CTTAGTTATC ATTAATGTAG TTCCTCATG 2940
 AACATGTGAT AATCTAATAC CTGTGAAAC TGACTAATCA GCTGCCAATA ATATCTAATA 3000
 TTTTTCATCA TGCAGAATT AATAATCATC ATACTCTAGA ATCTGTCTG TCACTCACTA 3060
 CATGAATAAG CAAATATTGT CTTCAAAAGA ATGCACAAGA ACCACAATTA AGATGTCATA 3120
 TTATTTTGAA AGTACAAAAT AACTAAAAG AGTGTGTGTG TATTACGCA GTTACTCGCT 3180
 TCCATTTTCA TGACCTTTCA ACTATAGGTA ATAACCTTCA GAGAAATTAA TTTAATATTA 3240
 GAATTTCTAT TATGAATCAT GTGAAAGCAT GACATTCGTT CACAATAGCA CTATTTTAAA 3300
 TAAATTATAA GCTTTAAGGT ACGAAGTATT TAATAGATCT AATCAAATAT GTTGATTATC 3360
 GGCTATAATA AAGCAGGAGC AATTATAAAA TCTTCAATCA ATTGAACCTT TACAAAACCA 3420
 CTGAGAAATT TCATGAGCAC TTTAAATCT GAACCTTCAA AGCTTGCTAT TAAATCATTT 3480
 AGAATGTTTA CATTTTACAA GGTGTGCTGG GTCATGTAAG ATATTAGACA CTAATATTTT 3540
 CATAGAAATT AGGCTGGAGA AAGAAGGAAG AAATGGTTTT CTTAAATACC TACAAAAAAG 3600
 TTACTGTGGT ATCTATGAGT TATCATCTTA GCTGTGTTAA AAATGAATTT TTACTATGGC 3660

AGATATGGTA TGGATCGTAA AATTTTAAGC ACTAAAAATT TTTTCATAAC CTTTCATAAT 3720
 AAAGTTTAAAT AATAGGTTTA TTAAGTGAAT TTCATTAGTT TTTTAAAAAGT GTTTTTGGTT 3780
 TGTGTATATA TACATATACA AATACAACAT TTACAATAAA TAAATAACTT GAAATTCTCA 3840
 AAAAAAAAAA AAAAAAAAAA AAAAA

Seq ID NO: 633 Protein sequence
 Protein Accession #: NP_003807.1

1 11 21 31 41 51
 | | | | |
 MGSGARFPSS TLRVRWLLLL GLVGPVLGAA RPFQQTSHL SSYEIITPWR LTRERREAPR 60
 PYSKQVSVYI QAEGKEHIH LERNKDLLPE DFVVYTYNKE GTLITDHPNI QNHCHYRGYV 120
 EGVHNSIAL SDCFLRLGLL HLENASYGIE PLQNSSHFEH IIVRMDVYK EPLKCGVSNK 180
 DIEKETAKDE EEEPPSMTQL LRRRAVLPO TRYVELFIVV DKERYDMMGR NQTAVREEMI 240
 LLANYLDSMY IMLNIRIVLV GLEIWTNGNL INIVGGAGDV LGNFVQWREK FLITRRRHDG 300
 AQLVLKKGFG GTAGMAFVGT VCSRSHAGGI NVFGQITVET FASIVAHELH HNLGMNHDDG 360
 RDCSCGAKSC IMNSGASGSR NFSSCSAEDF EKLTNLKGGN CLLNIPKPE AYSAAPSCGNK 420
 LVDAGEBCDC GTPKECELDP CCEGSTCKLK SFAECAYGDC CKDCRFLPGG TLCRGKTSEC 480
 DVPEYCNSSS QFCQPDVFIQ NGYPCQNNKA YCYNGMCQYY DAQCQVIFGS KAKAAPKDCF 540
 IEVNSKGRDR GNCGFSGNEY KKCATGNALC GKLCQENVQE IPVFGIVPAI IQTPSRGTCK 600
 WGVDFQLGSD VPDPMVNEG TKCGAGKICR NFQCVDAVL NYDCDVQKKC HGHGVCSNKK 660
 NCHCENGWAP PNCETKGYGG SVDSGPTYNE MNTALRDGLL VFFFLIVPLI VCAIFIFIKR 720
 DQLWRSYFRK KRSQTYESDG KNQANPSRQP GSVPRHVSVP TPPREVPIYA NRFAVPTYAA 780
 KQPQFPSPRP PPPQPKVSSQ GNLIIPARPAP APPLYSSLT

Seq ID NO: 634 DNA sequence
 Nucleic Acid Accession #: NM_002091.1
 Coding sequence: 56..503

1 11 21 31 41 51
 | | | | |
 AGTCTCTGCT CTTCCAGGCC TCTCCGGCGC GCTCCAAGGG CTTCCCGTCG GGACCATGCG 60
 CGGCAGTGAG CTCCCGCTGG TCCTGCTGGC GCTGGTCTCT TGCTAGCGC CCCGGGGGCG 120
 AGCGGTCCCG CTGCCTGCGG GCGGAGGGAC CGTGCTGACC AAGATGTACC CGCGCGGCAA 180
 CCCTGGGCG GTGGGGCACT TAATGGGGAA AAAGAGCACA GGGGAGTCTT CTTCTGTTTC 240
 TGAGAGAGGG AGCCTGAAGC AGCAGCTGAG AGAGTACATC AGGTGGGAAG AAGCTGCAAG 300
 GAATTGCTG GGTCTCATAG AAGCAAAGGA GAACAGAAAC CACCAGCCAC CTCAACCCAA 360
 GGCCTTGGGC AATCAGCAGC CTTCTGTTGG TTCAGAGGAT AGCAGCAACT TCAAAGATGT 420
 AGGTTCAAAA GGCAGAGTTG GTAGACTCTC TGCTCCAGGT TCTCAACGTG AAGGAAGGAA 480
 CCCCAGCTG AACACAGCAAT GATAATGATG GCCTCTCTCA AAAGAGAAAA ACAAAACCCC 540
 TAAGAGACTG AGTTCTGCAA GCATCAGTTC TACGGATCAT CAACAAGATT TCCTTGTGCA 600
 AAATATTGTA CTATTCTGTA TCTTTCATCC TTGACTAAAT TCGTGATTTT CAAGCAGCAT 660
 CTTCTGTTT AAACCTTGTT GCTGTGAACA ATTGTGAAA AGAGTCTTCC AATTAATGCT 720
 TTTTATATC TAGGCTACCT GTTGGTTAGA TTCAAGGCC CGAGCTGTGA CATTTCACAA 780
 TAAAGCTTA AACACAT

Seq ID NO: 635 Protein sequence
 Protein Accession #: NP_002082.1

1 11 21 31 41 51
 | | | | |
 MRGSELPLVL LALVLCCLAPR GRAVPLPAGG GTVLTKMYPR GNHWAVGHLM GKKSTGESSS 60
 VSERGSLKQQ LREYIRWEEA ARNLLGLIEA KENRNHQPPQ PKALGNQQPS WSEDSNFK 120
 DVGSKGKVG RLSAPGSQREG RNPQLNQQ

Seq ID NO: 636 DNA sequence
 Nucleic Acid Accession #: NM_016522.1
 Coding sequence: 265..1299

1 11 21 31 41 51
 | | | | |
 GCGGAAGCAG CGAGGAGGGA GCCCCCTTTG GCCGTCCTCC GTGGAACCGG TTTTCCGAGG 60
 CTGGCAAAAG CCGAGGCTGG ATTTGGGGGA GGAATATTAG ACTCGGAGGA GTCTGCGCGC 120
 TTTTCTCTCT CCCGCGCCTC CCGGTCGCGG CGGGTTCACC GCTCAGTCCC CGCGCTCGCT 180
 CCGCACCCCA CCCACTTCTC GTGCTCGCCC GGGGGGCGTG TGCCGTGCGG CTGCCGAGT 240
 TCGGGGAAGT TGTGGCTGTC GAGAATGGGG GTCTGTGGGT ACCTGTTTCT GCCCTGGAAG 300
 TGCTCTGTTG TCGTGTCTCT CAGGCTGCTG TTCTTTGTAC CCACAGGAGT GCCCGTGCAG 360
 AGCGGAGATG CCACCTTCCC CAAAGCTATG GACACCTGTA CGGTCCGCGA GGGGGAGAGC 420
 GCCACCTTCA GGTGCACTAT TGACAACCGG GTCACCCGGG TGGCTTGGCT AAACCGCAGC 480
 ACCATCTCT ATGCTGGGAA TGACAAGTGG TGCTGGATC CTCGCGTGGT CCTTCTGAGC 540
 AACACCCAAA CGCAGTACAG CATCGAGATC CAGAACGTGG ATGTGTATGA CGAGGGCCCT 600
 TACACCTGCT CGGTGCAGAC AGACAACAC CCAAGACCT CTAGGGTCCA CCTCATTGTG 660
 CAAGTATCTC CCAAATTTGT AGAGATTTCT TCAGATATCT CCATTAATGA AGGGAACAAT 720
 ATTAGCCTCA CCTGCATAGC AACTGGTAGA CCAGAGCCTA CGGTACTTGT GAGACATC 780
 TCTCCCAAAG CGGTGGCTTT TGTGAGTGAA GACGAATACT TGGAAATCA GGGCATCACC 840
 CGGGAACAGT CAGGGGACTA CGAGTGCACT GCCTCCAATG ACCTGGCCGC GCCCGTGGTA 900
 CGGAGAGTAA AGGTCAACGT GAACATATCA CCATACATTT CAGAAGCCAA GGGTACAGGT 960
 GTCCCGTGG GACAAAAGGG GACACTGCAG TGTGAAGCCT CAGCAGTCCC CTCAGCAGAA 1020
 TTCCAGTGGT ACAAGGATGA CAAAAGACTG ATTGAAGGAA AGAAAGGGGT GAAAGTGGAA 1080
 AACAGACCTT TCCTCTCAAA ACTCATCTTC TTCAATGTCT CTGAACATGA CTATGGGAAC 1140
 TACACTTGGG TGGCTCCCAA CAAGCTGGGC CACACCAATG CCAGCATCAT GCTATTGGT 1200
 CCAGCGCCCG TCAGCGAGGT GAGCAACGGC ACGTCGAGGA GGCAGGCTG CGTCTGGCTG 1260
 CTGCTCTTTC TGGTCTTGCA CCGTCTTCTC AAATTTTGAT GTGAGTGCCA CTTCCCCACC 1320
 CGGGAAGGCG TGCCGCCACC ACCACCACCA ACACAACAGC AATGGCAACA CCGACAGCAA 1380
 CCAATCAGAT ATATACAGAT GAAATTAGAA GAAACACAGC CTCATGGGCA AGAAATTTGA 1440
 GGGAGGGGAA CAAAGAATAC TTTGGGGGGA AAAGAGTTT AAAAAGAAA TTGAAATTTG 1500
 CCTTCAGAT ATTAGGTAC AATGGAGTTT TCTTTTCCCA AACGGGAAGA ACACAGCACA 1560

CCCGGCTTGG ACCCACTGCA AGCTGCATCG TGCAACCTCT TTGGTGCCAG TGTGGGCAAG 1620
 GGCTCAGCCT CTCTGCCAC AGACTGCCCC CACGTGGAAC ATTCTGGAGC TGGCCATCCC 1680
 AAATTC AATC AGTCCATAGA GACGAACAGA ATGAGACCTT CCGGCCCAAG CGTGGCGCTT 1740
 CCGGCCCAAG CGTGGCGCTG CCGGCACCTT GGTAGACTGT GCCACCACGG CGTGTGTGT 1800
 GAAACGTGAA ATAAAAAGAG CAAAAA AAAAAA

Seq ID NO: 637 Protein sequence
 Protein Accession #: NP_057606.1

1 11 21 31 41 51
 | | | | |
 MGVCGYLFLP WKCLVVSRLR LLFLVPTGVP VRSGDATFPK AMDNVTVRQG ESATLRCTID 60
 NRVTRVAVLN RSTILYAGND KWCLDPRVVL LSNTQTQYSI EIQNVVDVDE GPYTCVQTD 120
 NHPKTSRVHL IVQVSPKIVE ISSDISINEG NNISLTCIAT GRPEPTVTWR HISP KAVGFV 180
 SEDYLEIQG ITRQSGDYE CSANNDVAAP VVRRVKVTVN YPPYISEAKG TGVPGVQKGT 240
 LQCEASAVPS AEFQWYKDDK RLIEGKKGVK VENRFPLSKL IFFNVSEHDY GNYTCVASNK 300
 LGHTNASIML FPGAVSEVS NGTSRRAGCV WLLPLLVHL LKLF

Seq ID NO: 638 DNA sequence
 Nucleic Acid Accession #: NM_012261.1
 Coding sequence: 203..1045

1 11 21 31 41 51
 | | | | |
 GATTGTCTCT GCCAGCAGCT GTCGGTGCCG CGCTCGACAC CGAGTCCTAG CTAGGCGCTC 60
 ACAGAATACG CGCTCCCTTC CTCCTCCCTTC TCTGTCCCTC GCCTCTCGCT CACCCCGGCC 120
 CACTCCAGCG GCGACTTTGA GGGATTCCCT CTCTGGCGGC CTCTGCAGCA GCACAGCCGG 180
 CCTCATTCGG GGCATTCGGA GTATGGATCT CCAAGGAAGA GGGTCCCA GCATCGACAG 240
 ACTTCGAGTT CTCTGATGT TGTTCATAC AATGGCTCAA ATCATGGCAG AACAGAAGT 300
 GGAATATCTC TCAGGCTTTT CCACTAACCC TGAAAAAGAT ATATTGTGG TCGGGAAAA 360
 TGGGACGACG TGTCTCATGG CAGAGTTTGC AGCCAAATTT ATTGTACCTT ATGATGTGTG 420
 GGCAGCAAC TACGTAGATC TGATCACAGA ACAGGCCGAT ATCGCATTGA CCGGGGAGC 480
 TGAGGTGAAG GGCCTGTGT GCCACAGCCA GTCGGAGCTG CAAGTGTCTT GGTGGATCG 540
 CGCATATGCA CTCAAATGTC TCTTTGTAAA GGAAGGCCAC AACATGTCCA AGGGACCTGA 600
 GGCAGCTTGG AGGCTGAGCA AAGTGCAGTT TGTCTACGAC TCCTCGGAGA AAACCCACTT 660
 CAAAGACGCA CTCAGTGTCT GGAAGCACAC AGCCAACTCG CACCACCTCT CTGCCTTGGT 720
 CACCCCGCTT GTGAAGTCTT ATGAGTGTCA AGCTCAACAA ACCATTTCAC TGGCCTCTAG 780
 TGATCCGCGA AAGACGGTCA CCATGATCCT GTCTGCGGTC CACATCCAAC CTTTGTGACAT 840
 TATCTCAGAT TTTGTCTTCA GTGAAGAGCA TAAATGCCCA GTGGATGAGC GGGAGCAACT 900
 GGAAGAAACC TTGCCCTTGA TTTTGGGGCT CATCTTGGGC CTCGTATCA TGGTAACACT 960
 CGCGATTTAC CACGTCCACC ACAAATGAC TGCCAACCCG GTGCAGATCC CTCGGGACAG 1020
 ATCCAGTAT AAGCATATGG GCTAGAGGCC GTTAGGCAG CACCCCTTAT TCCTGCTCCC 1080
 CCAACTGGAT CAGGTAGAAC AACAAAAAGCA CTTTTCATC TTGTACACGA GATACACCAA 1140
 CATAGCTACA ATCAACAGG CCTGGGTATC TGAGGCTTGC TTGGCTTGTG TCCATGCTTA 1200
 AACCCACGGA AGGGGAGAC TCTTTCGGAT TTGTAGGGTG AAATGGCAAT TATTCTCTCC 1260
 ATGCTGGGGA GGAGGGGAGG AGGGTCTCAG ACAGCTTTTC TGCTCATGGT GGCTTGGCTT 1320
 TGACTCTCCA AAGAGCAATA AATGCCACTT GGAGCTGTAT CTGGCCCAA AGTTTAGGGA 1380
 TTGAAAAATC GCTTCTTTGA GGAGGAAACC CCTTAGGTT CAGAAGAATA TGGGTGCTT 1440
 TGCTCCCTTG GACACAGCTG GCTTATCCTA TACAGTTGTC AATGCACACA GAATCAAC 1500
 TCATGCTCCC TGCAGCAAGA CCCCTGAAAG TGATTCATGC TTCTGGCTGG CATTCTGCAT 1560
 GTTTAGTGAT TGTCTTGGGA ATGTTTCACT GCTACCCGCA TCCAGCGACT GCAGCACCAG 1620
 AAAACGACTA ATGTAACAT GCAGAGTTGT TTGGACTTCT TCCTGTGCCA GGTCCAAGTC 1680
 GGGGACCTG AAGAATCAAT CTGTGTGAGT CTGTTTTTCA AAATGAAATA AAACACACTA 1740
 TTCTCTGGC

Seq ID NO: 639 Protein sequence
 Protein Accession #: NP_036393.1

1 11 21 31 41 51
 | | | | |
 MDLQGRGVPS IDRLRVLLML FHTMAQIMAE QEVNLSGLS TNPEKDIFVV RENGTTCLMA 60
 EFAAKFIVPY DVWASNYVDL ITEQADIALT RGAEVKGRCG HSQSELQVFW VDRAYALKML 120
 FVKESHNMMSK GPEATWRLSK VQFVYDSSEK THFKDAVSAG KHTANSHLS ALVTPAGKSY 180
 BCQAQQTISL ASSDPQKTVT MILSAVHIQF FDIISDFVFS EEHKCPVDER EQLEETLPLI 240
 LGLILGLVIM VTLAIYVHH KMTANQVQIP RDRSQYKHM

Seq ID NO: 640 DNA sequence
 Nucleic Acid Accession #: NM_002993.1
 Coding sequence: 64..408

1 11 21 31 41 51
 | | | | |
 GGCACGAGCC AGTCTCCGCG CCTCCACCCA GCTCAGGAAC CCGCGAACCC TCTCTTGACC 60
 ACTATGAGCC TCCCGTCCAG CCGCGCGGCC CGTGTCCCGG GTCCTTCGGG CTCCTTGTGC 120
 GCGCTGCTCG CGCTGTCTGT CCGCTGACG CCGCGGGGGC CCCTCGCCAG CGCTGGTCTC 180
 GTCTCTGCTG TGCTGACAGA GCTGCGTTCG ACTTGTTTAC GCGTTACGCT GAGAGTAAAC 240
 CCAAAACGGA TTGTTAAACT GCAGGTGTTT CCGCAGGCC CGCAGTGCTC CAAGGTGGAA 300
 GTGGTAGCCT CCCTGAAGAA CGGAAGCAA GTTTGTCTGG ACCCGGAAGC CCCTTTCTA 360
 AAGAAAGTCA TCCAGAAAT TTTGGACAGT GGAACAAGA AAACTGAGT AACAAAAAG 420
 ACCATGCATC ATAAATTGC CCAGTCTTCA GCGGAGCAGT TTTCTGGAGA TCCCTGGACC 480
 CAGTAAGAAAT AAGAGGAAG GGTGGTTT TTTCCATTT CTACATGGAT TCCCTACTTT 540
 GAAGAGTGTG GGGGAAAGCC TACGCTTCTC CTGAAGTT ACAGCTCAGC TAATGAAGTA 600
 CTAATATAGT ATTTCCACTA TTTACTGTTA TTTTACCTGA TAAGTTATTG AACCTTTGG 660
 CAATTGACCA TATTGTAGC AAAGAATCAC TGGTTATTAG TCTTCAATG AATATTGAAT 720
 TGAAGATAAC TATTGTATT CTATCATACA TTCCTAAAG TCTTACCGAA AAGGCTGTGG 780
 ATTTCTGATG GAAATAATGT TTTATTAGTG TGCTGTTGAG GGAGGTATCC TGTGTTCTT 840
 ACTCACTCTT CTCATAAAT AGGAAATATT TAGTTCTGT TTTCTGGGG AATATGTTAC 900

TCTTTACCT AGGATGCTAT TTAAGTTGTA CTGTATTAGA AACTGGGTG TGTACATCCG 960
 TTATCTGTGC AGAATATATT TCCTTATTCA GAATTTCTAA AAATTTAAGT TCTGTAAGGG 1020
 CTAATATATT CTCTTCCTAT GGTTTTAGAT GTTTGATGTC TTCTTAGTAGT GGCATAATGT 1080
 CATGATTTAC TCATTAAACT TTGATTTTGT ATGCTATTTT TTTACTATAG GATGACTATA 1140
 ATCTGGTCA CTAATATATAC ACTTTAGATA GATGAAGAAG CCCAAAAACA GATAAATTC 1200
 TGATTGCTAA TTTACATAGA AATGTATTCT CTGTTTGT TAAATAAAG CAAAATTAAC 1260
 AATGATCTGT GCTCTGCAAA GTTTTGAAAA TATATTTGAA CAATTTGAAT ATAAATTCAT 1320
 CATTAGTCC TCAAAATATA TACAGCATG CTAAGATTTT CAGATATCTA TTGTGGATCT 1380
 TTTAAAGGTT TTGACCATTT TGTATGAGG AATTATACAT GTATCACATT CACTATATTA 1440
 AAATTGCACT TTTATTTTCT CCTGTGTGTC ATGTTGGTTT TTGGTACTTG TATTGTCTAT 1500
 TGGAGAAACA ATAAAGATT TCTAAACCAA AAAAAA AAAA

Seq ID NO: 641 Protein sequence
 Protein Accession #: NP_002984.1

1 11 21 31 41 51
 MSLPSSRAAR VPGPSGSLCA LLALLLLLTTP PGPLASAGPV SAVLTELRCT CLRVTLRVNP 60
 KTIGKLQVFP AGPQCSKEV VASLKNKQV CLDPEAPFLK KVIQKILDSG NKKN

Seq ID NO: 642 DNA sequence
 Nucleic Acid Accession #: NM_013271.1
 Coding sequence: 27..809

1 11 21 31 41 51
 TCCGAGCCA GGCTCGCTGG GGCAGCATGG CGGGGTCGCC GCTGCTCTGG GGGCCGCGGG 60
 CCGGGGGCGT CGGCTTTTGG GTGCTGCTGC TGCTCGGCCT GTTTCGCGCG CCCCCCGCGC 120
 TCTGCGCGCG GCGCGTAAAG GAACCCGCG GCCTAAGCGC AGCGTCTCCG CCCTTGCGTG 180
 AGACTGGCGC TCCTCGCGCG TTCCGGCGGT CAGTGCCCGC AGGTGAGCGC GCGGGGCGCG 240
 TGCAGGAGCT GCGCGCGCGC CTGGCGCATC TGCTGGAGGC CGAACGTGAG GAGCGGGCGC 300
 GGGCCGAGGC GCAGGAGGCT GAGGATCAGC AGGCGCGCGT CCTGGCGCAG CTGCTGCGCG 360
 TCTGGGGCGC CCCCCGCAAC TCTGATCCGG CTCTGGGCCT GGACGACGAC CCGACGCGC 420
 CTGCGAGCCA GCTCGCTCGC GCTCTGCTCC GCGCCCGCCT TGACCCCTGCC GCCCTAGCAG 480
 CCCAGCTTGT CCGCGCGCGC GTCCCCGCGC CGGCGCTCCG ACCCGGGGCC CCGGTCTACG 540
 ACGACGGCCC CGCGGGCCCG GATGCTGAGG AGGCGAGCGA CGAGACACCC GACGTGGACC 600
 CCGAGCTGTT GAGGTACTTG CTGGGACGGA TTCTTGCGGG AAGCGCGGAC TCCGAGGGGG 660
 TGGCAGCCCC GCGCGGCTCT CGCCGTGCGC CCGACCACGA TGTGGGCTCT GAGCTGCCCC 720
 CTGAGGGCGT GCTGGGGGCG CTGCTGCGTG TGAACGCCT AGAGACCCCG GCGCCCCAGG 780
 TGCTGCAAG CCGCTCTTTG CCACCTGAG CACTGCGCGG ATCCCGTGCA CCCTGGGACC 840
 CAGAAAGTGC CCGCCATTC CGCCACCAGG ACTTCTCCCC GCCAGCACGT CCAGAGCAAC 900
 TTACCCCGGC CAGCCAGCCC TCTCACCCGA GGATCCCTAC CCCCTGGCCC ACAATAACAT 960
 GATCTGAGC

Seq ID NO: 643 Protein sequence
 Protein Accession #: NP_037403.1

1 11 21 31 41 51
 MAGSPLLWGP RAGGVGLLV LLLGLFRPPP ALCARPVKEP RGLSAASPPL AETGAPRRFR 60
 RSVPRGEAAG AVQELARALA HLLEAERQER ARAEAQEAED QQARVLAQLL RVWGAPRNSD 120
 PALGLDDDDP APAQALARAL LRRLDPAAL AAQLVPAPVP AAALRPFPV YDDGPAGPDA 180
 BEAGDETPDV DPELLRYLLG RILAGSADSE GVAAPRRLLR AADHDVGSSEL FPEGVLGALL 240
 RVKRLTPAP QVPARRLLPP

Seq ID NO: 644 DNA sequence
 Nucleic Acid Accession #: NM_002214
 Coding sequence: 681..2990

1 11 21 31 41 51
 CCCAGAGCCG CCTCCCCCTG TTGCTGGCAT CCGAGCTTC CTCCCTTGCC AGCCAGGACG 60
 CTGCCGACTT GTCTTTGGCC GCTGCTCCGC AGACGGGGCT GCAAAGCTGC AACTAATGGT 120
 GTTGGCCTCC CTGCCCACTT GTGGAAGCAA CTGCGCTGAT TGATGCGCCA CAGACTTTT 180
 TCCCTCGAC CTGCGCGCGC TACCTCCCA CAGATCCAGC ATCACCAGT GAATGTACAT 240
 TAGGGTGGTT TCCCCCCAG CTTCGGGCTT TGTTTGGGTT TGATGTGTT TGGCTCTTCG 300
 CTAAGCTGAT TTATGCAAGA GAAGCCCCAC CGGCTGGAGA GAAACAAAG CTCTTTTCTT 360
 TGTCCCGGAG CAGGCTGCGG AGCCCTTGCA GAGCCCTCTC TCCAGTCGCC GCGGGGCCCT 420
 TGGCCGTCGA AGGAGGTGCT TCTCGCGGAG ACCGCGGGAC CCGCCGTGCC GAGCCGGGAG 480
 GGCCTAGGG GCCCTGAGAT GCCGAGCGGT GCCCGGGGCC GCTTACCTGC ACCGCTTGCT 540
 CCGAGCCGCG GGGTCCGCCT GCTAGGCCTG CGGAAACGCT CCTAGCGACA CTCGCCCGCG 600
 GGCCCCGAGG TCGCCCGGGA GGCCGAGCCC GCGTCCGGAA GGCAGCCAGG CCGCGGGCGC 660
 GGGCGGGGCT GTTTTGCAAT ATGTGCGGCT CGGCCCTGGC TTTTITTTACC GCTGCATTTG 720
 TCTGCCTGCA AAACGACCGG CGAGGTCCCG CCTCGTTTCT CTGGCAGCC TGGGTGTTT 780
 CACTTGTCTT TGGACTGGGC CAAGGTGAAG ACAATAGATG TGCACTTTCA AATGCAGCAT 840
 CCTGTGCCAG GTGCTTGGC CTGGGTCCAG AATGTGGATG GTGTGTTCAA GAGGATTTC 900
 TTTCAAGTGG ATCAAGAAGT GAACGTTGTG ATATGTTTC CAATTTAATA AGCAAAGGCT 960
 GCTCAGTTGA TTCAATAGAA TACCATCTG TGCACTGTTA AATACCCACT GAAATGAAA 1020
 TTAATACCCA GGTGACACCA GGAGAAGTGT CTATCCAGCT GCGTCCAGGA GCCGAAGCTA 1080
 ATTTTATGCT GAAAGTTTAT CCTCTGAAGA AATATCCTGT GGATCTTTAT TATCTTGTG 1140
 ATGTCTCAGC ATCAATGCAC AATAATATAG AAAAAATAAA TTCCGTTTGA AACGATTAT 1200
 CTAGAAAAAT GGCATTTTTC TCCCGTACT TTCGTTTGG ATTTGGCTCA TACGTTGATA 1260
 AAACAGTTTC ACCATACATT AGCATCCACC CCGAAGGAT TCATAATCAA TGCAGTGACT 1320
 ACAATTTAGA CTGATGCTCT CCCATGGAT ACATCCATGT GCTGTCTTTC ACAGAGAACA 1380
 TCAGTAGATT TGAGAAAGCA GTTCATAGAC AGAAGATCTC TGGAAACATA GATACACCA 1440
 AAGGAGGTTT TGACGCCATG CTTACGGCAG CTGTCTGTGA AAGTCATATC GGATGGCGAA 1500
 AAGAGGCTAA AAGATTGCTG CTGGTGATGA CAGATCAGAC GTCTCATCTC GCTCTTGATA 1560

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GCAAATTGGC AGGCATAGTG GTGCCCAATG ACGGAAACTG TCATCTGAAA AACAACTGCT 1620
ACGTCAAATC GACAACCATG GAACACCCCT CACTAGGCCA ACTTTCAGAG AAATTAATAG 1680
ACAACAACAT TAAATGTATC TTTGCAGTTC AAGGAAAAACA ATTTTCATGG TATAAGGATC 1740
TTCTACCCCT CTGTGCCAGG ACCATTGCTG GTGAAATAGA ATCAAAGGCT GCAAACCTCA 1800
ATAATTTGGT AGTGGGAAGC TATCAGAAGC TCATTTTCAG AGTGAAAGTT CAGGTGGAAA 1860
ACCAGGTACA AGGCATCTAT TTTAACATTA CCGCCATCTG TCCAGATGGG TCCAGAAAAGC 1920
CAGGCATGGA AGGATGACGA AACGTGACGA GCAATGATGA AGTTCTTTTC AATGTAACAG 1980
TTACAATGAA AAAATGTGAT GTCCACAGGAG GAAAAAACTA TGCAATAATC AAACCTATTG 2040
GTTTTAATGA AACCGCTAAA ATTCATATAC ACAGAAACTG CAGCTGTGAG TGTGAGGACA 2100
ACAGAGGACC TAAAGGAAAG TGTGTAGATG AAACCTTTCT AGATTCCAAG TGTTCCTAGT 2160
GTGATGAGAA TAAATGTATC TTTGATGAAG ATCAGTTTTT TTCTGAGAGT TGCAAGTCAC 2220
ACAAGGATCA GCCTGTTTGC AGTGGTCGAG GAGTTTGTGT TTGTGGGAAA TGTTCATGTC 2280
ACAAAATTAA GCTTGGAAAA GTGTATGGAA AATACTGTGA AAAGGATGAC TTTTCTTGTC 2340
CATATCACCA TGGAAATCTG TGTGCTGGGC ATGGAGAGTG TGAAGCAGGC AGATGCCAAT 2400
GCTTCAGTGG CTGGGAAGGT GATCGATGCC AGTGCCCTTC AGCAGCAGCC CAGCACTGTG 2460
TCAATTCAAA GGGCCAAAGT GTCCAGTGGAA GAGGCACGTG TGTGTGTGGA AGGTGTGAGT 2520
GCACCGATCC CAGGAGCATC GGCCGCTTCT GTGAACACTG CCCCACCTGT TATACAGCCT 2580
GCAAGGAAAA CTGGAATTGT ATGCAATGCC TTCACCTCA CAATTTGTCT CAGGCTATAC 2640
TTGATCAGTG CAAAACCTCA TGTGCTCTCA TGGAAACAACA GCATTATGTC GACCAAACTT 2700
CAGAAATGTT CTCAGGCCA AGCTACTTGA GAATATTTT CATCATTTT ATAGTTTACAT 2760
TCTTGATTGG GTTGCTTAAA GTCCTGATCA TTAGACAGGT GATACTACAA TGGAAATAGTA 2820
ATAAAATTAA GTCCTCATCA GATTACAGAG TGTGAGCCTC AAAAAAGGAT AAGTTGATT 2880
TGCAAAAGTG TTGCACAAGA GCAGTCACCT ACCGACGTGA GAAGCCTGAA GAAATAAAAA 2940
TGGATATCAG CAAATTAAT GCTCATGAAA CTTTCAGGTG CAACTTCTAA AAAAAGATTT 3000
TTAAACACTT AATGGGAAAC TGGAAATTGT AATAATTGCT CCTAAAGATT ATAATTTTAA 3060
AAGTCACAGG AGGAGACAAA TTGCTCACGG TCATGCCAGT TGCTGGTTGT ACACCTCGAAC 3120
GAAGACTGAC AAGATCTCTC ATCATGATGT GACTCACATA GCTGCTGACT TTTTCAGAGA 3180
AAAAATGTGTC TTACTACTGT TTAGAGACTAG TGTGTTGTA GCACCTTACT GTAATATATA 3240
ACTTATTTAG ATCAGCATAG AATGTAGATC CTCTGAAGAG CACTGATTAC ACTTTACAGG 3300
TACCTGTTAT CCCTACGCTT CCCAGAGAGA ACAATGCTGT GAGAGAGTTT AGCATTGTGT 3360
CACTACAAGG GTACAGTAAT CCCTGCACTG GACATGTGAG GAAAAAATA ATCTGGCAAG 3420
TATATTTCAA GGTTCGCAAA CACTTCAACA GTTGGTGGTT GAATAGACAA GAACAGCTAG 3480
ATGAATAAAT GATTGCTGTT TCACTCTTTC AAGAGGTGAA CAGATACAAC CTTAATCTTA 3540
AAAGATTATT GCTTTTTTAA GTGTGTAGTT TTATGCATGT GTGTTTATGG TTTGCTTATT 3600
TTTGCAAGAT GGATACTAAT TCCAGCATTC TCTCCTCTT GCCTTTATGT TTTGTTTTCT 3660
TTTTTACAGG ATAAGTTTAT GTATGTCACA GATGACTGGA TTAATTAAGT GCTAAGTTAC 3720
TACTGCCATA AAAAATAAT AATACAATGT CACTTTATCA GAATACTAGT TTTAAAAGCT 3780
GAATGTTAA

Seq ID NO: 645 Protein sequence
Protein Accession #: NP_002205

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60

1 11 21 31 41 51
MCGSALAFPT AAFVCLQNDR RGPASFLWAA WVFSVLVLGLG QGEDNRCASS NAASCARCLA 60
LGPECGWCQV EDFISGGSRS ERCDIVSNLI SKGCSVDSIE YPSVHVIIPT ENEINTQVTP 120
GEVSIQLRPG AEANFMLKVH PLKKYPVDLY YLVDVSASMH NNIEKLNSVG NDLSRKMAFF 180
SRDFRLGFGS YVDKTVSPYI SIHPERIHNQ CSDYNLDCMP PHGYIHVLSL TENITEFEKA 240
VHRQKISGNI DTPEGGFDM LQAAVCESHI GWRKEAKRL LVMTDQTSHL ALDSKLAGIV 300
VPNDGNCHLK NNIVYKSTIM EHPSLQQLSE KLIDNNINVI FAVQKQFHW YKDLLPLLP 360
TIAGEIESKA ANLNNLVVEA YQKLISEVKV QVENQVQGIY FNITAICPDG SRKPGMEGCR 420
NVTSDNEVLK NVTVMKKKCH VTGGKNYAI KPIGFNETAK IHIHRNCSCQ CEDNRGPKGK 480
CVDETFLDSK CFQCDENKCH FDEDDFSSSES CKSHKDQPV C SGRGVVCVCGK CSCHKIKLGK 540
VYGKYCEKDD FSCPHYHGNL CAGHGECEAG RCQCFSWEG DRCQCPSAAA QHCVNSKGQV 600
CSGRGTCVCG RCECTDPRSI GRFCEHCPTC YTACKENWNC MQCLHPHNLS QAILDQCKTS 660
CALMEQQUHYV DQTSBCEPSS SYLRIFFIIF IVTFLIGLLK VLIIRQVILQ WNSNKKIKSS 720
DYRVSASKKD KLILQSVCTR AVTYRREKPE BIKMDISKLN AHETFRCNF

Seq ID NO: 646 DNA sequence
Nucleic Acid Accession #: NM_003318.1
Coding sequence: 1..2574

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80
85

1 11 21 31 41 51
ATGGAATCCG AGGATTTAAG TGGCAGAGAA TTGACAATTG ATTCCATAAT GAACAAAGTG 60
AGAGACATTA AAAATAAGTT TAAAAATGAA GACCTTACTG ATGAACTAAG CTTGAATAAA 120
ATTTCTGCTG ATACTACAGA TAACTCGGGA ACTGTTAACC AAATTATGAT GATGGCAAAC 180
AACCAGAGG ACTGTTGAG TTTGTTGCTC AAACCTAGAGA AAAACAGTGT TCCGCTAAGT 240
GATGCTCTTT TAAATAAATT GATTGGTCTG TACAGTCAAG CAATTGAAGC GCTTCCCCCA 300
GATAAATATG GCCAAATGA GAGTTTTGCT AGAATTCAAG TGAGATTGTC TGAATTAATA 360
GCTATTCAAG AGCCAGATGA TGCACGTGAC TACTTTCAAA TGGCCAGAGC AAAGTGCAG 420
AAATTGCTT TTGTTTATAT ATCTTTTGCA CAATTGTAAC TGTACACAAG TAATGTCAAA 480
AAAAGTAAAC AACTTCTTCA AAAAGCTGTA GAACGTGGAG CAGTACCACT AGAAATGCTG 540
GAAATTGCCC TGGCGAATTT AAACCTCCAA AAAAGCAGC TGCTTTCAGA GGAGGAAAAG 600
AAGAATTAT CAGCATCTAC GGTATTAACT GCCCAAGAAT CATTTTCCGG TTCCTTGGG 660
CATTTACAGA ATAGGAACAA CAGTTGTGAT TCCAGAGGAC AGACTACTAA AGCCAGGTTT 720
TTATATGGAG AGAACATGCC ACCACAAGAT GCAGAAATAG GTTACCCGAA TTCAATTGAGA 780
CAAACATAAC AACTTAAACA GTCATGCCCA TTTGGAAGAG TCCAGTTTAA CCTTCTAAAT 840
AGCCAGATT GTGATGTGAA GACAGATGAT TCAGTTGTAC CTTGTTTTAT GAAAAGACAA 900
ACCTCTAGAT CAGAATGCCG AGATTGGTT GTGCCCTGGT CTAACCAAG TGGAAATGAT 960
TCCTGTGAAT TAAGAAATTT AAAGTCTGTT CAAAATAGTC ATTTCAAGGA ACCTCTGGTG 1020
TCAGATGAAA AGAGTCTGTA ACTTATTATT ACTGATTCAA TAACCCTGAA GAATAAAACG 1080
GAATCAAGTC TTCTAGCTAA ATTAGAAGAA ACTAAAGAGT ATCAAGAACC AGAGGTTCCA 1140
GAGAGTAACC AGAAACAGTG GCAATCTAAG AGAAAGTCAG AGTGATTAA CCAGAATCCT 1200
GCTGCATCTT CAAATCACTG GCAGATTCCG GAGTTAGCCC GAAAAGTTAA TACAGAGCAG 1260
AAACATACCA CTTTGTAGCA ACCTGTCTTT TCAGTTTCAA AACAGTCACC ACCAATATCA 1320
ACATCTAAT GGTGTGACCC AAAATCTATT TGTAAGACAC CAAGCAGCAA TACCTTGGAT 1380

	GATTACATGA	GCTGTTTTAG	AACTCCAGTT	GTAAAGAATG	ACTTTCACC	TGCTTGTCAG	1440
	TTGTCAACAC	CTTATGGCCA	ACCTGCCTGT	TTCCAGCAGC	AACAGCATCA	AATACTTGCC	1500
	ACTCCACTTC	AAAATTTACA	GGTTTTAGCA	TCTTCTTCAG	CAAATGAATG	CATTTCGGTT	1560
5	AAAGGAAGAA	TTTATTCCAT	TTTAAAGCAG	ATAGGAAGTG	GAGGTTCAAG	CAAGGTATTT	1620
	CAGGTGTTAA	ATGAAAAGAA	ACAGATATAT	GCTATAAAAT	ATGTGAACCT	AGAAGAAGCA	1680
	GATAACCAAA	CTCTTGATAG	TTACCGGAAC	GAAATAGCTT	ATTTGAATAA	ACTACAACAA	1740
	CACAGTGATA	AGATCATCCG	ACTTTATGAT	TATGAAATCA	CGGACCAGTA	CATCTACATG	1800
	GTAAATGGAGT	GTGGAAATAT	TGATCTTAAT	AGTTGCTTA	AAAAGAAAAA	ATCCATTGAT	1860
10	CCATGGGAAC	GCAAGAGTTA	CTGGAATAAT	ATGTTAGAGG	CAGTTCACAC	AATCCATCAA	1920
	CATGGCATTG	TTACAGTGA	TCTTAAACCA	GCTAACTTTC	TGATAGTTGA	TGGAATGCTA	1980
	AAGCTAAATTG	ATTTTGGGAT	TGCAAAACCA	ATGCAACCAG	ATACAACAAG	TGTTGTTAAA	2040
	GATTCCTCAGG	TTGGCACAGT	TAATTATATG	CCACCAGAAG	CAATCAAAGA	TATGTCTTCC	2100
	TCCAGAGAGA	ATGGGAAATC	TAAGTCAAAG	ATAAGCCCCA	AAAGTGATGT	TTGGTCTTCA	2160
15	GGATGTATTT	TGTACTATAT	GACTTACGGG	AAAACACCAT	TTCAGCAGAT	AATTAATCAG	2220
	ATTTCTAAAT	TACATGCCAT	AATTGATCCT	AATCATGAAA	TTGAATTTCC	CGATATTCCA	2280
	GAGAAAGATC	TTCAGAGTGT	GTTAAAGTGT	TGTTTAAAAA	GGGACCCAAA	ACAGAGGATA	2340
	TCCATTCCTG	AGCTCCTGCG	TCATCCCTAT	GTTCAAATTC	AAACTCATCC	AGTTAAACCA	2400
	ATGGCCCAAGG	GAACCACTGA	AGAAATGAAA	TATGTTCTGG	GCCAACTTGT	TGGTCTGAAT	2460
20	TCTCCTAACT	CATTTTGAAA	AGCTGCTAAA	ACTTTATATG	AACACTATAG	TGGTGGTGAA	2520
	AGTCATAATT	CTTCATCCTC	CAAGACTTTT	GAAAAAATAA	GGGGAATAAA	ATGA	

Seq ID NO: 647 Protein sequence
Protein Accession #: NP_003309.1

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	NPEDWLSLLL	KLEKNSVPLS	DALLNKLIGR	YSQAIKALFP	DKYQONESFA	RIQVRFAELK	120
	AIQEPDDARD	YFQMARANCK	KFAFVHISFA	QFELSQGNVK	KSKQLLQKAV	ERGAUPEML	180
30	EIALRNLNLQ	KKQLLSSEEEK	KNLSASTVLT	AQESFSGSLG	HLQNRNNSCD	SRGQTTKARF	240
	LYGENMPPQD	ABIGYRNLRL	QTNKTKQSCP	FGRVPVNLIN	SPDCDVKTDD	SVVPCFMKRO	300
	TSRSECRDLV	VPGSKPSGND	SCELRNLKSV	QNSHFKEPLV	SDEKSSSELI	ITDITLKNKT	360
	ESSLLAKLEE	KEYEQEPFVP	ESNQKQWQSK	RKSECINQNP	AASNHWQIP	ELARKVNTAQ	420
	KHTTFEQPVF	SVSKQSPPI	TSKWDFPKSI	CKTPSSNTLD	DYMSCFRTPV	VKNDFPPACQ	480
35	LSTPYGQAPC	FQQQHQHILA	TPLQNLQVLA	SSSANECISV	KGRYISILKQ	IGSGSSSKVF	540
	QVLNEKKQIY	AIKYVNLBEE	DNQTLDSYRN	EIAYLNKLQO	HSDKIIRLYD	YEITDQYIYM	600
	VMECCNIDLN	SWLKKKKSID	PWERKSYWKN	MLEAVHTIHQ	HGIVHSDLKP	ANFLIVDGML	660
	KLIDFGIANQ	MQPDITTSVVK	DSQVGTVNYM	PPEAIKDMSS	SRENGKSKSK	ISPKSDVWSL	720
40	GCILYMYTYG	KTFPQQIINQ	ISKHLAIIIDP	NHEIEFPDIP	EKDLQDVLKC	CLKRDPKQRI	780
	SIPLELAHPY	VQIQTHPYNQ	MAKGTTEEMK	YVLGQLVLGN	SPNSILKAAK	TLYEHVSGGE	840
	SHNSSSKTFF	EKKRGGK					

Seq ID NO: 648 DNA sequence
Nucleic Acid Accession #: NM_015507
Coding sequence: 241..1902

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50	CGCCCTGCCC	GCGGTGCTGC	GCCTCCCCCTC	CCAGACTGCA	GGGACAGCAC	CCGGTAACTG	120
	CGAGTGGAGC	GGAGGACCCG	AGCGGCTGAG	GAGAGAGGAG	GCGGCGGCTT	AGCTGCTACG	180
	GGGTCCGGCC	GGCGCCCTCC	CGAGGGGGGC	TCAGGAGGAG	GAAGGAGGAC	CCGTGCGGAG	240
	ATGCTCTGCG	CTGTGAGCCT	TGCGCTCCCG	CTGCTGCTCT	CCTGGGTGGC	AGGTGGTTTC	300
55	GGGAACGCGG	CCAGTGCAAG	GCATCACGGG	TTGTTAGCAT	CGGCACGTCA	GCCTGGGGTC	360
	TGTCACTATG	GAACATAAAT	GGCCTGCTGC	TACGGCTGGA	GAAGAAACAG	CAAGGGAGTC	420
	TGTGAAGCTA	TATCGGACCC	TGGATGTAAG	TTTGGTGAGT	GCGTGGGACC	AAACAAATGC	480
	AGATGCTTTC	CAGGATACAC	CGGGAACACC	TGCAGTCAAG	ATGTGAATGA	GTGTGGAATG	540
	AAACCCCGGC	CATGCCAACA	CAGATGTGTG	AATACACACG	GAAGCTACAA	GTGCTTTTGC	600
60	CTCAGTGGCC	ACATGCTCAT	GCCAGATGCT	ACGTGTGTGA	ACTCTAGGAC	ATGTGCCATG	660
	ATAAACTGTC	AGTACAGCTG	TGAAGACACA	GAAGAAGGGC	CACAGTGCCT	GTGTCCATCC	720
	TCAGGACTCC	GCCTGGCCCC	AAATGGAAGA	GACTGTCTAG	ATATTGATGA	ATGTGCCCTC	780
	GGTAAAGTCA	TCTGTCCCTA	CAATCGAAGA	TGTGTGAACA	CATTGTGAAG	CTACTACTGC	840
	AAATGTCACA	TTGGTTTCGA	ACTGCAATAT	ATCAGTGGAC	GATATGACTG	TATAGATATA	900
65	AATGAATGTA	CTATGGATAG	CCATACGTGC	AGCCACCATG	CCAATTGCTT	CAATACCCAA	960
	GGGTCTCTCA	AGTGTAAATG	CAAGCAGGGA	TATAAAGGCA	ATGGACTTCG	GTGTTCTGCT	1020
	ATCCCTGAAA	ATTCTGTGAA	GGAAGTCCCT	AGAGCACCTG	GTACCATCAA	AGACAGAATC	1080
	AAGAAGTTGC	TTGCTCACAA	AAACAGCATG	AAAAAGAAGG	CAAAAAATTA	AAATGTTACC	1140
	CCAGAACCCA	CCAGGACTCC	TACCCCTAAG	GTGAACCTGC	AGCCCTTCAA	CTATGAAGAG	1200
70	ATAGTTTCCA	GAGGCGGGAA	CTCTCATGGA	GGTAAAAAAG	GGAATGAAGA	GAAATGAAA	1260
	GAGGGGCTTG	AGGATGAGAA	AAGAGAAGAG	AAAGCCCTGA	AGAATGACAT	AGAGGAGCGA	1320
	AGCCTGCGAG	GAGATGTGTT	TTTCCTTAAG	GTGAATGAAG	CAGGTGAATT	CGGCCTGATT	1380
	CTGGTCCAAA	GGAAAGCGCT	AACCTCCAAA	CTGGAACATA	AAGATTTAAA	TATCTCGGTT	1440
	GACTGCAGCT	TCAATCATGG	GATCTGTGAC	TGGAAACAGG	ATAGAGAAGA	TGATTTTGAC	1500
75	TGGAATCCTG	CTGATCGAGA	TAATGCTATT	GGCTTCTATA	TGGCAGTTCC	GGCCTTGGCA	1560
	GGTCACAAGA	AAGACATTGG	CCGATTGAAA	CTTCTCTTAC	CTGACCTGCA	ACCCCAAGAG	1620
	AACCTCTGTT	TGCTCTTTGA	TTACCGGCTG	GCCGGAGACA	AAGTCGGGAA	ACTTCGAGTG	1680
	TTTGTGAAAA	ACAGTAACAA	TGCCCTGGCA	TGGGAGAAGA	CCACGAGTGA	GGATGAAAAA	1740
	TGGAAGACAG	GGAAATTTCA	GTTGTATCAA	GGAATGATG	CTACCAAAAG	CATCATTTTT	1800
80	GAAGCAGAAC	GTGGCAAGGG	CAAAACCGGC	GAAATCGCAG	TGGATGGCGT	CTTGCTTGTT	1860
	TCAGGCTTAT	GTCAGATAG	CCTTTTATCT	GTGGATGACT	GAATGTTACT	ATCTTTATAT	1920
	TTGACTTTGT	ATGTCAGTTC	CCTGGTTTTT	TTGATATTGC	ATCATAGGAC	CTCTGGCATT	1980
	TTAGAATTAC	TAGCTGAAA	ATTGTAATGT	ACCAACAGAA	ATATTATTGT	AGATGCCTTT	2040
	TCTTGATATA	GATATGCCAA	TATTTGCTTT	AAATATCATA	TCAGTGTATC	TTCTCAGTCA	2100
	TTTCTGAATC	TTTCCACATT	ATATTATAAA	ATATGGAAAT	GTCAGTTTAT	CTCCCTCCTT	2160
85	CAGTATATCT	GATTGTGATC	AGTAAGTTGA	TGAGCTTCTC	TCTACAACTA	TTCTAGAAAA	2220
	TAGAAAAAAA	AGCACAGAGA	AATGTTTAA	TGTTTGACTC	TTATGATACT	TCTTGGAAAC	2280
	TATGACATCA	AAGATAGACT	TTTGCTTAAG	TGGCTTAGCT	GGGTCTTTCA	TAGCCAAACT	2340

TGATATTTTA AATCTTTGT AATAATAATA TCCAAATCAT CAAAAAATAA AAAAAATA

Seq ID NO: 649 Protein sequence
Protein Accession #: NP_056322

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CEATCEPGCK	FGECVGPNC	RCFPGYTGT	CSQDVNECGM	KPRPCQHRV	NTHGSYKCF	120
LSGHMLMPDA	TCVNSRTCAM	INCQYSCEDT	BEGPQCLCPS	SGLRLAPNGR	DCLDIDECAS	180
GKVICPNRR	CVNFTGSYYC	KCHIGFELQY	ISGRYDCIDI	NECTMDSHTC	SHHANCFTNQ	240
GSFKCKCKQG	YKGNGLRCSA	IPENSVKEVL	RAPGTIKDRI	KKLLAHKNSM	KKKAKIKNVT	300
PEPTRTPTPK	VNLQFPNVEE	IVSRGGNSHG	GKKGNEEKMK	EGLEDEKREE	KALKNDIEER	360
SLRGDVFFPK	VNEAGEFLGI	LVQRKALTSK	LEHKDLNISV	DCSFNHGICD	WKQDREDDFD	420
WNPADRDNAI	GFYMAVPPALA	GHKKDIGRLK	LLLPDLQPQS	NFCLLFDYRL	AGDKVKGKLRV	480
FVKNSNNALA	WEKTTSEDEK	WKTGKIQLYQ	GTDATKSIIF	EAERGKGKTG	EIAVDGVLLV	540
SGLCPDSLLS	VDD					

Seq ID NO: 650 DNA sequence
Nucleic Acid Accession #: NM_003506.1
Coding sequence: 259..2379

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TTAGACGGGG	ACGGGAAGGG	ACAGCGGCCT	TCGACCGCCC	CCCGAGTAAT	TGACCCAGGA	120
CTCATTTTCA	GGGAAGCCTG	AAAAAGAGTA	AAATAGTGAA	ATGAGGAATT	TGAACATTTT	180
ATCTTTGGAT	GGGATCTTTC	TGAGGATGCA	AAGAGTGATT	CATCCAAGCC	ATGTGGTAAA	240
ATCAGGAATT	TGAAGAAAAT	GGAGATGTTT	ACATTTTGTG	TGACGTGTAT	TTTCTACCC	300
CTCCTAAGAG	GGCAGAGTCT	CTTCACCTGT	GAACCAATTA	CTGTTCCAG	ATGTATGAAA	360
ATGGCTTACA	ACATGACCTT	TTTCCCTAAT	CTGATGGGTC	ATTATGACCA	GAGTATTGCC	420
GCGGTGGAAA	TGGAGCATTT	TCTTCTCTCT	GCAAACTCTG	AATGTTTACC	AAACATTGAA	480
ACTTTCCTCT	GCAAGACATT	TGTACCAACC	TGCATAGAAC	AAATTCATGT	GGTTCACCT	540
TGTCGTAAAC	TTTGTGAGAA	AGTATATTCT	GATTGCAAAA	AATTAATTGA	CACTTTGGG	600
ATCCGATGGC	CTGAGGAGCT	TGAATGTGAC	AGATTACAAT	ACTGTGATGA	GACTGTTCTT	660
GTAACCTTTG	ATCCACACAC	AGAATTTCTT	GGTCTCTAGA	AGAAAACAGA	ACAAGTCCAA	720
AGAGACATTG	GATTTTGGTG	TCCAAGGCAT	CTTAAGACTT	CTGGGGGACA	AGGATATAAG	780
TTTCTGGGAA	TTGACCAAGT	TGCGCCTCCA	TGCCCCCAACA	TGTATTTTAA	AAGTGATGAG	840
CTAGAGTTTG	CAAAAAGTTT	TATTGGAACA	GTTTCAATAT	TTTGTCTTTG	TGCAACTCTG	900
TTCACATTCC	TTACTTTTTT	AATTGATGTT	AGAAGATTCA	GATACCCAGA	GAGACCAATT	960
ATATATTACT	CTGTCTGTTA	CAGCATTTGA	TCTCTATGT	ACTTCATTGG	ATTTTGTCTG	1020
GGCGATAGCA	CAGCCTGCAA	TAAGGCAGAT	GAGAAGCTAG	AACCTGGTGA	CACGTGTTGC	1080
CTAGGCTCTC	AAAATAAGGC	TTGACCCGTT	TTGTTTCATG	TTTTGTATTT	TTTCAAAATG	1140
GCTGGCATTG	TGTGGTGGGT	GATTCTTACC	ATTACTTGGT	TCTTAGCTGC	AGGAAGAAAA	1200
TGGAGTTGTG	AAGCCATCGA	GCAAAAAGCA	GTGTGGTTTC	ATGCTGTTGC	ATGGGGAACA	1260
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GGAGTTTGCT	TTGTGGGCTT	TTATGACCTG	GATGCTTCTC	GCTACTTTGT	ACTCTTGCCA	1380
CTGTGCTTTT	GTGTGTTTGT	TGGGCTCTCT	CTTCTTTTAG	CTGGCATTAT	TTCTTAAAT	1440
CATGTTTCGAC	AAGTCATACA	ACATGATGGC	CGGAACCAAG	AAAAACTAAA	GAAATTTATG	1500
ATTTCGAATTG	GAGTCTTCAG	CGGCTTGAT	CTTGTGCCAT	TAGTGACACT	TCTCGGATGT	1560
TACGTCTATG	AGCAAGTGA	CAGGATTACC	TGGGAGATAA	CTTGGGTCTC	TGATCATTTG	1620
CGTCAGTACC	ATATCCCATG	TCCTTATCAG	GCAAAAAGCA	AAGCTCGACC	AGAATTGGCT	1680
TTATTTATGA	TAAAATACCT	GATGACATTA	ATTGTTGGCA	TCTCTGTGTT	CTTCTGGGTT	1740
GGAAGCAAAA	AGACATGCAC	AGAATGGGCT	GGGTTTTTTA	AACGAAATCG	CAAGAGAGAT	1800
CCAAATCAGT	AAAGTCGAAG	AGTACTACAG	GAATCATGTG	AGTTTTTCTT	AAAGCAATAT	1860
TCTAAAGTTA	AACACAAAAG	GAAGCACTAT	AAACCAAGTT	CACACAAGCT	GAAGGTCATT	1920
TCCAAATCCA	TGGGAACGAG	CACAGGAGCT	ACAGCAAAATC	ATGGCACTTC	TGCAGTAGCA	1980
ATTACTAGCC	ATGATTACCT	AGGACAAGAA	ACTTTGACAG	AAATCCAAAC	CTCACCAGAA	2040
ACATCAATGA	GAGAGGTGAA	AGCGGACGGA	GCTAGCACCC	CCAGGTTAAG	AGAACAGGAC	2100
TGTGGTGAAC	CTGCCCTGCG	AGCAGCATCC	ATCTCCAGAC	TCTCTGGGGA	ACAGGTTCGAC	2160
GGGAAGGGCC	AGGCAGGCG	TGTATCTGAA	AGTGCGCGGA	GTGAAGGAAG	GATTAGTCCA	2220
AAGAGTGATA	TTACTGACAC	TGGCCTGGCA	CAGAGCAACA	ATTTGCAGGT	CCCCAGTTCT	2280
TCAGAACCAA	GCAGCCTCAA	AGGTTCCACA	TCTCTGCTTG	TTCAACCCAGT	TTCAGGAGTG	2340
AGAAAAGAGC	AGGGAGGTGG	TTGTCTATCA	GATACTTGAA	GAACATTTTC	TCTCGTTACT	2400
CAGAAAGCAA	TTTGTGTTAC	ACTGGAAGTG	ACCTATGCAC	TGTTTTGTAA	GAATCACTGT	2460
TACGTTCTTC	TTTTGCACCT	AAAGTTGCAT	TGCCTACTGT	TATACTGGAA	AAAATAGAGT	2520
TCAAGAATAA	TATGACTCAT	TTCACACAAA	GGTTAATGAC	AACATATATC	CTGAAAAACG	2580
AAATGTGCAG	GTTAATAATA	TTTTTTTAAAT	AGTGTGGGAG	GACAGAGTTA	GAGGAATCTT	2640
CCTTTTCTAT	TTATGAAGAT	TCTACTCTTG	GTAAGAGTAT	TTTAAGATGT	ACTATGCTAT	2700
TTTACCTTTT	TGATATAAAA	TCAAGATATT	TCTTTGCTGA	AGTATTTAAA	TCTTATCTCT	2760
GTATCTTTT	ATACATATTT	GAAAATAAGC	TTATATGTAT	TTGAACTTTT	TTGAAATCCT	2820
ATTCAGATAT	TTTTATCATG	CTATTGTGAT	ATTTTAGCAC	TTTGGTAGCT	TTTACACTGA	2880
ATTTCTAAGA	AAATTGTATA	ATAGTCTTCT	TTTATACTGT	AAAAAAGAT	ATACCAAAAA	2940
GTCTTATAAT	AGGAATTTAA	CTTTAAAAAC	CCACTTATTG	ATACCTTACC	ATCTAAAAATG	3000
TGTGATTTT	ATAGTCTCGT	TTTAGGAATT	TCACAGATCT	AAATTTATGA	ACTGAAATAA	3060
GGTGCTTACT	CAAGAGGTGT	CCACTATTGA	TGTATTATG	CTGCTCACTG	ATCCTTCTGC	3120
ATATTAAAAA	TAAATGTCC	TAAAGGGTTA	GTAGACAAAA	TGTTAGTCTT	TTGTATATTA	3180
GGCCAGGTGC	AATTGACTTC	CCTTTTTTAA	TGTTTCATGA	CCACCCATTG	ATTGTATTAT	3240
AACCACTTAC	AGTTGCTTAT	ATTTTGTGTT	TAACTTTTGT	TTTCTTAACA	TTTAGAATAT	3300
TACATTTTGT	ATTATACAGT	ACCTTTCTCA	GACATTTTGT	AG		

Seq ID NO: 651 Protein sequence
Protein Accession #: NP_003497.1

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 LECDRLLQYCD ETVPVTFDPH TEFLGPQKKT EQVQRDIGFW CPRHLKTSGG QGYKFLGIDQ 180
 CAPPCPNMYF KSDBLEFAKS FIGTVSIFCL CATLFTFLTF LIDVRRFRYP ERPIIYYSVC 240
 YSIVSLMYFI GFLGDSSTAC NKADKLELG DTVVLGSONK ACTVLFMLLY FFTMAGTVWW 300
 VILTTTWFLA AGRKWSCEAI EQKAVWFHAV AWGTPGFLTV MLLALNKVEG DNISGVCPVG 360
 LYDLDAASYF VLLPLCLCVF VGLSLLLAGI ISLNHVRQVI QHDGRNQEKI KKFMRIGVVF 420
 SGLYLVPLVT LLGCYVVEQV NRIWEITWV SDHCRQYHIP CPYQAKAKAR PELALFMIKY 480
 LMTLIVGISA VFWVGSKKT C TEWAGFFKRN RKRDPISER RVLQESCEFF LKHNSKVKHK 540
 KKHYKPSHHK LKVISKSMGT STGATANHGT SAVAITSHDY LGQETLTEIQ TSPETSMREV 600
 KADGASTPRL REQDCGEPAS PAASISRLSG EQVDCKGQAG SVSESARSEG RISPKSDITD 660
 TGLAQSNLQ VPSSSEPSL KGSTSLLVHP VSGVRKEQGG GCHSDT

Seq ID NO: 652 DNA sequence
 Nucleic Acid Accession #: NM_014791.1
 Coding sequence: 171..2126

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 TCCGCCCCCTC AGGTTCTTTT TCTAATTCCA AATAAACTTG CAAGAGGACT ATGAAAGATT 180
 ATGATGAAC TCTCAAATAT TATGAATTAC ATGAAACTAT TGGGACAGGT GGCTTTGCAA 240
 AGGTCAAAC TGCCTGCCAT ATCCTTACTG GAGAGATGGT AGCTATAAAA ATCATGGATA 300
 AAAACACACT AGGAGTGAT TTGCCCCGGA TCAAAACGGA GATTGAGGCC TTGAAGAACC 360
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 GTGGATTCTC ACCATTTGAT GATGATAATG TAATGGCTTT ATACAAGAAG ATTATGAGAG 840
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 CTACCACTAG ATTAGTGAA TCCAGATCAAC TGTTGAATGA AATAATGTCT ATTCTTCAA 1920
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 TGGGTATCAG GAGGCAGCG CTTAAGGGCG ATGCTGGGT TTACAAAAGA TTAGTGAAG 2100
 ACATCCTATC TAGCTGCAAG GTATAATTGA TGGATTCTTC CATCTGCCG GATGAGTGTG 2160
 GGTGTGATAC AGCCTACATA AAGACTGTTA TGATCGCTTT GATTTTAAAG TTCATTGAA 2220
 CTACCAACTT GTTTCTAAG AGCTATCTTA AGACCAATAT CTCTTTGTTT TTAACAAAA 2280
 GATATTATTT TGTGTATGAA TCTAAATCAA GCCCATCTGT CATTTATGTTA CTGTCTTTT 2340
 TAATCATGTG GTTTTGTATA TTAATAATTG TTGACTTTCT TAGATTCACT TCCATATGTG 2400
 AATGTAAGCT CTAACTATG TCTCTTTGTA ATGTGTAATT TCTTCTGAA ATAAACCAT 2460
 TTGTAATAT

Seq ID NO: 653 Protein sequence
 Protein Accession #: NP_055606.1

1 11 21 31 41 51
 | | | | |
 MKDYDELLKY YELHETIGTG GFAKVKLACH ILTGEMVAIK IMDKNTLGS DLPRIKTEIEA 60
 LKNLRHQHIC QLYHVLETAN KIFMVLEYCP GGELEFDYIIS QDRLESEETR VVFRQIVSAV 120
 AYVHSQGYAH RDLKPENLLF DEYHKLKID PGLCAKPKGN KDYLQTCG SLAYAAPELI 180
 QGKSYLGSEA DVWSMGILLY VLMCGFLPFD DDNVMALYKK IMRGKYDVPK WLSPPSILL 240
 QQMLQVDEPK RISMKNLLNH PWIMQDYNYP VEWQSKNPF IHLDDDCVTEL SVHHRNNRQT 300
 MEDLISLWQY DHLTATYLLL LAKKARGKPV RLRLSSFS CGQASATPFTDI KSNWNWLEDV 360
 TASDKNYVAG LIDYDWCEDD LSTGAATPRT SQFTKYWTES NGVESKSLTP ALCRTPANKL 420
 KNKENVYTPK SAVKNEEYFM FPEPKTPVNK NQHKREILTT PNRYTTPSKA RNQLCKETPI 480
 KIPVNSTGTD KLMTGVISPE RRCRSVELDL NQAHMEETPK RKGAKVFGSL ERGLDKVITV 540
 LTRSKRKGSA RDGPRRLKLH YNVTTTRLVN PDQLLNEIMS ILPKKHVDV KGYTLKCQT 600
 QSDFGKVTMQ FELEVCQLQK PDVVGIRQR LKGDWVYKR LVEDILSSCK V

Seq ID NO: 654 DNA sequence
 Nucleic Acid Accession #: NM_000582
 Coding sequence: 88..990

1 11 21 31 41 51
 | | | | |
 GCAGAGCACA GCATCGTCGG GACCAGACTC GTCTCAGGCC AGTTGCAGCC TTCTCAGCCA 60
 AACGCCGACC AAGGAAAAC CACTACCATG AGAATTGCAG TGATTGCTT TTGCTCCTA 120

GGCATCACCT GTGCCATACC AGTTAAACAG GCTGATTCTG GAAGTTCTGA GGAAAAGCAG 180
 CTTTACAACA AATACCCAGA TGCTGTGGCC ACATGGCTAA ACCCTGACCC ATCTCAGAAG 240
 CAGAATCTCC TAGCCCAACA GACCCCTCCA AGTAAGTCCA ACGAAAGCCA TGACCACATG 300
 GATGATATGG ATGATGAAGA TGATGATGAC CATGTGGACA GCCAGGACTC CATTGACTCG 360
 AACGACTCTG ATGATGTAGA TGACACTGAT GATTCTCACC AGTCTGATGA GTCTCACCAT 420
 TCTGATGAAT CTGATGAAC TGTCACTGAT TTTCCACCGG ACCTGCCAGC AACCGAAGTT 480
 TTCACTCCAG TTGTCCCCAC AGTAGACACA TATGATGGCC GAGGTGATAG TGTGGTTTAT 540
 GGACTGAGGT CAAAATCTAA GAAATTTTCG AGACCTGACA TCCAGTACCC TGATGTCTACA 600
 GACGAGGACA TCACCTCACA CATGGAAGC GAGGAGTTGA ATGGTGCATA CAAGGCCATC 660
 CCCGTTGCCC AGGACCTGAA CGCGCCTTCT GATTGGGACA GCCGTGGGAA GGACAGTTAT 720
 GAAACGAGTC AGCTGGATGA CCAGAGTGCT GAAACCCACA GCCACAAGCA GTCAGATTA 780
 TATAAGCGGA AAGCCAATGA TGAGAGCAAT GAGCATTCCG ATGTGATGTA TAGTCAGGAA 840
 CTTTCCAAAG TCAGCCGTGA ATTCCACAGC CATGAATTTC ACAGCCATGA AGATATGCTG 900
 GTTGTAGACC CCAAAGTAA GGAAGAAGAT AAACACCTGA AATTTCGTAT TTCTCATGAA 960
 TTAGATAGTG CATCTTCTGA GGTCAATTAA AAGGAGAAAA AATACAATTT CTCACTTTGC 1020
 ATTTAGTCAA AAGAAAAAAT GCTTTATAGC AAAATGAAAG AGAACATGAA ATGCTTCTTT 1080
 CTCAGTTTAT TGGTTGAATG TGTATCTATT TGAGTCTGGA AATAACTAAT GTGTTTGATA 1140
 ATTAGTTTAG TTTGTGGCTT CATGGAAACT CCCTGTAAC TAAAAGCTTC AGGGTTATGT 1200
 CTATGTTTAT TCTATAGAAG AAATGCAAAAC TATCACTGTA TTTTAATATT TGTATTCTC 1260
 TCATGAATAG AAAATTTATG AGAAGCAAAAC AAAATACTTT TACCCACTTA AAAAGAGAAT 1320
 ATAACATTTT ATGTCACATAT AATCTTTTGT TTTTAAAGTT AGTGTATATT TTGTTGTGAT 1380
 TATCTTTTGT TGGTGTGAAT AAATCTTTTA TCTTGAATGT AATAAGAATT TGGTGGTGTC 1440
 AATTGCTTAT TTGTTTCCC ACGGTGTGCC AGCAATTAAT AAAACATAAC CTTTTTTACT 1500
 GCCTAAAAAA AAAAAAATAA AAAA

Seq ID NO: 655 Protein sequence
 Protein Accession #: NP_000573

1 11 21 31 41 51
 | | | | |
 MRIAVICFCL LGITCAIPVK QADSGSSEK QLYNKYPDAV ATWLNPDPSQ KQNLAPQTL 60
 PSKSNESHHD MDDMDDEDD DHVDSQDSID SNDSDDVDDT DDSHQSDSH HSDESEDLVT 120
 DFPTDLPAE VFTPVVPTVD TYDGRGDSVV YGLRSKSKKF RRPDIQYFDA TDEDITSHME 180
 SEELNGAYKA IPVAQDLNAP SDWDSRGKDS YETSQLDDQS AETHSHKQSR LYKRKANDES 240
 NEHSDVIDSQ ELSKVSREHF SHEFHSHEDM LVVDFPKSKEE DKHLKFRISH ELDSASSEVN

Seq ID NO: 656 DNA sequence
 Nucleic Acid Accession #: NM_003108.1
 Coding sequence: 76..1401

1 11 21 31 41 51
 | | | | |
 GGGGTGGGAG GGGGAGGGGG ACCTCCGCAC GAGACCCAGC GGCCCGGGTT GGAGCGTCCA 60
 GCCCTGCAAC GGATCATGGT GCAGCAGGCG GAGAGCTTGG AAGCGGAGAG CAACCTGCCC 120
 CGGGAGGCGC TGGACACGGA GGAGGGCGAA TTCATGGCTT GCAGCCCGGT GGCCCTGGAC 180
 GAGAGCGACC CAGACTGGTG CAAGACGGCG TCGGGCCACA TCAAGCGGCC GATGAACGCG 240
 TTCATGGTAT GGTCCAAGAT CGAACGCGAG AAGATCATGG AGCAGTCTCC GGACATGCAC 300
 AACGCCGAGA TCTCCAAGAG GCTGGGCAAG CGCTGGAAAA TGCTGAAGGA CAGCGAGAAG 360
 ATCCCGTTCA TCCGGGAGGC GGAGCGGCTG CGGCTCAAGC ACATGGCCGA CTACCCCGAC 420
 TACAAGTACC GGCCCCGGAA AAAGCCCAAA ATGGACCCCT CGGCCAAGCC CAGCGCCAGC 480
 CAGAGCCAG AGAAGAGCGC GGCCGGCGGC GGCGGCGGGA GCGCGGGCGG AGGCGCGGGC 540
 GGTGCAAGA CCTCCAAGG CTCCAGCAAG AAATGCGGCA AGCTCAAGGC CCCGCGGGC 600
 GCGGGCGCCA AGGCGGGCGC GGGCAAGGCG GCCCAGTCCG GGGACTACGG GGGCGCGGGC 660
 GACGACTACG TGCTGGGCG CCGTGGCGTG AGCGGCTCGG GCGGCGGCGG CGCGGGCAAG 720
 ACGGTCAAGT GCGTGTCTCT GGATGAGGAC GACGACGACG ACGACGACGA CGACGAGCTG 780
 CAGCTGCAGA TCAACACAGA GCCCGACGAG GAGGACGAGG AACCAACGCA CCAGCAGCTC 840
 CTGCAGCCGC CGGGCGGCGC GCGGTGCGAG CTGCTGAGAC GCTACAACGT CGCCAAAGTG 900
 CCCGCCAGCC CTACGCTGAG CAGCTCGGCG GAGTCCCCCG AGGGAGCGAG CCTCTACGAC 960
 GAGGTGCGGG CCGGCGCGAC CTCGGGCGCC GGGGGCGGCA GCGGCTCTA CTACAGCTTC 1020
 AAGAACATCA CCAAGCAGCA CCCGCGCGCG CTCGCGCAGC CCGCGCTGTC GCCCGCTGCC 1080
 TCGCGCTCGG TGTCCACCTC CTCGTCCAGC AGCAGCGGCA GCAGCAGCGG CAGCAGCGGC 1140
 GAGGACGCGC ACGACCTGAT GTTCGACCTG AGCTTGAATT TCTCTCAAAG CGCGCACAGC 1200
 GCCAGCGAGC AGCAGCTGGG GGGCGGCGCG GCGGCGCGGA ACCTGTCCCT GTCGCTGGTG 1260
 GATAAGGATT TGGATTCGTT CAGCGAGGCG AGCCTGGGCT CCCACTTCGA GTTCCCGGAC 1320
 TACTGCACGC CGGAGCTGAG CGAGATGATC GCGGGGACT GGCTGGAGGC GAACTTCTCC 1380
 GACCTGGTGT TCACATATTG AAAGGCGCCC GCTGCTCGCT CTTTCTCTCG GAGGGTGCAG 1440
 AGCTGGGTTC CTTGGGAGGA AGTTGTAGTG GTGATGATGA TGATGATGAT AATGATGATG 1500
 ATGATGGTGG TGTGTATGGT GCGGTGGTA GGGTGGAGGG GAGAGAAGAA GATGCTGATG 1560
 ATATTGATAA GATGTCGTGA CGCAAAGAAA TTGGAAGAAA TGATGAAAT TTTGGTGGAG 1620
 TTAAAGTGAA ATGAGTAGTT TTTAAACATT TTTCTGTCC TTTTCTGTG CCCCCTCCCT 1680
 TCCTTTATCG TGTCTCAAGG TAGTTGCATA CCTAGTCTGG AGTTGTGATT ATTTTCCCAA 1740
 AAAATGTGTT TTTGTAATTA CTATTCTTT TTCCTGAAAT TCGTGATTGC AACAAAGGCA 1800
 GAGGGGGCGG CGCGGCGGAG GGGAGGTAGG ACCCGCTCCG GAAGGCGCTG TTTGAAGCTT 1860
 GTCGGTCTTT GAAGTCTGGA AGACGTCTGC AGAGGACCTT TTTGGCAGCA CAACTGTTAC 1920
 TCTAGGGAGT TGGTGGAGAT ATTTTTTTTT CTTAAGAGAA CTTAAGAAC TGGTGATTTT 1980
 TTTTAAACAA AAAAAGGG

Seq ID NO: 657 Protein sequence
 Protein Accession #: NP_003099.1

1 11 21 31 41 51
 | | | | |
 MVQQAESLEA ESNLPREALD TEEGEFMACS PVALDESDDP WCKTASGHIK RPMNAPMVWS 60
 KIERRKIMEQ SPDMHNAEIS KRLGKRWKML KDSEKIPFIR EAERLRLKHM ADYDPYKYRP 120
 RKKPKMDPSA KPSASQSPBK SAAGGGGSSA GGGAGGAKTS KGSKKCGKL KAPAAAGAKA 180
 GAGKAAQSGD YGGAGDDYVL GSLRVSGSGG GGAGKTVKCV FLDEDDDDDD DDELDLQIK 240

QEPDEDEREP PHQQLLQPPG QPQSLLRRY NVAKVPASPT LSSSAESPEG ASLYDEVVRAG 300
 ATSGAGGGSR LYYSFKNITK QHPPLAQA LSPASSRSVS TSSSSSSGSS SGSSGEDADD 360
 LMFDSLNFPS QSAHSASEQQ LGGGAAGNL SLSLVDKLDL SFSEGLGSH FEPDYCTPE 420
 LSEMIAGDWL EANFSDLVFT Y

Seq ID NO: 658 DNA sequence
 Nucleic Acid Accession #: NM_001719
 Coding sequence: 123..1418

1 11 21 31 41 51
 | | | | |
 GGGCGCAGCG GGGCCCGTCT GCAGCAAGTG ACCGACGGCC GGGACGGCCG CCTGCCCCCT 60
 CTGCCACCTG GGGCGGTGCG GGCCCGGAGC CCGAGGCCCG GGTAGCGCGT AGAGCCGCGC 120
 CGATGCACGT GCGCTCACTG CGAGCTGCGG CGCCGCACAG CTTCTGTGCG CTCTGGGCAC 180
 CCCTGTTTCT GCTGCGCTCC GCCCTGGCCG ACTTCAGCCT GGACAACGAG GTGCACCTCGA 240
 GCTTCATCCA CCGCGCCTCC CGCAGCCAGG AGCGCGGGA GATGCAGCGC GAGATCCTCT 300
 CCAATTTTGGG CTTGCCCCAC CGCCCGCGCC CGCACCTCCA GGGCAAGCAC AACTCGGCAC 360
 CCATGTTTCT GCTGGACCTG TACAACGCCA TGGCGGTGGA GGAGGGCGGC GGGCCCGCGC 420
 GCCAGGGCTT CTCCTACCCC TACTCAGTAC CCAGGGCCCC CCTCTGGCCA 480
 GCCTGCAAGA TAGCCATTTC CTACCCGACG CCGACATGGT CATGAGCTTC GTCAACCTCG 540
 TGGAAACATGA CAAGGAATTC TTCCACCCAC GCTACCACCA TCGAGAGTTC CGGTTTGATC 600
 TTTTCAAGAT CCCAGAAGGG GAAGCTGTCA CGGCAGCCGA ATTCCGGATC TACAAGGACT 660
 ACATCCGGGA ACGCTTCGAC AATGAGACGT TCCGGATCAG CGTTTATCAG GTGCTCCAGG 720
 AGCACTTGGG CAGGAATTCG GATCTCTTCC TGCTCGACAG CCGTACCCTC TGGGCTCCGG 780
 AGGAGGGCTG GCTGGTGTTC GACATCAGAG CCACCCAGCA CCACTGGGTG GTCAATCCGC 840
 GGCACAACCT GGGCCTGCAG CTCTCGGTGG AGACGCTGGA TGGGCAGAGC ATCAACCCCA 900
 AGTTGGCGGG CCTGATTTGG CGGCACGGGC CCCAGAACAA CGAGCCCTTC ATGGTGGCTT 960
 TCTTCAAGCG CACGGAGTTC CACTTCGCGA GCATCCGGTC CACGGGGAGC AAACAGCGCA 1020
 GCCAGAACCG CTCAAGACG CCCAAGAACC AGGAAGCCCT GCGGATGGCC AACGTGGCAG 1080
 AGAACAGCAG CAGCGACCAG AGGCAGGCCT GTAAGAAGCA CGAGCTGTAT GTCAGCTTCC 1140
 GAGACCTGGG CTGGCAGGAC TGGATCATCG CGCCTGAAGG CTACGCCGCC TACTACTGTG 1200
 AGGGGGAGTG TGCCTTCCTT CTGAACCTCT ACATGAACGC CACCAACCAC GCCATCGTGC 1260
 AGACGCTGGT CCATTCATC AACCOCGAAA CGGTGCCCAA GCCCTGTCTGT GCGCCACGCG 1320
 AGCTCAATGC CATCTCCGTC CTCTACTTCG ATGACAGCTC CAACGTCATC CTGAAGAAAT 1380
 ACAGAAACAT GGTGGTCCGG GCCTGTGGCT GCCACTAGCT CACTCCGAGAA TTCAGACCTT 1440
 TTGGGGCCAA GTTTTCTCGG ATCTCTCCAT GCTCGCCTTG GCCAGGAACC AGCAGACCAA 1500
 CTGCCCTTTG TGAGACCTTC CCTCCCTAT CCCCAACTTT AAAGTGTGA GAGTATTAGG 1560
 AAACATGAGC AGCATATGGC TTTTGATCAG TTTTTCAGTG GCAGCATCCA ATGAACAAGA 1620
 TCCTACAAGC TGTGCAGGCA AAACCTAGCA GGAAAAAACA ACAACGCATA AAGAAAAATG 1680
 GCCGGGCCAG GTCATTGGCT GGGGAAGTCT AGCCATGCAC GGACTCGTTT CCAGAGGTAA 1740
 TTATGAGCGC CTACCAGGCA GGCCACCCAG CCGTGGGAGG AAGGGGGCGT GGCAAGGGGT 1800
 GGGCACAATT GTGTCTGTGC GAAAGGAAAA TTGACCCGGA AGTTCTGTGA ATAAATGTCA 1860
 CAATAAACCG AATGAATG

Seq ID NO: 659 Protein sequence
 Protein Accession #: NP_001710

1 11 21 31 41 51
 | | | | |
 MHVRSRAAA PHSFVALWAP LFLRLSALAD FSLDNEVHSS FIHRLRSQE RREMQRILS 60
 ILGLPHRPRP HLQGHNSAP MFMLDLYNAM AVEEGGGPGG QGFSYPYKAV FSTQGPPLAS 120
 LQDSHFLEDA DMVMSFVNLV EHDKEFFPHR YHREFRFDL SKIPEGEAVT AAEFRIYKDY 180
 IRERDNETF RISVYQVLQE HLGRESDLFL LDSRLWASE EGWLVDITA TSNHWVNNPR 240
 HNLGLQLSVE TLDGQSINPK LAGLIGRHCP QNKQPFMVAF FKATEVHFPS IRSTGSKQRS 300
 QNRSKTPKNQ EALRMANVAE NSSSDQRQAC KKHLYVSFR DLGWQDWIIA PEGYAAYYCE 360
 GECAFPLNSY MNATNHAIVQ TLVHFINFET VPKPCCAPTQ LNAISVLVFD DSSNVILKKY 420
 RNMVVRACGC H

Seq ID NO: 660 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 211..1895

1 11 21 31 41 51
 | | | | |
 GGATCTGAGG GGCGCCAGT CACTTCCTCC ACGTTCTCGT GCTGGGCGGG AGGAGCGGAT 60
 GGGGCTTGGG AGGCAGCCTG CTCTCCAGTC CCTATCCACC CACAGGTTT TTGGGTCGGA 120
 GAGGAATTAT CTGATAAAAT TCCTGGGTTA ATATTTTAA AAACGGAGAG TTTTAAAAA 180
 TGATTTTTTT CCCTCGAAAA TGACCTTTT ATGCTTCGAA GCAGTTTGTC AACCAGCATA 240
 GTGCTTTTTC TTTTCTCTTC TTTTCTACG ATAAATGAAA GCATTTCTTC AAGAAAAAGG 300
 CACAGGTTCC TTGAACAGCT GGATCTGAT GGCACCATTA CTATAGAGGA GCAGATTGTC 360
 CTTGTGCTGA AAGCGAAAGT ACAATGTGAA CTCACATCA CAGCTCAACT CCAGGAGGGA 420
 GAAGGTAATT GTTCCCTGTA ATGGGATGGA CTCATTTGTT GGCCAGAGG AACAGTGGGG 480
 AAAATATCGG CTGTCCATG CCTCCTTAT ATTTATGACT TCAACCATAA AGGAGTTGCT 540
 TTCCGACACT GTAACCCCA TGAACATGG GATTTTATGC ACAGCTTAAA TAAACATGG 600
 GCCAATTATT CAGACTGCCT TCGCTTTCTG CAGCCAGATA TCAGCATAGG AAAGCAAGAA 660
 TTCTTTGAAC GCCTCTATGT AATGTATACC GTTGGCTACT CCATCTCTTT TGGTTCCTTG 720
 GCTGTGGCTA TCTCATCAT TGGTTACTTC AGACGATTGC ATTGCACTAG GAACTATATC 780
 CACATGCACT TATTTGTGTC TTTTATGCTG AGAGCTACAA GCATCTTTGT CAAAGACAGA 840
 GTAGTCCATG CTCACATAGG AGTAAAGGAG CTGGAGTCCC TAATAATGCA GGATGACCCA 900
 CAAAATCCA TTGAGGCCAAC TTCTGTGGAC AAATCACAAT ATATCGGGTG CAAGATTGCT 960
 GTTGTGATGT TTATTTACTT CCTGGCTACA AATTATTATT GGATCCTGGT GGAAGGTCTC 1020
 TACCTGCATA ATCTCATCTT TGTGGCTTTC TTTTCGGACA CCAATACTT GTGGGGCTTC 1080
 ATCTTGATAG GCTGGGGGTT TCCAGCAGCA TTTGTGTCAG CATGGGCTGT GGCACGAGCA 1140
 ACTCTGGCTG ATGCGAGGTG CTGGGAACCT AGTGTCTGAG ACATCAAGTG GATTATCAA 1200
 GCACCGACT TAGCATCTAT TGGGCTGAAT TTTATCTGT TTCTGAATAC GGTTAGAGTT 1260
 CTAGCTACCA AAATCTGGGA GACCAATGCA GTTGGGCATG ACACAAGGAA GCAATACAGG 1320
 AAATGGCCA AATCGACACT GGTCTGTGTC CTAGTCTTTG GAGTGCATTA CATCGTGTTC 1380

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GTATGCCTGC CTCACCTCCTT CACTGGGCTC GGGTGGGAGA TCCGCATGCA CTGTGAGCTC 1440
 TTCTTCAACT CCTTTCAGGG TTTCTTTGTG TCTATCATCT ACTGCTACTG CAATGGAGAG 1500
 GTTCAGGCAG AGGTGAAGAA GATGTGGAGT CGGTGGAATC TCTCCGTGGA CTGGAAAAGG 1560
 ACACGCCCAT GTGGGAGCCG CAGATGCGCG TCAGTGCTCA CCACCGTGAC GCACAGCACC 1620
 AGCAGCCAGT CACAGGTGGC GGCCAGCACA CGCATGGTGC TTATCTCTGG CAAAGCTGCC 1680
 AAGATCGCCA GCAGACAGCC TGACAGCCAC ATCACTTTAC CTGGCTATGT CTGGAGTAAC 1740
 TCAGAGCAGG ACTGGCTGCC ACACCTCTTC CACGAGGAGA CCAAGGAAGA TAGTGGGAGG 1800
 CAGGAGATG ATATTCTAAT GGAGAAGCCT TCCAGGCCTA TGAATCTAA CCCAGACACT 1860
 GAAGGATGCC AAGGAGAAAC TGAGGATGTT CTCTGA

Seq ID NO: 661 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MLRSSLSSTSI VLFLFSSFSST INESSRKR HRFLEQLDSD GTITIEEQIV LVLKAKVQCE 60
 LNITAQLQEG EGNCFPEWDG LICWPRGTVG KISAVPCPPY IYDFNHKGVA FRHCNPNGTW 120
 DFMHSLNKTW ANYSDCLRFL QPDISIGKQE FFERLYVMYT VGYISFSGSL AVAILIIGYF 180
 RRLHCTRNYY HMLFVSFML RATSIFVKDR VVHAHIGVKE LESLIMQDDP QNSIEATSVD 240
 KSQYIGCKIA VVMFYFLAT NYIWLVEGL YLHNLIFVAF FSDTKYLWGF ILIGWGFPA 300
 FVAAWAVARA TLADARCWEL SAGDIKWIYQ ABILAAIGLN FILFLNTVRV LATKIWETNA 360
 VGHDTRKQYR KLAKSTLVLV LVFGVHYIVF VCLPHSFTGL GWEIRMHCEL FFNSFQGFV 420
 SIIYCYCNGE VQAEVKMWS RWNLSVDWKR TPPCGRRCG SVLTTVTHTS SSQSQVAAS 480
 RMVLISGKAA KIASRQPDH ITLPGYVWSN SEQDCLPHSF HEETKEDEGR QGDDILMEKP 540
 SRPMESNPDT EGCQGETEDV L

Seq ID NO: 662 DNA sequence
 Nucleic Acid Accession #: NM_005048
 Coding sequence: 143..1795

1 11 21 31 41 51
 GGCCGGTGGC CCGGGCCCGA CCACCCAGC TGCGCGTCGT TACTGGCCAC AAGTTTGCTC 60
 TGGGCCAGCC AAGTTGGCAA CTTGGAAGCT TCTCCCGGGC TCTGGAGGAG GGTCCCTGCT 120
 TCTTCTTACA GCCGTTCGGG GCATGGCCGG GCTGGGGGCG TCGCTCCACG TCTGGGGTTG 180
 GCTAATGCTC GGCAGCTGCC TCCTGGCCAG AGCCAGCTG GATTCTGATG GCACCATTAC 240
 TATAGAGGAG CAGATTGTCT TGTGCTGAA AGCGAAAGTA CAATGTGAAC TCAACATCAC 300
 AGCTCAACTC CAGGAGGAG AAGGTAATTG TTTCCCTGAA TGGGATGGAC TCATTGTGTG 360
 GCCCAGAGGA ACAGTGGGGA AAATATCGGC TGTTCATGCT CCTCCTTATA TTTATGACTT 420
 CAACCATAAA GGAGTTGCTT TCCGACACTG TAACCCCAAT GGAACATGGG ATTTTATGCA 480
 CAGCTTAAAT AAAACATGGG CCAATTATTC AGACTGCCTT CGCTTCTGCG AGCCAGATAT 540
 CAGCATAGGA AAGCAAGAAT TCTTTGAACG CCTCTATGTA ATGTATACCG TTGGCTACTC 600
 CATCTCTTTT GGTTCCTTGG CTGTGGCTAT TCTCATCATT GGTACTTCA GACGATTGCA 660
 TTGCACTAGG AACTATATCC ACATGCACTT ATTTGTGTCT TTCATGTGTA GAGCTACAA 720
 CATCTTTGTC AAAGACAGAG TAGTCCATGC TCACATAGGA GTAAAGGAGC TGGAGTCCCT 780
 AATAATGCAG GATGACCCAC AAAATTCAT TGAGGCAACT TCTGTGGACA AATCACAATA 840
 TATCGGGTGC AAGATTGCTG TTGTGATGTT TATTTACTTC CTGGCTACAA ATTATTATG 900
 GATCTGTGTC GAAGGTCTCT ACCTGCATAA TCTCATCTTT GTGGCTTTCT TTTCCGACAC 960
 CAAATACCTG TGGGGCTTCA TCTTGATAGG CTGGGGGTTT CCAGCAGCAT TTGTGTCAGC 1020
 ATGGGCTGTG GCACGAGCAA CTCTGGCTGA TGCGAGGTGC TGGGAACCTA GTGCTGGAGA 1080
 CATCAAGTGG ATTTATCAAG CACCGATCTT AGCAGCTATT GGGCTGAATT TTATTCTGTT 1140
 TCTGAATACG GTTAGAGTTC TAGCTACCAA AATCTGGGAG ACCAATGCAG TTGGGCATGA 1200
 CACAAGGAAG AACTACAGGA AACTGGCCAA ATCGACACTG GTCCTGGTCC TAGTCTTTGG 1260
 AGTGCAATAC ATCGTGTTCG TATGCCTGCC TCACTCCTTC ACTGGGCTCG GGTGGGAGAT 1320
 CCGCATGCAC TGTGAGCTCT TCTTCAACTC CTTTCAGGGT TTCTTTGTGT CTATCATCTA 1380
 CTGCTACTGC AATGGAGAGG TTCAGGCAGA GGTGAAGAAG ATGTGGAGTC GGTGGAATCT 1440
 CTCCTGTGAC TGGAAAAGGA CACCGCCATG TGGCAGCCGC AGATCGCGCT CAGTGCTCAC 1500
 CACCGTGACG CACAGCACC ACGAGCATC ACAGGTGGCG GCCAGCACAC GCATGGTGCT 1560
 TATCTCTGGC AAAGCTGCCA AGATCGCCAG CAGACAGCCT GACAGCCACA TCACTTTACC 1620
 TGGCTATGTC TGGAGTAAT CAGAGCAGGA CTGCTGCCA CACTCTTTCC ACGAGGAGAC 1680
 CAAGGAAGAT AGTGGGAGGC AGGGAGATGA TATTCTAATG GAGAAGCCTT CCAGGCCATAT 1740
 GGAATCTAAC CCAGACACTG AAGGATGCCA AGGAGAAACT GAGGATGTTC TCTGAATGGA 1800
 CATTTGTGGC TGACTTTTCAT GGGCTGGTCC AATGGCTGGT TGTGTGAGAG GGCTTGGCTG 1860
 ATACTCCTAT GCTTGAGTTC AAAGGCTGAA AATTCACTTA AGGTGTTACT TAATAATAGT 1920
 TTTTAGGCTC CATGAATTGG CTCCTGTAAA TACTAACGAC ATGAAAATGC AAGTGTCAAT 1980
 GGAGTAGTTT ATTACCTTCT ATTGGCATCA AGTTTTCTCT TAAATTAATG TATGGTATTT 2040
 GCTCTGTGAT TGTTCATTTT TTTCTGCTAC TTTTGGGTAG AAAAAAGATT CAATTGCTTG 2100
 GCTGTAGCTT TCTCTCATAT ATATCACCTT AAATATAATG AAGATCTTTT AGTGTGTATC 2160
 ATTTTCTTTT TAGAACTAG TATTCTCTTA TTTCTTACTT TAATGTACTT CTATCACTGC 2220
 ATTTATTTTG CCTGTGCATA GGAGCAATTA GGATCTAAAA AAATATATGG GAAGATAAAA 2280
 GATCTAAGAA CAAGTACTTG CTGGAAAAAT AGTTGGCTGG ACATTGATAA AATAATGCAT 2340
 TTATAACAAT TACATGTGTT TTTGGGAACA AGGAAAAATT CTCAAAAAAG AATATTTTAC 2400
 ACATCCCTTC TTTTGAATGG CCTCTTTGTG ACCAGCCAGA CCTCAGGTCT TCACTCTTTC 2460
 TTCTTTGTAA AGCATGTCTAT GTGGAAAGAT TTCCTCAGTT AGTGAGCTTG TGTCTGCAAA 2520
 TTGATTTTGT TTGTAATGTA TTTTGATAGC AAATCATGCT GCATCTATAT CTTTTTCTTG 2580
 TTTGAGCTGT TACTACATTT TACATGGCAT GTGGGATCAA TTAATAATTT GTTTTAAAAA 2640
 T

Seq ID NO: 663 Protein sequence
 Protein Accession #: NP_005039

1 11 21 31 41 51
 MAGLGASLHV WGLWMLGSCL LARAQLDSDG TITIEEQIVL VLKAKVQCEL NITAQLQEGE 60
 GNCFFPEWDGL ICWPRGTVGK ISAVPCPPYI YDFNHKGVA RHCNPNGTWD FMHSLNKTWA 120
 NYSDCLRFLO PDISIGKQEF FFERLYVMYT VGYISFSGSLA VAILIIGYFR RLHCTRNYYH 180
 MHLFVSFMLR ATSIFVKDRV VHAHIGVKEL ESLIMQDDPQ NSIEATSVDK SQYIGCKIAV 240

VMFYFLATN YYWILVEGLY LHNLIFFVAFF SDTKYLWGF IIGWGFPAAF VAAWAVARAT 300
 LADARCWELS AGDIKWIYQA PILAAIGLNF ILFLNIVRVL ATKIWETNAV GHDTRKQYRK 360
 LAKSTLVLVL VFGVHYIVFV CLPHSFTGLG WEIRMHCELF FNSFQGFVS IIYCYCNGEV 420
 QAEVKMWSR WNLVDWKRT PPCGSRRCGS VLT'TVTHSTS SQSQVAASR MVLISGKAAK 480
 IASRQPDHSI TLPGVVWSNS EQDCLPHSFH BETKEDSGRQ GDDILMEKPS RPMESNPDTE 540
 GCQGETEDVL

Seq ID NO: 664 DNA sequence
 Nucleic Acid Accession #: NM_012152
 Coding sequence: 43..1104

1 11 21 31 41 51
 CTTCTTTAAA TTTCTTTCTA GGATGTTTAC TTCTTCTCCA CAATGAATGA GTGTCACTAT 60
 GACAGACACA TGGACTTTTT TTATAATAGG AGCAACACTG ATACTGTGCA TGA CTGGACA 120
 GGAACAAAGC TTGTGATTGT TTTGTGTGTT GGGACGTTTT TCTGCCTGTT TATTTTTTTT 180
 TCTAATCTCT TGGTCATCGC GGCAGTGATC AAAACAGAAA AATTTCATT CCCCTTCTAC 240
 TACCTGTTGG CTAATTTAGC TGCTGCCGAT TTCTTCGCTG GAATTGCCTA TGTATTCTCTG 300
 ATGTTTAACA CAGGCCAGT TTCAAAAAC TTGACTGTCA ACCGCTGGTT TCTCCGTCAG 360
 GGGCTTCTGG ACAGTAGCTT GACTGCTTCC CTCACCAACT TGCTGGTTAT CGCCGTGGAG 420
 AGGCACATGT CAATCATGAG GATGCGGGTC CATAGCAACC TGACCAAAA GAGGGTGACA 480
 CTGCTCATTT TGCTTGTCTG GGCCATCGCC ATTTTATAGG GGGCGGTCCC CACACTGGGC 540
 TGGATTGCCC TCTGCAACAT CTCTGCCCTG TCTTCCCTGG CCCCATTTA CAGCAGGAGT 600
 TACCTTGTGT TCTGGACAGT GTCCAACTTC ATGGCCTTCC TCATCATGTT TGTGGTGATC 660
 CTGCGGATCT ACGTGATCGT CAAGAGGAAA ACCAACGTCT TGTCTCCGCA TACAAGTGGG 720
 TCCATCAGCC GCCGGAGGAC ACCCATGAAG CTAATGAAGA CGGTGATGAC TGTCTTAGGG 780
 GCGTTTGTGG TATGTGTGAG CCGGGCCCTG GTGGTTCTGC TCCTCGACGG CCTGAAGTGC 840
 AGGCAGTGTG GCGTCGACGA TGTGAAAAGG TGGTTCCTGC TGCTGGCGCT GCTCAACTCC 900
 GTCGTGAACC CCATCATCTA CTCCTACAA GACGAGGACA TGTATGGCAC CATGAAGAAG 960
 ATGATCTGCT GCTTCTCTCA GGAGAACCCA GAGAGGCGTC CCTCTCGCAT CCCCTCCACA 1020
 GTCCTCAGCA GGAGTGACAC AGGCAGCCAG TACATAGAGG ATAGTATTAG CCAAGGTGCA 1080
 GTCTGCAATA AAAGCACTTC CTAAACTCTG GATGCCTCTC GGCCCAACCA GGTGATGACT 1140
 GTCTTAGG

Seq ID NO: 665 Protein sequence
 Protein Accession #: NP_036284

1 11 21 31 41 51
 MNECHYDKHM DFFYNRSNTD TVDDWTGTKL VIVLCVGTFF CLFIFFSNLS VIAAVIKNRK 60
 PHFPFYLLA NLAAADFFAG IAYVFLMFT GPVSKTLTVN RWFLRQGLLD SSLTASLTNL 120
 LVIAVERHMS IMRMVRHNSL TKKRVTLLIL LVWAIAMFMG AVPTLGNWCL CNISACSSLA 180
 PIYSRSLVF WTVSNLMAFL IMVVYLRIRI VYVKKRKNVL SPHTSGSISR RRTPMKLMKT 240
 VMTVLGAFFV CWTPLGLVLL LDGLNCRQCG VQHVKRWFL LALLNSVNP IIYSYKDEDM 300
 YGTMKKMICC FSQENPERRP SRIPSTVLSR SDTGSQYIED SISQGAVCNK STS

Seq ID NO: 666 DNA sequence
 Nucleic Acid Accession #: NM_002821
 Coding sequence: 150..3362

1 11 21 31 41 51
 AACTCCCGCC TCGGGACGCC TCGGGGTCGG GCTCCGGCTG CGGCTGCTGC TCGCGCGCCC 60
 GCGCTCCGGT GCGTCCGCTT CCTGTGCCG CCGCGAGCA GTCTGCGGCC CGCGTGCAGC 120
 CCTCAGCTCC TTTTCTGAG CCCGCCGCGA TGGGAGCTGC GCGGGGATCC CCGGCCAGAC 180
 CCCGCCGGTT GCCTCTGCTC AGCGTCTGCT TGCTGCCGCT GCTGGGCGGT ACCCAGACAG 240
 CCATTGTCTT CATCAAGCAG CCGTCTCTCC AGGATGCACT GCAGGGGCGC CGGGCGCTGC 300
 TTCGTGTGTA GGTGAGGCT CCGGGCCCGG TACATGTGTA CTGGCTGCTC GATGGGGCCC 360
 CTGTCCAGGA CACGGAGCGG CGTTTCGCCC AGGGCAGCAG CCTGAGCTTT GCAGCTGTGG 420
 ACCGGCTGCA GGACTCTGGC ACCTTCCAGT GTGTGGCTCG GGATGATGTC ACTGGAGAAG 480
 AAGCCCGCAG TCCCAACGCC TCCTTCAACA TCAAATGGAT TGAGGCAGGT CCTGTGGTCC 540
 TGAAGCATCC AGCCTCGGAA GCTGAGATCC AGCCACAGAC CCAGGTCACA CTTCTGTTGCC 600
 ACATTGATGG GCACCTCCGG CCCACCTACC AATGGTTCGG AGATGGGACC CCCCTTTCTG 660
 ATGGTCAGAG CAACCAACACA GTCAGCAGCA AGGAGCGGAA CCTGACGCTC CGGCCAGCTG 720
 GTCCTGAGCA TAGTGGGCTG TATTCTGCTC GCGCCACAG TGCTTTTGGC CAGGCTTGCA 780
 GCAGCCAGAA CTTACACCTT AGCATTGCTG ATGAAAGCTT TGCCAGGGTG GTGCTGGCAC 840
 CCCAGGACGT GGTAGTAGCG AGGTATGAGG AGGCCATGTT CCATTGCCAG TTCTCAGCCC 900
 AGCCACCCCC GAGCCTGCAG TGGCTCTTTG AGGATGAGAC TCCCATCACT AACCCAGTTC 960
 GCCCCCCACA CCTCCGAGAG GCCACAGTGT TTGCCAACGG GTCTCTGCTG CTGACCCAGG 1020
 TCCGGCCACG CAATGACAGG ATCTACCGCT GCATTGGCCA GGGGCAGAGG GGCCCAACCA 1080
 TCATCTTGGA AGCCACACTT CACCTAGCAG AGATTGAAGA CATGCCGCTA TTTGAGCCAC 1140
 GGGTGTTTAC AGCTGGCAGC GAGGAGCGTG TGACCTGCCT TCCCCCAAG GGTCTGCCAG 1200
 AGCCAGCGCT GTGGTGGGAG CACGCGGGAG TCCGGCTGCC CACCCATGGC AGGGTCTACC 1260
 AGAAGGGCCA CGAGCTGGTG TTGGCCAATA TTGCTGAAAG TGATGCTGGT GTCTACACCT 1320
 GCCACGCGGC CAACCTGGCT GGTGAGCGGA GACAGGATGT CAACATCACT GTGGCCACTG 1380
 TGCCCTCTCG GCTGAAGAG CCCCAAGACA GCCAGCTGGA GGAGGGCAAA CCCGGCTACT 1440
 TGGATTGCGT GACCCAGGCC ACACCAAAAC CTACAGTTGT CTGGTACAGA AACCAAGATG 1500
 TCATCTCAGA GGACTCACGG TTCGAGGTCT TCAAGAATGG GACCTTGCGC ATCAACAGCG 1560
 TGGAGGTGTA TGTATGGGCA TGGTACCGTT GTATGAGCAG CACCCAGGCC GGCAGCATCG 1620
 AGGCAGCAGC CCGTGTCCAA GTGCTGGAAA AGCTCAAGTT CACACCACCA CCCAGCCAC 1680
 AGCAGTGCAT GGAGTTTGAC AAGGAGGCCA CGGTGCCCTG TTCAGCCACA GGCCGAGAGA 1740
 AGCCCACTAT TAAGTGGGAA CGGGCAGATG GGAGCAGCCT CCCAGAGTGG GTGACAGACA 1800
 ACCTGGGAC CCGTCACTTT GCCCGGGTGA CTCGAGATGA CGCTGGCAAC TACACTTGCA 1860
 TTGCTCCCAA CGGGCCGAGG GGCCAGATTC GTGCCCATGT CCAGCTCACT GTGGCAGTTT 1920
 TTATCACTTT CAAAGTGGAA CCAGAGCGTA CGACTGTGTA CCAGGGCCAC ACAGCCCTAC 1980
 TGCAGTGCAG GGCCAGGGG GACCCCAAGC CGCTGATTCA GTGGAAGGC AAGGACCGCA 2040
 TCCTGGACCC CACCAAGCTG GGACCCAGGA TGCACATCTT CCAGAATGGC TCCCTGGTGA 2100

	TCCATGACGT	GGCCCTGAG	GACTCAGGCC	GCTACACCTG	CATTGCAGGC	AACAGCTGCA	2160
	ACATCAAGCA	CACGGAGGCC	CCCCTCTATG	TCGTGGACAA	GCCTGTGCCG	GAGGAGTCGG	2220
	AGGGCCCTGG	CAGCCCTCCC	CCCTACAAGA	TGATCCAGAC	CATTGGGGTTG	TCGGTGGGTG	2280
5	CGCTGTGGC	CTACATCATT	GCCGTGCTGG	GCCTCATGTT	CTACTGCAAG	AAGCGCTGCA	2340
	AAGCCAAAGC	GCTGCAGAAG	CAGCCCGAGG	GCGAGGAGCC	AGAGATGGAA	TGCCTCAACG	2400
	GAGGGCCTTT	GCAGAACGGG	CAGCCCTCAG	CAGAGATCCA	AGAAGAAGTG	GCCTTGACCA	2460
	GCTTGGGCTC	CGGCCCGCGG	GCCACCAACA	AACGCCACAG	CACAAGTGAT	AAGATGCACT	2520
	TCCACGGTTC	TAGCCTGCAG	CCCATCACCA	CGCTGGGGAA	GAGTGAGTTT	GGGGAGGTGT	2580
10	TCCTGGCAAA	GGCTCAGGGC	TTGGAGGAGG	GAGTGGCAG	GACCTTGTA	CTTGTGAAGA	2640
	GCCTGCAGAC	GAAGGATGAG	CAGCAGCAGC	TGGACTTCCG	GAGGGAGTTG	GAGATGTTTG	2700
	GGAAAGCTGAA	CCACGCCAAC	GTGTTGCGGC	TCCTGGGGCT	GTGCCGGGAG	GCTGAGCCCC	2760
	ACTACATGGT	GCTGGAATAT	GTGGATCTGG	GAGACCTCAA	GCAGTTCCTG	AGGATTTCCTA	2820
	AGAGCAAGGA	TGAAAAATTG	AAGTCACAGC	CCCTCAGCAC	CAAGCAGAAG	GTGGCCCTAT	2880
	GCACCCAGGT	AGCCTTGGGC	ATGGAGCACC	TGTCCAACAA	CCGCTTTGTG	CATAAGGACT	2940
15	TGGCTGCGCG	TAACCTGCTG	GTCAGTGCCC	AGAGACAAGT	GAAGGTGTCT	CCCCTGGGCT	3000
	TCAGCAAGGA	TGTGTACAAC	AGTGAGTACT	ACCACTTCCG	CCAGGCTTGG	GTGCCGCTGC	3060
	GCTGGATGTC	CCCCGAGGCC	ATCCTGGAGG	GTGACTTCTC	TACCAAGTCT	GATGTCTGGG	3120
	CCTTCGGTGT	GCTGATGTGG	GAAGTGTTTA	CACATGGAGA	GATGCCCATC	GGTGGGCAGG	3180
20	CAGATGATGA	AGTACTGCA	GATTTGCAGG	CTGGGAAGGC	TAGACTTCCT	CAGCCCGAGG	3240
	GCTGCCCTTC	CAAACTCTAT	CGGCTGATGC	AGCGCTGCTG	GGCCCTCA3C	CCCAAGGACC	3300
	GGCCCTCCTT	CAGTGAGATT	GCCAGCGCCC	TGGGAGACAG	CACCGTGGAC	AGCAAGCCGT	3360
	GAGGAGGGAG	CCCCCTCAGG	ATGGCCTGGG	CAGGGGAGGA	CATCTCTAGA	GGGAAGCTCA	3420
	CAGCATGATG	GGCAAGATCC	CTGTCTCCT	GGGCCCTGAG	GTGCCCTAGT	GCAACAGGCA	3480
25	TTGCTGAGGT	CTGAGCAGGG	CCTGGCCTTT	CCTCCTCTTC	CTCACCCCTCA	TCCTTTGGGA	3540
	GGCTGACTTG	GACCCAAAT	GGGCGACTAG	GGCTTTGAGC	TGGGCAGTTT	CCCCTGCCAC	3600
	CTCTTCCTCT	ATCAGGACAC	GTGTGGGTGC	CACAGGTAAC	CCCAATTCTC	GGCCTTCAAC	3660
	TTCTCCCTTT	GACCGGGTCC	AACCTCTCCA	CTCATCTGCC	AACCTTGCTT	GGGGAGGGCT	3720
	AGGCTTGGGA	TGAGCTGGGT	TTGTGGGGAG	TTCTTAATA	TTCTCAAGTT	CTGGGCACAC	3780
30	AGGGTTAATG	AGTCTCTTGC	CCACTGGTCC	ACTTGGGGTG	CTAGACCAGG	ATTATAGAGG	3840
	ACACAGCAAG	TGAGTCCCTC	CCACTCTGGG	CTTGTGCACA	CTGACCCAGA	CCACAGCTCT	3900
	CCCCACCCTT	CTCTCTTTTC	CTCATCTTAA	GTGCCTGGCA	GATGAAGGAG	TTTTCAGGAG	3960
	CTTTTGACAC	TATATAAACC	GCCCTTTTTG	TATGCACCAC	GGGCGGCTTT	TATATGTAAT	4020
	TGCAGCGTGG	GGTGGGTGGG	CATGGGAGGT	AGGGGTGGGC	CCTGGAGATG	AGGAGGGTGG	4080
35	GCCATCCTTA	CCCCACACTT	TTATTTGTGT	CGTTTTTTGT	TTGTTTTGTT	TTTTTGTTTT	4140
	TGTTTTTGT	TTTACACTCG	CTGCTCTCAA	TAAATAAGCC	TTTTTTTA		

Seq ID NO: 667 Protein sequence
Protein Accession #: NP_002812

	1	11	21	31	41	51	
	MGAARGSPAR	PRRLPLLSVL	LLPLLGQT	AIVFIKQPS	QDALQGRRL	LRCEVEAPGP	60
	VHVYLLDGA	PVQDTERRFA	QSSLSFAAV	DRLQDSGTQ	CVARDDVTGE	EARSANASFN	120
45	IKWIEAGPVV	LKHPASEAEI	QPQTQVTLRC	HIDGHPRTY	QWFRDGTPLS	DQGSNHTVSS	180
	KERNLTLRPA	GPEHSLYSC	CAHSAFGQAC	SSQNFTLSIA	DESFAVVLA	PQDVVVARYE	240
	EAMFHCQPSA	QPPSLQWL	EDETPITNRS	RPPHLRRATV	FANGSLLLTQ	VRPRNAGIYR	300
	CIGQQRGPP	IILEATLHLA	EIDEMPLFEP	RVFTAGSEER	VTCLPPKGLP	EPVSWWEHAG	360
	VRLPTHGRVY	QKGHELVLAN	IAESDAGVYT	CHAANLAGQR	RQDVNITVAT	VPSWLKKPQD	420
50	SOLEBGPY	LDCLTQATPK	PTVVYRNQM	LISEDSRFEV	FKNGTLRINS	VEVYDGTWYR	480
	CMSSTPAGSI	BAQARVQVLE	KLKFTPPPQP	QQCMEFDKEA	TVPCSATGRE	KPTIKWERAD	540
	GSSLEPWVTD	NAGTLHFARV	TRDDAGNYTC	IASNGPQGOI	RAHVQLTVAV	FITFKVEPER	600
	TTVYQGHATL	LQCEAQGDPK	PLIQWKGKDR	ILDPTKLGP	MHIFQNGSLV	IHDVAPEDSG	660
	RYTCIAGNSC	NIKHTEARPL	VVDKPVPEES	EGPGSPPPYK	MIQTIGLSVG	AAVAYIIAVL	720
55	GLMFYCKKRC	KAKRLQKQPE	GEEPEMECLN	GGPLQNGQPS	AEIQEVALT	SLGSGPAATN	780
	KRHSTSDKMH	FPRSLQPI	TLGKSEFGEV	FLAKAQGLEE	GVAETLVLVK	SLQTKDEBQQ	840
	LDFFRELEMF	GKLNHANVVR	LLGLCREAEP	HYMVLEYVDL	GDLKQFLRIS	KSKDEKLKSK	900
	PLSTKQKVAL	CTQVALGMEH	LSNNRFVHKD	LAARNCLVSA	QRQVKVSALG	LSKDVYNSEY	960
60	YHFRQAWVPL	RWMSEPAILE	GDFSTKSDVW	AFGLMWVEVF	THGEMPHGGQ	ADDEVLAIDLQ	1020
	AGKARLPQPE	GCPSKLYRLM	QRCWALSPKD	RPSFSEIASA	LGDSTVDSKP		

Seq ID NO: 668 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1389

	1	11	21	31	41	51	
	ATGGGCTACC	AGAGGCAGGA	GCCTGTCTATC	CCGCCGCAGA	GAGATTTAGA	TGACAGAGAA	60
	ACCCTTGT	CTGAACATGA	GTATAAAGAG	AAAACCTGTC	AGTCTGCTGC	TCTTTTAAAT	120
70	GTTGTCAACT	CGATTATAGG	ATCTGGTATA	ATAGGATTGC	CTTATTCAAT	GAAGCAAGCT	180
	GGGTTCCTT	TGGGAATATT	GCTTTTATTC	TGGGTTTCAT	ATGTTACGGA	CTTTTCCCTT	240
	GTTTATTGA	TAAAGGAGG	GGCCCTCTCT	GGAACAGATA	CCTACCAAGT	TTTGGTCAAT	300
	AAAACCTTCG	GCTTTCAGG	GTATCTGCTC	CTCTCTGTTT	TTCAGTTTTT	GTATCCTTTT	360
	ATAGCAATGA	TAAGTACAA	TATAATAGCT	GGAGATACTT	TGAGCAAAGT	TTTCAAAGA	420
75	ATCCAGGAG	TTGATCCTGA	AAACGTGTTT	ATTGGTCGCC	ACTTCATTAT	TGGACTTTCC	480
	ACAGTTACCT	TTACTCTGCC	TTTATCCTTG	TACCGAAATA	TAGCAAAGCT	TGGAAGGTC	540
	TCCCTCATCT	CTACAGGTTT	AACAACCTG	ATTCTTGAA	TTGTAATGGC	AAGGGCAATT	600
	TCACCTGGTC	CACACATACC	AAAAACAGAA	GACGCTGGG	TATTTGCAAA	GCCCAATGCC	660
	ATTCAAGCGG	TCGGGGTTAT	GTCCTTTGCA	TTTATTGTC	ACCATAACTC	CTTCTTAGTT	720
80	TACAGTTCTC	TAGAGAACCC	CACAGTAGCT	AAGTGGTCCC	GCCTTATCCA	TATGTCCATC	780
	GTGATTTCTG	TATTTATCTG	TATATCTTTT	GCTACATGTG	GATACTTGAC	ATTTACTGGC	840
	TTACCCCAAG	GGGACTTATT	TGAAAATTAC	TGCAGAAATG	ATGACCTGGT	AACATTTGGA	900
	AGATTTTGT	ATGGTGTGAC	TGTCAATTTG	ACATACCCTA	TGGAATGCTT	TGTGACAGA	960
	GAGGTAATTG	CCAATGTGTT	TTTTGGTGGG	AATCTTTTAT	CGGTTTTCCA	CATTGTTGTA	1020
85	ACAGTGATGG	TCATCACTGT	AGCCACGCTT	GTGTCATTGC	TGATTGATTG	CCTCGGGATA	1080
	GTTCTAGAAC	TCAATGTGTC	GCTCTGTGCA	ACTCCCTCA	TTTTTATCAT	TCCATCAGCC	1140
	TGTTATCTGA	AACGTCTGTA	AGAACCAAGG	ACACACTCCG	ATAAGATTAT	GTCTTGTGTC	1200
	ATGCTTCCCA	TTGGTGCTGT	GGTGATGGTT	TTTGATTTCG	TCATGGCTAT	TACAAATACT	1260

CAAGACTGCA CCCATGGGCA GGAAATGTTC TACTGCTTTC CTGACAATTT CTCTCTCACA 1320
 AATACCTCAG AGTCTCATGT TCAGCAGACA ACACAACCTT CTACTTTAAA TATTAGTATC 1380
 TTTCAATGA

Seq ID NO: 669 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MG YQRQEPVI PPQRDLDDRE TLVSEHEYKE KTCQSAALFN VVNSIIIGSGI IGLPYSMKQA 60
 GFPLGILLLF WVSVYVDRSL VLLIKGGALS GTDTYQSLVN KTFGFPGLYL LSVLQFLYPF 120
 IAMISYNIIA GDTLSKVFQR IPGVDPENVF IGRHFIIGLS TVTFTLPLSL YRNI AKLGKV 180
 SLISTGLTTL ILGIVMARAI SLGPHIPKTE DAWVFAKPN IAQAVGVMSFA FICHNSFLV 240
 YSSLEPTVA KWSRLIHMSI VISVFICIF ATCGYLTFTG FTQGDLEFNY CRNDDLVTFG 300
 RFCYGVTVIL TYPMECFVTR EVIANVFFGG NLSSVFHIVV TVMVITVATL VSLLDCLGI 360
 VLELNGVLCA TPLIFIIPSA CYLKLSEEP THSDKIMSCV MLPIGAVVMV FGFVMAITNT 420
 QDCTHGQEMF YCFPDNFSLT NTSSEHVQQT TQLSTLNISI FQ

Seq ID NO: 670 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..1284

1 11 21 31 41 51
 ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGCAGA GAGGATTGCC TTATTCAATG 60
 AAGCAAGCTG GGTTCCTTT GGGATATTTG CTTTATTCT GGGTTTCATA TGTACAGAC 120
 TTTTCCCTFG TTTTATTGAT AAAAGGAGGG GCCCTCTCTG GAACAGATAC CTACCAGTCT 180
 TTGGTCAATA AAACCTTCGG CTTTCCAGGG TATCTGCTCC TCTCTGTTCT TCAGTTTTTG 240
 TATCCTTTTA TAGCAATGAT AAGTACAAAT ATAATAGCTG GAGATACTTT GAGCAAAGTT 300
 TTTCAAAGAA TCCAGGAGT TGA TCTGAA AACGTGTTA TTGGTCGCCA CTTTATTATT 360
 GGACTTTCCA CAGTACCTT TACTCTGCCT TTATCCTTGT ACCGAAATAT AGCAAAGCTT 420
 GGAAAGGTCT CCCTCATCTC TACAGGTTTA ACAACTCTGA TTCTTGGAA TGTAAATGGCA 480
 AGGGCAATTT CACTGGGTCC ACACATACCA AAAACAGAAG ACGCTTGGGT ATTTGCAAAG 540
 CCCAATGCCA TTCAGCGGT CGGGGTTATG TCTTTTGCAT TTATTGCCA CCATAACTCC 600
 TTCTTAGTTT ACAGTTCTCT AGAAGAACC ACAGTAGCTA AGTGGTCCCG CCTTATCCAT 660
 ATGTCCATCG TGATTCTGT ATTTATCTGT ATATTCTTTG CTACATGTGG ATACTTGACA 720
 TTTACTGGCT TCACCCAAAG GGACTTATTT GAAAATTACT GCAGAAATGA TGACCTGGTA 780
 ACATTGGAA GATTTGTGTA TGGTGTCACT GTCATTTTGA CATACCCCTAT GGAATGCTTT 840
 CTGACAAGAG AGGTAATTGC CAATGTGTTT TTTGGTGGGA ATCTTTCATC GGTTTTCCAC 900
 ATTGTGTAA CAGTGATGGT CATCACTGTA GCCACGCTTG TGTCAATTGCT GATTGATTGC 960
 CTCGGGATAG TTCTAGAAT CAATGGTGTG CTCTGTGCAA CTCCTCAT TTTTATCATT 1020
 CCATCAGCCT GTTATCTGAA ACTGTCTGAA GAACCAAGGA CACACTCCGA TAAGATTATG 1080
 TCTTGTGTCA TGCTTCCCAT TGGTGTCTGT GTGATGGTTT TTGATTGCT CATGGCTATT 1140
 ACAATACTC AAGACTGCAC CCATGGGCAG GAAATGTTCT ACTGCTTTCC TGACAATTT 1200
 TCTCTACAA ATACCTCAGA GTCTCATGTT CAGCAGACAA CACAACCTTC TACTTTAAAT 1260
 ATTAGTATCT TTCAACTCGA GTAA

Seq ID NO: 671 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MG YQRQEPVI PPQRGLPYSM KQAGFPLGIL LLFWVS YVTD FSLVLLIKGG ALSGDTYQS 60
 LVNKTFFGFP YLLSLVQLF YPFIAMISYN IAGDTLSKV QRI PGVDPE NVFGRHFII 120
 GLSTVTFTLP LSLYRNIAKL GKVSLISTGL TTLILGIVMA RAISLGHIP KTEDAWVFAK 180
 PNAIQAQVGM SFAPICHNS FLVYSSLEEP TVAKWSRLIH MSIVISVFIC IFFATCGYLT 240
 FTGFTQGDLE ENYCRNDDL TFGRCYGVV VILTYPMECF VTREVIANVF FGNLSSVFH 300
 IIVTVMLVIT ATLVSLLIDC LGIVLELNGV LCATPLIFII PSACYLKLSE EPRTHSDKIM 360
 SCVMLPIGAV VMVFGFVMAI TNTQDCTHQG EMFYCFPDNF SLTNTSESHV QTTQLSTLN 420
 ISIFQLE

Seq ID NO: 672 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..1203

1 11 21 31 41 51
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 AAAGGAGGGG CCTCTCTG GACAGATACC TACCAGTCTT TGGTCAATAA AACTTTCGGC 120
 TTTCCAGGGT ATCTGCTCCT CTCTGTTCTT CAGTTTTTGT ATCCTTTTAT AGCAATGATA 180
 AGTTACAATA TAATAGCTTG AGATACTTG AGCAAAGTTT TTCAAAGAAT CCCAGGAGTT 240
 GATCTGAAAC ACGTGTATAT TGGTGCACC TTTTATTATG GACTTTCCAC AGTTACCTTT 300
 ACTCTGCCTT TATCTTGTA CCGAAATATA GCAAAGCTTG GAAAGGTCTC CCTCATCTCT 360
 ACAGGTTTAA CAACTCTGAT TCTTGGAAAT GTAATGGCAA GGGCAATTTC ACTGGGTCCA 420
 CACATACCAA AAACAGAAGA CGCTTGGGTA TTTGCAAAGC CCAATGCCAT TCAAGCGGTC 480
 GGGGTTATGT CTTTGTGATT TATTTGCCAC CATAACTCCT TCTTAGTTTA CAGTTCTCTA 540
 GAAGAACCAC CAGTAGCTAA GTGGTCCGCG CTTATCCATA TGTCCATCGT GATTTCGTGA 600
 TTTATCTGTA TATTTCTTGC TACATGTGGA TACTTGACAT TTACTGGCTT CACCAAGGG 660
 GACTTATTTG AAATATTCTG CAGAAATGAT GACCTGGTAA CATTGGGAAG ATTTTGTATT 720
 GGTGTCACTG TCATTTTGAC ATACCCTATG GAATGCTTTG TGACAAGAGA GGTAAATGCC 780
 AATGTGTTT TTGGTGGGAA TCTTTCATCG GTTTTCCACA TTGTGTGAAC AGTGATGGTC 840
 ATCACTGTAG CCACGCTTGT GTCAATGCTG ATTGATTGCC TCGGGATAGT TCTAGAACTC 900
 AATGGTGTGC TCTGTGAAC TCCCTCATTT TTTATCATTC CATCAGCCTG TTATCTGAAA 960
 CTGTCTGAAG AACCAAGGAC ACACCTCCGAT AAGATTATGT CTTGTGTCAT GCTTCCCAT 1020
 GGTGCTGTGG TGATGGTTT TGGATTCTGT ATGGCTATTA CAAATACTCA AGACTGCACC 1080
 CATGGGCAGG AAATGTTCTA CTGCTTCCCT GACAAATTTCT CTCTCACAAA TACCTCAGAG 1140
 TCTCATGTT AGCAGACAAC ACAACTTTCT ACTTTAAATA TTAGTATCTT TCAACTCGAG 1200

TAA

Seq ID NO: 673 Protein sequence
Protein Accession #: Eos sequence

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1      11      21      31      41      51
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SYNTIAGDTL SKVQRIPIGV DPENVFIGRH FIIGLSTVTF TLPLSLYRNI AKLGKVSLS 120
TGLTTLILGI VMARAIISLGP HIPKTEDAWV FAKPNAIQAV GVMSFAFICH HNSFLVYSSL 180
EEPTVAKWSR LIHMSIVISV PICIFFATCG YLTFGTGFTQG DLFFENYCRND DLVTFGRFCY 240
GVTVILTYPM ECFVTREIVIA NVFFGGNLSS VFHIVVTVMV ITVATLVSLI IDCGLVLEL 300
NGVLCATPLI FIIPSACYLK LSEEPRTSHD KIMSCVMLPI GAVVMVFGFV MAITNTQDCT 360
HGQEMFYCFP DNFLTNTISE SHVQTTQLS TLNISIFQLE

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Seq ID NO: 674 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1140

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1      11      21      31      41      51
|      |      |      |      |      |
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CCAGGGTATC TGCTCCTCTC TGTTCTTCAG TTTTGTATC CTTTATAGC AATGATAAGT 120
TACAAATATA TAGCTGGAGA TACTTTGAGC AAAGTTTTTC AAAGAATCCC AGGAGTTGAT 180
CCTGAAAACG TGTATTATGG TCGCCACTTC ATTATTGGAC TTTCCACAGT TACCTTTACT 240
CTGCCTTTAT CCTGTACCG AAATATAGCA AAGCTTGGAA AGGCTCCCT CATCTCTACA 300
GGTTTAACAA CTCTGATTCT TGGAAATTGA ATGGCAAGGG CAATTTCAC TGGTCCACAC 360
ATACCAAAAA CAGAAGACGC TTGGGTATTT GCAAAGCCCA ATGCCATTCA AGCGGTGCGG 420
GTTATGTCCT TTGCATTAT TGGCCACCAT AACTCCTTCT TAGTTTACAG TTCTCTAGAA 480
GAACCCACAG TAGCTAAGTG GTCCCGCCTT ATCCATATGT CCATCGTGAT TTCTGTATTT 540
ATCTGTATAT TCTTTGCTAC ATGTGGATAC TTGACATTTA CTGGCTTCAC CCAAGGGGAC 600
TTATTTGAAA ATTACTGCAG AAATGATGAC CTGGTAACAT TTGGAAGATT TTGTTATGGT 660
GTCACTGTCA TTTTGACATA CCCTATGGAA TGCTTTGTGA CAAGAGAGGT AATTGCCAAT 720
GTGTTTTTTG GTGGGAATCT TTCATCGGTT TTCCACATTG TTGTAACAGT GATGGTCATC 780
ACTGTAGCCA CGCTTGTGTC ATTGCTGATT GATTGCCTCG GGATAGTTCT AGAACTCAAT 840
GGTGTGCTCT GTGCAACTCC CCTCATTTTT ATCATTCCAT CAGCCTGTTA TCTGAAACTG 900
TCTGAAGAAC CAAGGACACA CTCGATAAG ATTATGCTTT GTGTCATGCT TCCATTGGT 960
GCTGTGGTGA TGGTTTTTGG ATTGCTCATG GCTATTACAA ATACTCAAGA CTGCACCCAT 1020
GGGCAGGAAA TGTCTACTGT CTTTCTGAC AATTCTCTC TCACAAATAC CTCAGAGTCT 1080
CATGTTCAAG ACACAACACA ACTTCTACT TTAATATTA GTATCTTTCA ACTCGAGTAA

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Seq ID NO: 675 Protein sequence
Protein Accession #: Eos sequence

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1      11      21      31      41      51
|      |      |      |      |      |
MGYQRQEPVI PPQVNKTGFG PGYLLLSVLQ FLYPFIAMIS YNIIAGDTLS KVFQRIPIVD 60
PENVFIGRHF IIGLSTVFTF LPLSLYRNIA KLGKVSLSIT GLTTLILGIV MARAISLGP 120
IPKTEDANVF AKPNAIQAVG VMSFAFICH NSFLVYSSLE EPTVAKWSRL IHMSIVISVF 180
ICIFFATCGY LFTFTGTQGD LFENYCRNDD LVTFRFCYV VTVILTYPM ECFVTREIVIA 240
VFFGGNLSSV FHVIVVTVMV TVATLVSLI DCLGIVLELN GVLCAATPLIF FIIPSACYLKL 300
SEEPRTSHDK IMSCVMLPIG AVVMVFGFVM AITNTQDCTH GQEMFYCFPD NFSLTNTSES 360
HVQTTQLST LNISIFQLE

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Seq ID NO: 676 DNA sequence
Nucleic Acid Accession #: NM_006853.1
Coding sequence: 26..874

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1      11      21      31      41      51
|      |      |      |      |      |
AGGAATCTGC GCTCGGGTTC CGCAGATGCA GAGGTGAGG TGGCTGCGGG ACTGGAAGTC 60
ATCGGGCAGA GGTCTCACAG CAGCCAAGGA ACCTGGGGCC CGCTCCTCCC CCTCCAGGC 120
CATGAGGATT CTGCAGTTAA TCCTGCTTGC TCTGGCAACA GGGCTTGTAG GGGGAGAGC 180
CAGGATCATC AAGGGGTTCG AGTGCAAGCC TCACTCCAG CCCTGGCAGG CAGCCCTGTT 240
CGAGAAGACG CGGTACTCT GTGGGGCGAC GCTCATCGCC CCCAGATGTC TCCTGACAGC 300
AGCCCACTGC CTCAGCCCC GCTACATAGT TCACCTGGGG CAGCACAAAC TCCAGAAGGA 360
GGAGGGCTGT GAGCAGACCC GGACAGCCAC TGAGTCTTTC CCCACCCCG GCTTCAACAA 420
CAGCCTCCCC AACAAAGACC ACCGCAATGA CATCATGCTG GTGAAGATGG CATCGCCAGT 480
CTCCATACCC TGGGCTGTGC GACCCCTCAC CCTCTCCTCA CGCTGTGTCA CTGCTGGCAC 540
CAGCTGCCTC ATTTCCGGCT GGGGCGACAC GTCCAGCCCC CAGTTACGCC TGCCCTCACAC 600
CTTGGCATGC GCCAACATCA CCATCATTTGA GCACCAAGAG TGTGAGAACG CCTACCCCG 660
CAACATCACA GACACCATGG TGTGTGCCAG CGTGCAGGAA GGGGGCAAGG ACTCCTGCCA 720
GGGTGACTCC GGGGGCCCTC TGGTCTGTAA CCAGTCTCTT CAAGGCATTA TCTCCTGGGG 780
CCAGGATCCG TGTGCGATCA CCCGAAAGCC TGGTGTCTAC ACGAAAGTCT GCAAAATATG 840
GGACTGGATC CAGGAGACGA TGAAGAACAA TTAGACTGGA CCCACCCACC ACAGCCCATC 900
ACCTCCATT TCCACTTGGT GTTTGGTTCC TGTTCACCT GTTAATAAGA AACCTAAGC 960
CAAGACCTCT TACGAACATT CTTTGGGCTC CTGGACTAC AGGAGATGCT GTCACTTAAT 1020
AATCAACCTG GGGTTCGAAA TCAGTGAGAC CTGGATTCAA ATCTGCCTT GAAATATTGT 1080
GACTCTGGGA ATGACACAC CTGTTTGTG CTCTGTTGTA TCCCAGCCC CAAAGACAGC 1140
TCCTGGCCAT ATATCAAGGT TTCAATAAAT ATTTGCTAAA TGAGTG

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Seq ID NO: 677 Protein sequence
Protein Accession #: NP_006844.1

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1      11      21      31      41      51
|      |      |      |      |      |
MRILQLILLA LATGLVGGET RIIKGFECKP HSQPWQAALF EKTRLLCGAT LIAPRWLLTA 60

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AHCLKPRYIV HLQOHNLQKE EGCEQTRTAT ESFPHPGFNN SLPNKDHRND IMLVKMASPV 120
 SITWAVRPLT LSSRCVTAGT SCLISGWGST SSPQLRLPHT LRCANITIE HQKCENAYPG 180
 NITDTMVCAS VQEGGKDSQ GDSGGPLVCN QSLQGIISWG QDPCAITRKP GVTYTKVCKYV 240
 DWIQETMKNN

Seq ID NO: 678 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..933

1	11	21	31	41	51	
ATGTGCACGA	ATGGACGGTG	CATCCCGGGC	GCCTGGCAGT	GTGACGGGCT	GCCTGACTGC	60
TTCGACAAGA	GTGATGAGAA	GGAGTGCCCC	AAGGCTAAGT	CGAAATGTGG	CCCGACCTTC	120
TTCCCTCTGT	CCAGCGGCAT	CCATTGCATC	ATTGGTCGCT	TCCGGTGCAA	TGGGTTTGAG	180
GACTGTCCCG	ATGGCAGCGA	TGAAGAGAAC	TGCACAGCAA	ACCCCTCTGT	TTGCTCCACC	240
GCCCGCTACC	ACTGCAAGAA	CGGCCTCTGT	ATTGACAAGA	GCTTCATCTG	CGATGGACAG	300
AATAACTGTC	AAGACAACAG	TGATGAGGAA	AGCTGTGAAA	GTCTCAAGA	ACCCGGCAGT	360
GGGCAGGTGT	TTGTGACTTC	AGAGAACCAA	CTTGTGTATT	ACCCAGCAT	CACCTATGCC	420
ATCATCGGCA	GCTCCGTCAT	TTTGTGTCTG	GTGGTGGCCC	TGCTGGCACT	GGTCTTGAC	480
CACGAGCGGA	AGCGGAACAA	CCTCATGACG	CTGCCCGTGC	ACCGGCTGCA	GCACCTGTG	540
CTGCTGTCCC	GCCTGTGTGT	CCTGGACCAC	CCCCACCACT	GCAACGTCAC	CTACAACGTC	600
AATAATGGCA	TCCAGTATGT	GGCCAGCCAG	GCGGAGCAGA	ATGCGTCGGA	AGTAGGCTCC	660
CCACCTCTCT	ACTCCGAGGC	CTTGTCTGAC	CAGAGGCGTG	CGTGGTATGA	CCTTCCTCCA	720
CCGCGCTACT	CTTCTGACAC	GGAATCTCTG	AACCAAGCCG	ACCTGCCCCC	CTACCGCTCC	780
CGGTCCGGGA	GTGCCAACAG	TGCCAGCTCC	CAGGCAGCCA	GCAGCTCTCT	GAGCGTGGAA	840
GACACGAGCC	ACAGCCCGGG	GCAGCTGGC	CCCCAGGAGG	GCACTGTCTG	GCCGAGGGAC	900
TCTGAGCCCA	GCCAGGGCAC	TGAAGAAGTA	TAA			

Seq ID NO: 679 Protein sequence
 Protein Accession #: Eos sequence

1	11	21	31	41	51	
MCSNGRCIPG	AWQCDGLPDC	FDKSDEKECP	KAKSKCGPTF	FPCASGIHCI	IGRFRNGFE	60
DQPDGSDDEEN	CTANPLLCST	ARYHCKNGLC	IDKSFICDQG	NNQDNDSEDE	SCSSQEPFGS	120
GCQFVTSENG	LVYYPSTIYA	IIGSSVIFVL	VVALLALVLH	HQRKRNNLMT	LPVHRLQHPV	180
LLSLRLVLHD	PHHCNVTYNV	NNGIQYVASQ	AEQNASEVGS	PPSYSEALLD	QRPAYWDLPP	240
PPYSSDTESL	NQADLPYRS	RSGSANSASS	QAASSLLSVE	DTSHSPGQPG	PQEGTAEPRD	300
SEPSQGTEEV						

Seq ID NO: 680 DNA sequence
 Nucleic Acid Accession #: S78203.1
 Coding sequence: 1..2190

1	11	21	31	41	51	
ATGAATCCTT	TCCAGAAAAA	TGAGTCCAAG	GAAACTCTTT	TTTCACCTGT	CTCCATTGAA	60
GAGGTACCAC	CTCGACCACC	TAGCCCTCCA	AAGAAGCCAT	CTCCGACAA	CTGTGGCTCC	120
AACATATCCAC	TGAGCATTTG	CTTCATTGTG	GTGAATGAAT	TCTGCGAGCG	CTTTTCCTAT	180
TATGGAATGA	AAGCTGTGCT	GATCCTGTAT	TTCCCTGTATT	TCTGCACTG	GAATGAAGAT	240
ACCTCCACAT	CTATATACCA	TGCCTTCAGC	AGCCTCTGTT	ATTTTACTCC	CATCCTGGGA	300
GCGCCATTG	CTGACTCGTG	GTGGGAAAAA	TTCAAGACAA	TCATCTATCT	CTCCTTGGTG	360
TATGTCTCTG	GCCATGTGAT	CAAGTCCTTG	GGTGCCCTTAC	CAATACTGGG	AGGACAAGTG	420
GTACACACAG	TCCTATCATT	GATCGGCCTG	AGTCTAATAG	CTTTGGGGAC	AGGAGGCATC	480
AAACCTCTGT	TGGCAGCTTT	TGGTGGAGAC	CAGTTTGAAG	AAAAACATGC	AGAGGAACGG	540
ACTAGATACT	TCTCAGTCTT	CTACCTGTCC	ATCAATGCAG	GGAGCTTGAT	TTCTACATTT	600
ATCACACCA	TGCTGAGAGG	AGATGTGCAA	TGTTTGGGAG	AAGACTGCTA	TGCATTGGCT	660
TTTGGAGTTC	CAGGACTGCT	CATGGTAATT	GCACTTGTTG	TGTTTGCAAT	GGGAAGCAAA	720
ATATACAATA	AACCAACCCC	TGAAGGAAAC	ATAGTGGCTC	AAGTTTTCAA	ATGTATCTGG	780
TTTGCTATT	CCAATCGTTT	CAAGAACCGT	TCTGGAGACA	TTCCAAAGCG	ACAGCACTGG	840
CTAGACTGGG	CAGCTGAGAA	ATATCCAAAG	CAGCTCATT	TGGATGTAAA	GGCACTGACC	900
AGGGTACTAT	TCCTTTATAT	CCCATTGCC	ATGTTCTGGG	CTCTTTTGA	TCAGCAGGGT	960
TCACGATGGA	CTTTGCAAGC	CATCAGGATG	AATAGGAATT	TGGGGTTTTT	TGTGCTTCAG	1020
CCGGACCAGA	TGCAGTTCT	AAATCCCTTT	CTGGTTCTTA	TCTTCATCCC	GTTGTTTGAC	1080
TTTGTCAATT	ATCGTCTGGT	CTCCAAGTGT	GGAATTAACT	TCTCATCACT	TAGGAAAAATG	1140
GCTGTTGGTA	TGATCTAGC	GTGCCCTGGCA	TTTGCACTTG	CGGCAGCTGT	AGAGATAAAA	1200
ATAAATGAAA	TGGCCCCAGC	CCAGTCAGGT	CCCCAGGAGG	TTTTCTTACA	AGTCTTGAAT	1260
CTGGCAGATG	ATGAGGTGAA	GGTGACAGTG	GTGGGAAATG	AAAAACAATC	TCTGTTGATA	1320
GAGTCCATCA	AATCCTTTCA	GAAACACCA	CACATATCCA	AACTGCACCT	GAAACAAAAA	1380
AGCCAGGATT	TTCACTTCCA	CCTGAAATAT	CACAATTGT	CTCTCTACAC	TGAGCATTCT	1440
GTGCAGGAGA	AGAACTGGTA	CAGTCTTGTC	ATTCGTGAAG	ATGGGAACAG	TATCTCCAGC	1500
ATGATGGTAA	AGGATACAGA	AAGCAAAACA	ACCAATGGGA	TGACAACCGT	GAGGTTTGTT	1560
AACACTTTGC	ATAAAGATGT	CAACATCTCC	CTGAGTACAG	ATACCTCTCT	CAATGTTGGT	1620
GAAGACTATG	GTGTGTCTGC	TTATAGAAT	GTGCAAGAG	GAGAATACCC	TGCAGTGCAC	1680
TGTAGAACAG	AAGATAAGAA	CTTTCTCTCT	AATTTGGGTC	TTCTAGACTT	TGGTGCAGCA	1740
TATCTGTTTG	TTATTAATAA	TAACACCAAT	CAGGGCTCTC	AGGCCTGGAA	GATTGAAGAC	1800
ATTCCAGCCA	ACAAAATGTC	CATTGCGTGG	CAGCTACCAC	AATATGCCCT	GGTTACAGCT	1860
GGGGAGGTCA	TGTTCTCTGT	CACAGTCTT	GAGTTTCTT	ATTCTCAGGC	TCCCTTAGC	1920
ATGAAATCTG	TGCTCCAGGC	AGCTTGGCTA	TTGACAATTG	CAGTTGGGAA	TATCATCTGT	1980
CTTGTGTGG	CACAGTTTCA	TGGCCTGGTA	CAGTGGGCGG	AATTCATTTT	GTTCCTCTGC	2040
CTCCTGCTGG	TGATCTGCTT	GATCTTCTCC	ATCATGGGCT	ACTACTATGT	TCTGTAAAG	2100
ACAGAGGATA	TGCGGGGTCC	AGCAGATAAG	CACATTCTCT	ACATCCAGGG	GAACATGATC	2160
AAACTAGAGA	CCAGAGAGAC	AAAACCTCTGA				

Seq ID NO: 681 Protein sequence
 Protein Accession #: AAB34388.1

	1	11	21	31	41	51	
	MNPFQKNESK	ETLFSPVSIE	EVPPRPSPSP	KKPSPTICGS	NYPLSIAFIV	VNEFCERFSY	60
5	YGMKAVLILY	FLYFLHWNED	TSTSIYHAFS	SLCYFTPILG	AAIADSWLGK	FKTIIYLSLV	120
	YVLGHVTKSL	GALPILGGQV	VHTVLSLIGL	SLIALGTGGI	KPCVAAFEGD	QFEKHAEER	180
	TRYFSVFYLS	INAGSLISTF	ITPMLRGDVQ	CFGEDCYALA	FGVPGLLMVI	ALVVVFAMGSK	240
	IYNKPPPEGN	IVAQVPKCIW	FAISNRPKNR	SGDIPKRQHW	LDWAAEKYPK	QLIMDVKALT	300
10	RVLFLLYIPLP	MFWALLDQGG	SRWTLQAIRM	NRNLGFFVLQ	PDQMQLNPF	LVLIFIPLFD	360
	FVIYRLVSKC	GINFSSLRKM	AVGMILACLA	FAVAAAVEIK	INEMAPAQSG	PQEVFLQVLN	420
	LADDEVKVTV	VGNENNSLLI	ESIKSFQKTP	HYSKLHLKTK	SQDFHFLKY	HNLSLYTEHS	480
	VQEKWYSLV	IREDGNSISS	MMVKDTESKT	TNGMTTVRFV	NTLHKDVNIS	LSTDTSLVNG	540
	EDYGVSAVRT	VQGEYPAVH	CRTEKDNFSL	NLGLLDFGAA	YLFVITNNTN	QGLQAWKIED	600
	IPANKMSIAW	QLPQYALVTA	GEVMFSVTGL	EFYSQAPSS	MKSVLQAOWL	LTIAVGNIIV	660
15	LVVAFSGSLV	QWAEFILFSC	LLLVICLIFS	IMGYVVPVK	TEDMRGPADK	HIPHIQGNMI	720
	KLETKKTKL						

Seq ID NO: 682 DNA sequence
Nucleic Acid Accession #: NM_016077.1
Coding sequence: 128..667

	1	11	21	31	41	51	
	TCGCTTTGTG	ATTCTTGATC	CGGAACCTTG	TCACCCAGGA	ACCCCGGAAG	AGGTAGCTCA	60
25	CGCGATAGAA	ACCTGTTTCG	TTGCCCAGAA	GAAGGGAAGG	CGCGAGTGAG	GAAAGGAGGT	120
	ACTGTAGATT	CCCTCCAAAT	CCTTGGTTAT	GGAATATTTG	GCTCATCCCA	GTACACTCGG	180
	CTTGGCTGTT	GGAGTTGCTT	GTGGCATGTG	CCTGGGCTGG	AGCCTTCGAG	TATGCTTTGG	240
	GATGCTCCCC	AAAAGCAAGA	CGAGCAAGAC	ACACACAGAT	ACTGAAAGTG	AAGCAAGCAT	300
	CTTGGGAGAC	AGCGGGGAGT	ACAAGATGAT	TCTTGTGGTT	CGAAATGACT	TAAAGATGGG	360
	AAAAGGGAAG	TGGGCTGCCC	AGTGCTCTCA	TGCTGCTGTT	TCAGCCTACA	AGCAGATTCA	420
30	AAGAAGAAAT	CCTGAAATGC	TCAACAATG	GAATACTGT	GGCAGCCCA	AGGTGGTGGT	480
	CAAAGCTCCT	GATGAAGAAA	CCCTGATTGC	ATTATTGGCC	CATGCAAAAA	TGCTGGGACT	540
	GACTGTAAGT	TTAATTCAAG	ATGCTGGACG	TACTCAGATT	GCACCGGCT	CTCAAACTGT	600
	CCTAGGGATT	GGGCCAGGAC	CAGCAGACCT	AATTGACAAA	GTCAGTGGTC	ACCTAAAACT	660
	TTACTAGGTG	GACTTTGATA	TGACAACAAC	CCCTCCATCA	CAAGTGTGTT	AAGCCTGTCA	720
35	GATTCTAACA	ACAAAAGCTG	AATTCTTCA	CCCAACTTAA	ATGTTCTTGA	GATGAAAATA	780
	AAACCTATTC	CCATGTCTTA	AAAAAA				

Seq ID NO: 683 Protein sequence
Protein Accession #: NP_057161.1

	1	11	21	31	41	51	
	MPSKSLVMEY	LAHPSTLGLA	VGVACGMCLG	WSLRVCFGML	PKSKTSKTHY	DTESEASILG	60
45	DSGEYKMLIV	VRNDLKMKGK	KVAAQCASHA	VSAYKQIQRR	NPEMLKQWEY	CGQPKVVVKA	120
	PDEETLIALL	AHAKMLGLTV	SLIQDAGRTQ	IAPGSQTVLG	IGPGPADLID	KVTGHLKLY	

Seq ID NO: 684 DNA sequence
Nucleic Acid Accession #: NM_004864.1
Coding sequence: 26..952

	1	11	21	31	41	51	
	CGGAACGAGG	GCAACCTGCA	CAGCCATGCC	CGGGCAAGAA	CTCAGGACGG	TGAATGGCTC	60
55	TCAGATGCTC	CTGGTGTGTC	TGGTGCTCTC	GTGGCTGCCG	CATGGGGGCG	CCCTGTCTCT	120
	GGCCGAGGCG	AGCCGCGCAA	GTTTCCCAGG	ACCCCTCAGG	TTGCACTCCG	AAGACTCCAG	180
	ATTCCGAGAG	TTGCGGAAGC	GCTACGAGGA	CCTGCTAACC	AGGCTGCGGG	CCAACACAGG	240
	CTGGGAAGAT	TCAACACCGC	ACCTCGTCCC	GGCCCTGCA	GTCGGGATAC	TCACGCCAGA	300
	AGTGCGGCTG	GGATCCGGCG	GCCACCTGCA	CCTGCGTATC	TCTCGGGCCG	CCCTTCCCGA	360
60	GGGGCTCCCC	GAGGCTTCCC	GCCTTCACCG	GGCTCTGTTC	CGGCTGTCCC	CGACGGCGTC	420
	AAGGCTGCTG	GACGTGACAC	GACCGCTGCG	CGCTCAGCTC	AGCCTTGCAA	GACCCCAAGC	480
	GCCGCGGCTG	CACCTGCGAC	TGTCGCGGCC	GCCGTGCGAG	TCGGACCAAC	TGCTGGCAGA	540
	ATCTTCGTCC	GCACGGCCCC	AGCTGGAGTT	GCACTTGCGG	CCGCAAGCCG	CCAGGGGGCG	600
	CCGCAGAGCG	CGTGGCGGCA	ACGGGGACGA	CTGTCCGCTC	GGGCCCCGGC	GTGCTGCCCG	660
65	TCTGCACACG	GTCCGCGCGT	CGCTGGAAGA	CCTGGGCTGG	GCCGATTGGG	TGCTGTGCGC	720
	ACGGGAGGTG	CAAGTGACCA	TGTGCATCGG	CGCGTGCCCG	AGCCAGTTCC	GGGCGGCAAA	780
	CATGCACGCG	CAGATCAAGA	CGAGCCTGCA	CCGCCTGAAG	CCCGACACGG	AGCCAGCGCC	840
	CTGCTGCGTG	CCGCCCAGCT	ACAATCCCAT	GGTGCTCATT	CAAAAGACCG	ACACCGGGGT	900
	GTCGCTCCAG	ACCTATGATG	ACTTGTAGC	CAAAGACTGC	CAGTGCATAT	GAGCAGTCCT	960
70	GGTCTTCCA	CTGTGCACTT	GCGCGGGGGA	GGCGACCTCA	GTTGTCTGTC	CCTGTGGAAT	1020
	GGGCTCAAGG	TTCTGTAGAC	ACCCGATTCC	TGCCCAACA	GCTGTATTTA	TATAAGTCTG	1080
	TTATTTATTA	TTAATTTATT	GGGGTGACCT	TCTTGGGGAC	TCGGGGGCTG	GTCTGATGGA	1140
	ACTGTGTATT	TATTTAAATC	TCTGGTGATA	AAAATAAAGC	TGTCTGAAC	GTAAAAAATA	1200
	AAAA						

Seq ID NO: 685 Protein sequence
Protein Accession #: NP_004855.1

	1	11	21	31	41	51	
	MPGQELRTVN	GSQMLLVLLV	LSWLPHGGL	SLAEASRAS	PGPSELHSED	SRFRELKRY	60
80	EDLLTRLRAN	QSWEDSNLTL	VPAPAVRILT	PEVRLGSGGH	LHLRISRAL	PEGLPEASRL	120
	HRALFRLSPT	ASRSWDVTRP	LRRQLSLARP	QAPALHLRLS	PPPSQSDQLL	AESSSARPOL	180
	ELHLRPQAA	RRRARARNG	DDCPLGPGRC	CRLHTVRASL	EDLGWADWVL	SPREVQVTMC	240
85	IGACPSQFRA	ANMHAQIKTS	LHRLKPDTEP	APCCVPASYN	PMVLIQKIDT	GVSLQTYDDL	300
	LAKDCHCI						

Seq ID NO: 686 DNA sequence

Nucleic Acid Accession #: NM_002423.2
Coding sequence: 48..851

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5      1      11      21      31      41      51
      |      |      |      |      |      |
      ACCAAATCAA CCATAGGTCC AAGAACAATT GTCTCTGGAC GGCAGCTATG CGACTCACCG 60
      TGCTGTGTGC TGTGTGCCTG CTGCCTGGCA GCCTGGCCCT GCGCTGCCT CAGGAGGCGG 120
      GAGGCATGAG TGAGCTACAG TGGGAACAGG CTCAGGACTA TCTCAAGAGA TTTTATCTCT 180
      ATGACTCAGA AACAAAAAT GCCAACAGTT TAGAAGCCAA ACTCAAGGAG ATGCAAAAAT 240
10     TCTTTGGCCT ACCTATAACT GGAATGTTAA ACTCCGCGT CATAGAAATA ATGCAGAAGC 300
      CCAGATGTGG AGTGCCAGAT GTTGCAGAAT ACTCACTATT TCCAAATAGC CCAAAATGGA 360
      CTCCAAAGT GGTCACCTAC AGGATCGTAT CATATACTCG AGACTTACCG CATATTACAG 420
      TGGATCGATT AGTGTCAAAG GCTTTAAACA TGTGGGGCAA AGAGATCCCC CTGCATTTCA 480
      GGAAAGTTTG ATGGGGAACT GCTGACATCA TGATTGGCTT TGC CGCAGGA GCTCATGGGG 540
15     ATCTCTACCC ATTTGATGGG CAGGAAACA CGCTGGCTCA TGCCTTTGCG CTGGGACAG 600
      GTCTCGGAGG AGATGCTCAC TTCGATGAGG ATGAACGCTG GACGGATGGT AGCAGTCTAG 660
      GGATTAACCT CCTGTATGCT GCAACTCATG AACTTGGCCA TTCTTTGGGT ATGGGACATT 720
      CCTCTGATCC TAATGCAGTG ATGTATCCAA CCTATGGAAA TGGAGATCCC CAAAATTTTA 780
      AACTTTCCCA GGATGATATT AAAGGCATTG AGAAACTATA TGGAAAGAGA AGTAATTCAA 840
20     GAAAGAAATA GAAACTTCAG GCAGAACATC CATTATTCA TCATTGGAT TGTATATCAT 900
      TGTTCACAA TCAGAATTGA TAAGCACTGT TCCTCCACTC CATTTAGCAA TTATGTCACC 960
      CTTTTTTATT GCAGTTGGTT TTTGAATGTC TTCTACTCCT TTTATGGTT AAACCTCTTT 1020
      ATGGTGTGAC TGTGTCTTAT TCCATCTATG AGCTTGTGCA GTGCGCGTAG ATGTCAATAA 1080
25     ATGTTACATA CACAAATAAA TAAATGTTT ATTCATGGT AAATTTA

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Seq ID NO: 687 Protein sequence
Protein Accession #: NP_002414.1

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30     1      11      21      31      41      51
      |      |      |      |      |      |
      MRLTVLCAVC LLPGSLALPL PQEAGGMSEL QWEQAQDYLK RFYLYDSETK NANSLEAKLK 60
      EMQKFGLPI TGMNLSRVIE IMQKPRCGVP DVAEYSLFPN SPKWTSKVVT YRIVSYTRDL 120
      PHITVDR LVS KALNMWGKEI PLHFRKVVWG TADIMIGFAR GAHGDSPYFD GFGNTLAHAF 180
35     APGTGLGGDA HFDEDERWTD GSSLGINFLY AATHELGHSL GMGHSSDPNA VMYPTYGNND 240
      PQNFKLSQDD IKGIQKLYGK RSNRSRK

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Seq ID NO: 688 DNA sequence
Nucleic Acid Accession #: NM_005221.3
Coding sequence: 1..870

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40     1      11      21      31      41      51
      |      |      |      |      |      |
      ATGACAGGAG TGTTTGACAG AAGGGTCCCC AGCATCCGAT CCGGCGACTT CCAAGCTCCG 60
      TTCCAGACGT CCGCAGCTAT GCACCATCCG TCTCAGGAAT CGCCAACTTT GCCCGAGTCT 120
45     TCAGCTACCG ATTCTGACTA CTACAGCCCT ACGGGGGGAG CCCC GCACCG CTACTGCTCT 180
      CCTACCTCGG CTCTCTATGG CAAAGCTCTC AACCCCTACC AGTATCAGTA TCACGGCGTG 240
      AACGGCTCCG CCGGGAGCTA CCCAGCCAAA GCTTATGCCG ACTATAGCTA CGCTAGCTCC 300
      TACCACCAAGT ACGGCGGCGC CTACACCCGC GTCCCAAGCG CCACCAACCA GCCAGAGAAA 360
      GAAGTGACCG AGCCCGAGGT GAGAAATGGT AATGGCAAAC CAAAGAAAGT TCGTAAACCC 420
50     AGGACTATTT ATTCCAGCTT TCAGCTGGCC GCATTACAGA GAAGGTTTCA GAAGACTCAG 480
      TACCTCGCCT TGCCGGAACG CGCCGAGCTG GCCGCTCGC TGGGATTGAC ACAAACACAG 540
      GTGAAAATCT GGTTTTCAGAA CAAAAGATCC AAGATCAAGA AGATCATGAA AAACGGGGAG 600
      ATGCCCCCGG AGCACAGTCC CAGCTCCAGC GACCCAATGG CGTGTAACCT GCCCGAGTCT 660
55     CCAGCGGTGT GGGAGCCCCA GGGCTCGTCC CGCTCGCTCA GCCACCACCC TCATGCCCCAC 720
      CCTCCGACCT CCAACCAAGT CCCAGCGTCC AGCTACCTGG AGAACTCTGC ATCCTGGTAC 780
      ACAAGTGACG CCAAGCTCAAT CAATTCACAC CTGCCGCCGC CGGGCTCTCT ACAGCACCCG 840
      CTGGCGCTGG CCTCCGGGAC ACTCTATTAG

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Seq ID NO: 689 Protein sequence
Protein Accession #: NP_005212.1

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60     1      11      21      31      41      51
      |      |      |      |      |      |
      MTGVFDRRVP SIRSGDFQAP FQTSAMHHP SQESPTLPES SATDSDYYSPT TGGAPHGYCS 60
65     PTSASYGKAL NPYQYQYHGV NGSAGSYPAK AYADYSYASS YHQYGGAYNR VPSATNQPEK 120
      EVTEPEVRMV NGKPKKVRKP RTIYSSFQLA ALQRRFQKTQ YLALPERAEL AASLGLTQTQ 180
      VKIWFQNKRS KIKKIMKNGE MPPEHSPSSS DPMA CNSPQS PAVWEPQSSS RSLSHHPHAH 240
      PPTSINQSPAS SYLENSASWY TSAASSINSH LPFPGSLQHP LALASGTLV

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It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

WHAT IS CLAIMED IS:

- 1 1. A method of detecting a lung cancer-associated transcript in a cell
2 from a patient, the method comprising contacting a biological sample from the patient with a
3 polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence
4 as shown in Tables 1A-16.
- 1 2. The method of claim 1, wherein the polynucleotide selectively
2 hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1A-16.
- 1 3. The method of claim 1, wherein the biological sample is a tissue
2 sample.
- 1 4. The method of claim 1, wherein the biological sample comprises
2 isolated nucleic acids.
- 1 5. The method of claim 4, wherein the nucleic acids are mRNA.
- 1 6. The method of claim 4, further comprising the step of amplifying
2 nucleic acids before the step of contacting the biological sample with the polynucleotide.
- 1 7. The method of claim 1, wherein the polynucleotide comprises a
2 sequence as shown in Tables 1A-16.
- 1 8. The method of claim 1, wherein the polynucleotide is labeled.
- 1 9. The method of claim 8, wherein the label is a fluorescent label.
- 1 10. The method of claim 1, wherein the polynucleotide is immobilized on
2 a solid surface.
- 1 11. The method of claim 1, wherein the patient is undergoing a therapeutic
2 regimen to treat lung cancer.
- 1 12. The method of claim 1, wherein the patient is suspected of having lung
2 cancer.
- 1 13. A method of monitoring the efficacy of a therapeutic treatment of lung
2 cancer, the method comprising the steps of:

3 (i) providing a biological sample from a patient undergoing the therapeutic
4 treatment; and

5 (ii) determining the level of a lung cancer-associated transcript in the
6 biological sample by contacting the biological sample with a polynucleotide that selectively
7 hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16,
8 thereby monitoring the efficacy of the therapy.

1 14. The method of claim 13, further comprising the step of: (iii) comparing
2 the level of the lung cancer-associated transcript to a level of the lung cancer-associated
3 transcript in a biological sample from the patient prior to, or earlier in, the therapeutic
4 treatment.

1 15. The method of claim 13, wherein the patient is a human.

1 16. A method of monitoring the efficacy of a therapeutic treatment of lung
2 cancer, the method comprising the steps of:

3 (i) providing a biological sample from a patient undergoing the therapeutic
4 treatment; and

5 (ii) determining the level of a lung cancer-associated antibody in the biological
6 sample by contacting the biological sample with a polypeptide encoded by a polynucleotide
7 that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in
8 Tables 1A-16, wherein the polypeptide specifically binds to the lung cancer-associated
9 antibody, thereby monitoring the efficacy of the therapy.

1 17. The method of claim 16, further comprising the step of: (iii) comparing
2 the level of the lung cancer-associated antibody to a level of the lung cancer-associated
3 antibody in a biological sample from the patient prior to, or earlier in, the therapeutic
4 treatment.

1 18. The method of claim 16, wherein the patient is a human.

1 19. A method of monitoring the efficacy of a therapeutic treatment of lung
2 cancer, the method comprising the steps of:

3 (i) providing a biological sample from a patient undergoing the therapeutic
4 treatment; and

5 (ii) determining the level of a lung cancer-associated polypeptide in the
6 biological sample by contacting the biological sample with an antibody, wherein the antibody
7 specifically binds to a polypeptide encoded by a polynucleotide that selectively hybridizes to
8 a sequence at least 80% identical to a sequence as shown in Tables 1A-16, thereby
9 monitoring the efficacy of the therapy.

1 20. The method of claim 19, further comprising the step of: (iii) comparing
2 the level of the lung cancer-associated polypeptide to a level of the lung cancer-associated
3 polypeptide in a biological sample from the patient prior to, or earlier in, the therapeutic
4 treatment.

1 21. The method of claim 19, wherein the patient is a human.

1 22. An isolated nucleic acid molecule consisting of a polynucleotide
2 sequence as shown in Tables 1A-16.

1 23. The nucleic acid molecule of claim 22, which is labeled.

1 24. The nucleic acid of claim 23, wherein the label is a fluorescent label

1 25. An expression vector comprising the nucleic acid of claim 22.

1 26. A host cell comprising the expression vector of claim 25.

1 27. An isolated polypeptide which is encoded by a nucleic acid molecule
2 having polynucleotide sequence as shown in Tables 1A-16.

1 28. An antibody that specifically binds a polypeptide of claim 27.

1 29. The antibody of claim 28, further conjugated to an effector component.

1 30. The antibody of claim 29, wherein the effector component is a
2 fluorescent label.

1 31. The antibody of claim 29, wherein the effector component is a
2 radioisotope or a cytotoxic chemical.

1 32. The antibody of claim 29, which is an antibody fragment.

- 1 33. The antibody of claim 29, which is a humanized antibody
- 1 34. A method of detecting a lung cancer cell in a biological sample from a
2 patient, the method comprising contacting the biological sample with an antibody of claim
3 28.
- 1 35. The method of claim 34, wherein the antibody is further conjugated to
2 an effector component.
- 1 36. The method of claim 35, wherein the effector component is a
2 fluorescent label.
- 1 37. A method of detecting antibodies specific to lung cancer in a patient,
2 the method comprising contacting a biological sample from the patient with a polypeptide
3 encoded by a nucleic acid comprises a sequence from Tables 1A-16.
- 1 38. A method for identifying a compound that modulates a lung cancer-
2 associated polypeptide, the method comprising the steps of:
3 (i) contacting the compound with a lung cancer-associated polypeptide, the
4 polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least
5 80% identical to a sequence as shown in Tables 1A-16; and
6 (ii) determining the functional effect of the compound upon the polypeptide.
- 1 39. The method of claim 38, wherein the functional effect is a physical
2 effect.
- 1 40. The method of claim 38, wherein the functional effect is a chemical
2 effect.
- 1 41. The method of claim 38, wherein the polypeptide is expressed in a
2 eukaryotic host cell or cell membrane.
- 1 42. The method of claim 38, wherein the functional effect is determined by
2 measuring ligand binding to the polypeptide.
- 1 43. The method of claim 38, wherein the polypeptide is recombinant.

1 44. A method of inhibiting proliferation of a lung cancer-associated cell to
2 treat lung cancer in a patient, the method comprising the step of administering to the subject a
3 therapeutically effective amount of a compound identified using the method of claim 38.

1 45. The method of claim 44, wherein the compound is an antibody.

1 46. The method of claim 45, wherein the patient is a human.

1 47. A drug screening assay comprising the steps of
2 (i) administering a test compound to a mammal having lung cancer or a cell
3 isolated therefrom;
4 (ii) comparing the level of gene expression of a polynucleotide that selectively
5 hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16 in a
6 treated cell or mammal with the level of gene expression of the polynucleotide in a control
7 cell or mammal, wherein a test compound that modulates the level of expression of the
8 polynucleotide is a candidate for the treatment of lung cancer.

1 48. The assay of claim 47, wherein the control is a mammal with lung
2 cancer or a cell therefrom that has not been treated with the test compound.

1 49. The assay of claim 47, wherein the control is a normal cell or mammal.

1 50. A method for treating a mammal having lung cancer comprising
2 administering a compound identified by the assay of claim 47.

1 51. A pharmaceutical composition for treating a mammal having lung
2 cancer, the composition comprising a compound identified by the assay of claim 47 and a
3 physiologically acceptable excipient.

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PATENT COOPERATION TREATY

PCT

DECLARATION OF NON-ESTABLISHMENT OF INTERNATIONAL SEARCH REPORT

(PCT Article 17(2)(a), Rule 13ter.1(c) and 39)

Applicant's or agent's file reference 18501-15-3PC	IMPORTANT DECLARATION	Date of mailing (day/month/year) 15 AUG 2003
International application No. PCT/US02/12476	International filing date (day/month/year) 18 April 2002 (18.04.2002)	(Earliest) Priority date (day/month/year) 10 May 2001 (10.05.2001)
International Patent Classification (IPC) or both national classification and IPC IPC(7): C07H 21/02, 21/04; C12Q 1/68 and US Cl.: 435/6, 536/23.1, 23.5		
Applicant EOS BIOTECHNOLOGY, INC		

This International Searching Authority hereby declares, according to Article 17(2)(a), that **no international search report will be established** on the international application for the reasons indicated below.

1. ☐ The subject matter of the international application relates to:
 - a. ☐ scientific theories.
 - b. ☐ mathematical theories
 - c. ☐ plant varieties.
 - d. ☐ animal varieties.
 - e. ☐ essential biological processes for the production of plants and animals, other than microbiological processes and the products of such processes.
 - f. ☐ schemes, rules or methods of doing business.
 - g. ☐ schemes, rules or methods of performing purely mental acts.
 - h. ☐ schemes, rules or methods of playing games.
 - i. ☐ methods for treatment of the human body by surgery or therapy.
 - j. ☐ methods for treatment of the animal body by surgery or therapy.
 - k. ☐ diagnostic methods practised on the human or animal body.
 - l. ☐ mere presentations of information.
 - m. ☐ computer programs for which this International Searching Authority is not equipped to search prior art.

2. ☐ The failure of the following parts of the international application to comply with prescribed requirements prevents a meaningful search from being carried out:

☐ the description
☐ the claims
☐ the drawings

3. ☒ The failure of the nucleotide and/or amino acid sequence listing to comply with the standard provided for in Annex C of the Administrative Instructions prevents a meaningful search from being carried out:

☐ the written form has not been furnished or does not comply with the standard.
☒ the computer readable form has not been furnished or does not comply with the standard.

4. Further comments:

Name and mailing address of the ISA/US Mail Stop PCT, Attn: ISA/US Commissioner for Patents P.O. Box 1450 Alexandria, Virginia 22313-1450 Facsimile No. (703)305-3230	Authorized officer <div style="text-align: center;"> CARLA J. MYERS PRIMARY EXAMINER </div> Carla Myers Telephone No. 703-308-0196
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PATENT COOPERATION TREATY

From the INTERNATIONAL SEARCHING AUTHORITY

To:
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PCT

NOTIFICATION OF TRANSMITTAL OF THE INTERNATIONAL SEARCH REPORT OR THE DECLARATION

(PCT Rule 44.1)

Date of Mailing (day/month/year)	15 AUG 2003
Applicant's or agent's file reference 18501-15-3PC	FOR FURTHER ACTION See paragraphs 1 and 4 below
International application No. PCT/US02/12476	International filing date (day/month/year) 18 April 2002 (18.04.2002)
Applicant EOS BIOTECHNOLOGY, INC	

1. ☐ The applicant is hereby notified that the international search report has been established and is transmitted herewith.

Filing of amendments and statement under Article 19:

The applicant is entitled, if he so wishes, to amend the claims of the international application (see Rule 46):

When? The time limit for filing such amendments is normally two months from the date of transmittal of the international search report.

Where? Directly to the International Bureau of WIPO, 34, chemin des Colombettes
1211 Geneva 20, Switzerland, Facsimile No.: (41-22) 740.14.35

For more detailed instructions, see the notes on the accompanying sheet.

2. ☒ The applicant is hereby notified that no international search report will be established and that the declaration under Article 17(2)(a) to that effect is transmitted herewith.

3. ☐ With regard to the protest against payment of (an) additional fee(s) under Rule 40.2, the applicant is notified that:

☐ the protest together with the decision thereon has been transmitted to the International Bureau together with the applicant's request to forward the texts of both the protest and the decision thereon to the designated Offices.

☐ no decision has been made yet on the protest; the applicant will be notified as soon as a decision is made.

4. Reminders

Shortly after 18 months from the priority date, the international application will be published by the International Bureau. If the applicant wishes to avoid or postpone publication, a notice of withdrawal of the international application, or of the priority claim, must reach the International Bureau as provided in Rules 90 *bis*.1 and 90 *bis*.3, respectively, before the completion of the technical preparations for international publication.

Within 19 months from the priority date, but only in respect of some designated Offices, a demand for international preliminary examination must be filed if the applicant wishes to postpone the entry into the national phase until 30 months from the priority date (in some Offices even later); otherwise the applicant must, within 20 months from the priority date, perform the prescribed acts for entry into the national phase before those designated Offices.

In respect of other designated Offices, the time limit of 30 months (or later) will apply even if no demand is filed within 19 months.

See the Annex to Form PCT/IB/301 and, for details about the applicable time limits, Office by Office, see the *PCT Applicant's Guide*, Volume II, National Chapters and the WIPO Internet site.

Name and mailing address of the ISA/US Mail Stop PCT, Attn: ISA/US Commissioner for Patents P.O. Box 1450 Alexandria, Virginia 22313-1450 Facsimile No. (703)305-3230	Authorized officer <i>Valerie Bell-Harris for</i> Carla Myers Telephone No. 703-308-0196
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Form PCT/ISA/220 (April 2002)

(See notes on accompanying sheet)